

9.17 - 9.19



Carl R. Woese Institute for Genomic Biology

UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN

WELCOME

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DIVE INTO THE GLOBAL BIOFOUNDRY IINGITVVIII SPARK NERSHIPS, DFFINE THE

Join us at the Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign for Biofoundry Week, a global convergence of innovation in synthetic biology, Al, automation, and biomanufacturing.

BEST WISHES

Huimin Zhao



CARL R. WOESE INSTITUTE FOR GENOMIC BIOLOGY CONFERENCE ROOM 612

WEDNESDAY

6-8 p.m.

Welcoming Reception

Greetings from the NSF iBioFoundry Director $$\operatorname{\textsc{HUIMIN}}${\sc ZHAO}$$



NSF iBioFoundry Tours

Buffet & Drinks

Networking

THURSDAY

I HOTEL
CHANCELLOR BALLROOM

8:15-8:45am

Breakfast

Opening Remarks

Gene Robinson, PhD

Swanlund Chair of Entomology, Director, Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign

Welcoming Remarks

Huimin Zhao, PhD

Steven L. Miller Chair of Chemical and Biomolecular Engineering, Director, NSF iBioFoundry, University of Illinois Urbana-Champaign

Welcoming Remarks

Lars Nielsen, PhD

Chair, Global Biofoundry Alliance, Professor, University of Queensland

9:00-9:30am

The what and why (and how) of Cloud Labs

DJ Kleinbaum, PhD

Co-Founder, Emerald Cloud Labs

9:30-10:30am

BioF:GREAT

Lance Wells, PhD

Professor of Biochemistry & Molecular Biology, University of Georgia

Director, BioF:GREAT

iBioFoundry

Huimin Zhao, PhD

Steven L. Miller Chair of Chemical and Biomolecular Engineering, University of Illinois Urbana-Champaign

Director, NSF iBioFoundry

CREATE BIOFOUNDRY

Mark Blenner, PhD

Thomas & Kipp Gutshall Career Development Associate Professor of Chemical and Biomolecular Engineering, University of Delaware

Director, CREATE BIOFOUNDRY

AIRFoundry

Daeyeon Lee, PhD

Russell Pearce and Elizabeth Crimian Heuer Professor of Chemical and Biomolecular Engineering, University of Pennsylvania

Director, AIRFoundry

ExFAB

Ian Wheeldon, PhD

Professor Chemical and Environmental Engineering, University of California, Riverside

Co-Director, ExFAB

10:30-11:00am

Coffee Break

11:00am-12:00pm

London Biofoundry (United Kingdom)

Marko Storch, PhD

Director Biofoundry Operations, Co-Director Imperial Drug Discovery Hub, Imperial College London

VTT Biofoundry (Finland)

Jussi Jäntti, PhD

Principal Scientist, Research Team Leader, VTT Technical Research Centre of Finland

Kobe Biofoundry (Japan)

Tomohisa Hasunuma, PhD

Professor, Director, Engineering Biology Research Center, Kobe University

K-Biofoundry (South Korea)

Seung-Goo Lee, PhD

Director, Korea BioFoundry Project, Professor, Korea Research Institute of Bioscience & Biotechnology

12:00-1:00pm

Lunch & Networking

1:00-2:00pm

Shing Kwok, PhD

Program Manager, Biological and Environmental Research, Office of Science,DOE

Sridhar Raghavachari, PhD

Program Director, Directorate for Biological Sciences, Division of Biological Infrastructure, NSF

Wataru Mizunashi, PhD

Deputy Senior Manager, Frontier & Open Innovation Division, Mitsubishi Chemical Corporation

Paul Raterron, PhD

Program Director, Office of the Director, Office of International Science and Engineering, NSF

R. Todd Anderson, PhD

Division Director for Biological Systems Science, Office of Biological and Environmental Research, Office of Science, DOE

2:00-3:00pm

NSF Global Center for Biofoundry Applications Members Panel

Moderator: George Heintz, Managing Director, NSF iBioFoundry

Introduction of NSF Global Center for Biofoundry Applications

Huimin Zhao, PhD, Principal Investigator, NSF Global Center for Biofoundry Applications India Hook-Barnard, PhD, Outreach Thrust Co-Leader, CEO, Engineering Biology Research Consortium

Haseong Kim, PhD, Research Thrust Co-Leader, K-Biofoundry Kenichi Yoshida, PhD, Education and Workforce Development Thrust Co-Leader, Kobe Biofoundry

Emma Frow, PhD, Governance Thrust Co-Leader,

Arizona State University

3:00-3:30pm **Group Photo**

State Farm Center

PARALLEL SESSION START

3:30- 4:00pm	Organized Transfer to IGB for Ribbon Cutting Shuttle to IGB (Invite only)	3:30- 6:00pm	Vendor Display I Hotel
4:00- 4:40pm	Ribbon-Cutting & Inauguration Ceremony Gene Robinson, PhD; Timothy L. Killeen, PhD; Charles Lee Isbell Jr., PhD; Huimin Zhao, PhD; Sridhar Raghavachari, PhD	4:00- 6:30pm	Poster Session Chancellor Ballroom
4:40- 6:30pm	Reception		

PARALLEL SESSION ENDS RECONVENING AT I HOTEL

6:30-8:30pm Global Biofoundry Alliance Oeuduvre, Drinks & Networking

Poster Session, Chancellor Ballroom



8:15-**Breakfast & Kickoff** 8:45am George Heintz, Managing Director, NSF iBiofoundry 8:45-C1 Biofoundry: From Prototype to Commercial Launchpad 9:15am Jeffrey Vieregg, PhD, LanzaTech Chair: Huimin Zhao, PhD The future of Biofoundries in the World of AI 9:15-9:45am Will Serber, VP and General Manager, Automation, Ginkgo Bioworks Chair: Huimin Zhao, PhD 9:45-10:45 AM David Ross, PhD India Hook-Barnard, PhD **Corey Hudson** Theresa Good, PhD Chief Executive Officer, Head of Data, The Align Lead Scientist, Living Measurement Directorate Head of Biological Systems Foundry, National Institute Engineering Biology Research Foundation Sciences, NSF of Standards and Technology Consortium 10:45-**Coffee Break** 11:00am 11:00am-12:30pm **National Physical BRIGHT IBVT BioFoundry** Jülich Biofoundry Concordia A*STAR Biofoundry at the **SPARROW** Laboratory (Germany) Genome Foundry (Germany) (United Kingdom) (Canada) **DTU Biosustain Biofoundry** Cedric Meyer, PhD Stephan Noack, PhD (Denmark) (Singapore) Max Ryadnov, PhD Nicolas Gold, MSc,S candidate Group Head, enior Advisor, Adam M. Feist, PhD Clement Scipion, PhD NPL Fellow in Institute of Biochemical Quantitative Microbial Business Biometrology, Engineering, University Phenotyping; Professor of Scientist, A*STAR Professor of Development & of Stuttgart Co-Manager, Bioengineering Singapore Institute Engagement Jülich Biofoundry, Biophysics, Director, and Group Leader, of Food and Reference Biofoundry, Concordia Genome **BRIGHT Biofoundry** Forschungszentrum Biotechnology National Physical Foundry, Concordia & UCSD Biofoundry Jülich GmbH Innovation Laboratory University (USA) 12:30-**Lunch Break** 1:30pm 1:30-2:30pm Tools to Drive DBTL Efficiently, De-Risk **Innovative Lab Automation Technologies Automating and Accelerating** Scale-Up, and Prioritize High-Quality **Advancing Synthetic Biology** Biofoundry Innovation with TeselaGen's AI-Enabled Design-Build-Test-Learn Data Dr. Hille Tekotte **Platform** Maria Savino, PhD, MBA Senior Product Applications Specialist, Thermo Eduardo Abeliuk, PhD Global Segment Development Manager, Fisher Scientific Beckman Coulter Life Sciences CEO, TeselaGen Biotechnology

2:30-3:30pm

DOE Agile BioFoundry (USA) Australian G

Nathan Hillson, PhD

Senior Staff Scientist, Lawrence Berkeley National Lab; Lead Principal Investigator, DOE Agile BioFoundry

Australian Genome Foundry (Australia)

Briardo Llorente, PhD

Associate Professor, Chief Scientist, Australian Genome Foundry, School of Natural Sciences, Macquarie University

Shenzhen Biofoundry (China)

Fan Jin, PhD

Professor, Chief Engineer of the Shenzhen Infrastructure for Synthetic Biology, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences

Paris Biofoundry (France)

Stéphane Lemaire, PhD

Research Director CNRS, Department of Computational, Quantitative and Synthetic Biology, Sorbonne Université; Director, Paris Biofoundry

3:30-4:00pm

Coffee Break

4:00-6:00pm

SynCTI (Singapore)

Chueh Loo Poh, PhD

Director, Associate Professor, Synthetic Biology for Clinical and Technological Innovation (SynCTI), National University of Singapore

Estonian Biofoundry (Estonia)

Vallo Varik, PhD

Faculty of Science and Technology, Director, Estonian Biofoundry, University of Tartu

Toronto Biofoundry (Canada)

Celina Tufvegren Borgstrom, PhD

Project Manager, BEACON, Department of Chemical Engineering and Applied Chemistry, University of Toronto

Synthetic DNA Accelerator Lab (Germany)

Konrad Herbst, PhD

Head, Synthetic DNA Accelerator Lab, Center for Synthetic Genomics Heidelberg-Karlsruhe-Mainz, University of Heidelberg

IDEA Bio (Australia)

Justin Gareth Chitpin, PhD

Postdoctoral Fellow, Systems Biology at IDEA Bio, University of Queensland

SynBiofoundry@TUM (Germany)

Volker Sieber, PhD Professor, Chair, Chemistry of Biogenic Resources, TU München

DAMP Lab (USA)

Kristen Sheldon

Senior Laboratory Technologist, Boston University

RISE High-Throughput Centre (Sweden)—Zoom

Payam Ghiaci, PhD Leader, RISE High-Throughput Centre

6:00-6:10pm

Wrap-Up and Closing Remarks

pm Huimin Zhao & Lars Nielsen

6:10-8:00pm

Global Biofoundry Alliance Dinner, Drinks & Networking

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EDUARDO ABELIUK, PHD

CEO, TeselaGen

Eduardo Abeliuk, Ph.D., is the co-founder and CEO of TeselaGen Biotechnology, a U.S.based company at the intersection of biotechnology, artificial intelligence, and enterprise software. TeselaGen's cloud platform helps biofoundries and research organizations worldwide accelerate the design-build-test-learn cycle for biological products. Previously, Dr. Abeliuk was a research assistant at Stanford University, applying high-throughput genetic and molecular biology techniques to study bacterial cell division. His work has been published in leading journals, and he holds multiple U.S. patents in computational biology and Al. While at Stanford, he launched and sold the social networking application KissMe, and founded Umine.com, a platform for optimizing corporate human capital performance in developing countries. Earlier, he worked at SMaL Camera Technologies (acquired by Cypress Semiconductor) designing and implementing embedded image processing algorithms. He has consulted in biotechnology, enterprise software, and Al for organizations including Exabeam, Karius, and PwC, and serves as a collaborator with the Joint BioEnergy Institute, advisor to the Agile BioFoundry, board member at Sofofa Hub's Center for Translational Biotechnology, founding member of OpenBeaucheff's Investment Council, and counselor for The Nature Conservancy (Miami Council).

Dr. Abeliuk holds bachelor's degrees in Physics and Electrical Engineering from the University of Chile, an M.S. in Bioengineering, and a Ph.D. in Electrical Engineering from Stanford University.

Talk Title: Automating and Accelerating Biofoundry Innovation with TeselaGen's AI-Enabled Design-Build-Test-Learn Platform

Abstract: TeselaGen provides a cloud-based, Al-enabled software platform for biotechnology, designed to streamline and automate the full Design-Build-Test-Learn (DBTL) cycle. By combining molecular design tools, automated assembly planning, experiment tracking, and data analytics into a single, integrated environment, TeselaGen empowers biofoundries to accelerate the creation of genetically reprogrammed organisms and scale their innovation efforts efficiently. The platform is used by leading research institutions, industrial biotechnology companies, and members of the Global Biofoundries Alliance (GBA). Its modular architecture supports a wide range of applications, including synthetic biology, protein engineering, and metabolic pathway optimization. Researchers can design DNA, RNA, and protein constructs using multiple assembly strategies, manage large combinatorial libraries, and execute complex workflows from DNA assembly through strain development. The system integrates seamlessly with laboratory automation equipment—such as liquid handlers, colony pickers, and analytical instruments—ensuring



reproducible, high-throughput experimentation. A deeply integrated electronic lab notebook (ELN) and inventory management system centralizes experimental data, samples, and protocols, while built-in algorithms and machine learning capabilities provide predictive insights to improve design quality, anticipate performance, and guide each iteration of the DBTL cycle.

In this talk, I will present real-world examples of how TeselaGen is enabling GBA member biofoundries to address common challenges, from managing complex multi-gene assemblies to automating experimental workflows and integrating diverse data sources. These examples demonstrate measurable improvements in turnaround time, error reduction, and collaborative efficiency across multi-disciplinary teams.

I will also offer a glimpse of upcoming capabilities, including expanded AI-driven design recommendations, deeper integration with public and proprietary databases, and advanced security and compliance features. By fostering close collaboration with the GBA community, TeselaGen aims to contribute to a globally connected biofoundry network that accelerates safe, reliable, and impactful biotechnology innovation.



R. TODD ANDERSON, PHD

Division Director, Office of Science, Office of Biological and Environmental Research, U.S. Department of Energy (DOE)

Dr. Anderson serves as the Director of the Biological Systems Science Division within DOE's Office of Biological and Environmental Research (BER). The division manages basic science programs addressing the fundamental biology of plants and microbes of relevance to DOE's bioenergy and environmental missions. The current portfolio includes the Genomic Science Program, the DOE Bioenergy Research Centers, the DOE Joint Genome Institute, the DOE Systems Biology Knowledgebase, the National Microbiome Data Collaborative and, capabilities at the DOE Synchrotron Light and Neutron sources for Structural Biology and Bioimaging science.



MARK BLENNER, PHD

Gutshall Associate Professor of Chemical & Biomolecular Engineering,
Director NSF CREATE Biofoundry

Dr. Blenner is the Thomas & Kipp Gutshall Career Development Associate Professor of Chemical & Biomolecular Engineering at the University of Delaware. Prior to that, he was the McQueen Quattlebaum Associate Professor of Chemical and Biomolecular Engineering at Clemson University. He received his PhD in Chemical Engineering from Columbia University in 2009 and completed three years of postdoctoral training as an American Heart Association Postdoctoral Fellow and an NIH NRSA Postdoctoral Fellow at Harvard Medical School and Children's Hospital Boston. He has won numerous awards including the 2022 AIChE Food, Pharmaceutical, and Bioengineering Division Early Career Award, the 2021 ACS BIOT Young Investigator Award, and the 2019 Presidential Early Career Award for Scientists and Engineers (PECASE). He is on the Board of the Society of Industrial Microbiology & Biotechnology and ACS Biochemical Technology. His research is broadly focused on engineering biomolecular and cellular systems to produce fuels, chemicals, enzymes, biopharmaceuticals and biosensors. Some of the common threads across his lab's work are around using microbes for enabling a circular economy and addressing biomanufacturing-related problems arising from cell line design in both microbes and animal cells.

Talk Title: Towards Decentralized Disaggregated Biofoundries

Abstract: Our vision is to assemble a working model of a distributed biofoundry that may serve as a blueprint for future decentralized biofoundries. This will require a new approach that differs from existing centralized biofoundry models. Therefore, we established the Center for Robust, Equitable and Accessible Technology and Education (CREATE) for Next Generation BioFoundries. Our efforts internally and with users focus on technology development on reducing the resource intensity of the biofoundry Design-Build-Test-Learn (DBTL) cycle. To date we have generated user-friendly computational Design environments informed by systems and synthetic biology and associated Build pipelines that drive down the cost of gene assembly and focus on the agility needed to work with a wide range of systems. Test strategies emphasizing biosensors, scale-down models, and algorithm-guided combinatorial search space reduction; and Learn workflows aided by bioinformatics and artificial intelligence. These efforts will address DBTL bottlenecks and knowledge gaps that currently require expensive, unwieldy massively parallel experimental design. This innovation strategy and distributed structure will ensure that CREATE will deliver a model for self-sustaining distributed and democratized biofoundries. This new model will increase access, and therefore impact, of the transformative biofoundry design-build-testlearn (DBTL) cycle, helping researchers solve grand challenges in biology.



CELINA TUFVEGREN BORGSTROM, PHD

Project Manager, BEACON, BioZone, Department of Chemical Engineering and Applied Chemistry,
University of Toronto

Dr. Tufvegren Borgstrom completed her PhD in Applied Microbiology working with yeast for production of bioethanol from hemicellulosic biomass at Lund University, Sweden, in 2021. She then joined the Mahadevan lab at the University of Toronto, Canada, to work on metabolic engineering for production of value-added compounds from sustainable substrate streams. She soon started doing more lab and project management work, including project management of projects supported by Genome Canada, Ontario Genomics, and DARPA. She has experience in writing grant applications, interacting with both industry and government stakeholders, and managing research work.

Talk Title: BEACON: Bioengineering Facility to Accelerate Circular Bioeconomy in Ontario

Abstract: BioZone is a multidisciplinary centre for Applied Bioscience and Bioengineering within the University of Toronto's Faculty of Applied Science and Engineering. As such, we are strong proponents of using the most recent advances in technology, including automation and machine learning (ML), to tackle a wide range of challenges faced within industrial and environmental biotechnology. Although we currently do not house a centralized biofoundry, we have years of experience using liquid handlers, plate readers and other higher throughput equipment. This approach allows us to streamline very labor intensive workflows, including those requiring an anaerobic atmosphere. Our goal is to develop our infrastructure into a full-scale biofoundry targeted towards characterization of anaerobic organisms and proteins based on some pending applications. During my talk I will describe the proposed equipment and workflows of the planned foundry, from DNA assembly, transformation, protein extraction and enzyme assays to growth and metabolite analysis of wild type and engineered anaerobes from microliter to 0.5L scales. I will also discuss the added complexity of performing these workflows within controlled atmosphere enclosures. Specifically, we will also describe planned activities to generate data on microbial phenotypes along with associated computational workflows that can lead to a self driving lab for engineering proteins, enzymes, strains and communities under anaerobic conditions. Finally, we plan to use ML both in designing high-throughput experiments and in analyzing their results.



JING CHENG, PHD

Microbial Platform Coordinator, Concordia Genome Foundry, Concordia University

Dr. Jing Cheng brings over two decades of academic and industrial experience in molecular biology, synthetic biology, protein engineering, biochemistry, and bioinformatics. She currently serves as the Genome Foundry Microbial Platform Coordinator at Concordia University's Centre for Applied Synthetic Biology, where she leads microbial cell engineering projects and manages high-throughput platform operations. Dr. Cheng has extensive expertise in genome editing, gene synthesis, mutagenesis, and library construction. Her work includes synthetic natural product biosynthesis, protein interaction studies, and high-throughput screening. She has successfully constructed and screened yeast-based biosynthetic pathway libraries and developed mini-protein libraries targeting Flu and SARS-CoV-2 RBDs using yeast surface display. Her interdisciplinary approach combines wet lab experimentation with computational analysis, including bioinformatics and machine learning. She has published research contributed to studies on genome bioinformatics, protein engineering for enzyme discovery and optimization. Dr. Cheng's career includes roles at the University of Montreal's IRIC, SickKids Research Institute, McGill University, and the National Research Council of Canada. She has also worked in industry, applying advanced cloning and mutagenesis techniques to develop novel gene synthesis and assembly methods.

Talk Title: Accelerating Synthetic Biology in the Era of Big Data— Concordia Genome Foundry's Integrated High-Throughput Platform

Abstract: Accelerating Synthetic Biology in the Era of Big Data: Concordia Genome Foundry's Integrated High-Throughput Platform Concordia Genome Foundry has established a comprehensive high-through put (HTP) platform that comprise mammalian, microbial cell engineering, as well as microbial bioprocessing. By combining state-of-the-art automation, a custom Laboratory Information Management System (LIMS), advanced bioinformatics, and next-generation sequencing (NGS), we aim to accelerate synthetic biology research and innovation. Our mammalian platform leverages the Vantage liquid handling workstation, Lonza nucleofector, citation 5 reader and Cytek flow cytometry to develop iPSC and build CRISPR-based gene editing cell lines. On the microbial side, our workflows enable HTP cloning, gene editing, strain construction, and phenotypic characterization through automated colony picking (QPix), liquid handling (Echo, Lynx 900, Biomek i7), and phenotyping tools (Growth Profiler, EnSight plate reader). Our microbial bioprocessing infrastructure supports downstream processing and scaleup from 0.3L to 200L. This integrated HTP system, powered by LIMS and bioinformatics, enables parallel processing of hundreds to thousands of constructs, facilitating robust screening, phenotyping, and data analysis to significantly accelerate the design-build-test-learn (DBTL) cycle. As synthetic biology enters the era of big data, we embrace the rapid advancements and cost-efficiency of oligo pool synthesis and NGS by developing scalable workflows for diverse applications. One example is our integrated workflow that combines pooled oligo synthesis and pooled NGS with HTP automation to streamline large-scale construct and strain engineering. Pooled oligos allow the generation of tens of thousands of DNA variants in a single order, eliminating repetitive manual cloning.



Automated colony picking, liquid handling, followed by pooled NGS and big data analysis enable large-scale unique construct identification and validation. By transforming synthetic biology into a faster, more scalable, and data-rich process. Concordia Genome Foundry is reshaping how we explore and engineer biology at scale.



JUSTIN GARETH CHITPIN, PHD

Postdoctoral fellow, Integrated Design Environment for Advanced Biomanufacturing (IDEA Bio)
Biofoundry, University of Queensland

Dr Justin Chitpin is a postdoctoral fellow in Systems Biology at IDEA Bio. His current research interests lie at the intersection of mechanistic metabolic modelling and statistical analyses of -omics data. At IDEA Bio, Justin is leading the development of cutting-edge computational workflows that integrate bioreactor and high-throughput data for rational strain engineering. Dr Chitpin received his PhD in biochemistry with specialisation in bioinformatics at the University of Ottawa, where he developed mathematical models and algorithms to efficiently analyse steady state metabolic flux network. Dr Chitpin also holds a MSc in biochemistry from the University of Ottawa, where he developed machine learning models to identify lipid species from liquid chromatography coupled to tandem mass spectrometry data. Prior to this, he also worked on quantifying and correcting statistical biases in chromatin immunoprecipitation followed by sequencing data.

Talk Title: Implementation of a DBTL workflow in the operation of a fermentation Biofoundry

Abstract: IDEA Bio is a national NCRIS-BPA supported bioprocess facility hosted at The University of Queensland, providing end-to-end capabilities to accelerate biotechnology research and industry collaborations. Our platform integrates a Design-Build-Test-Learn (DBTL) pipeline, enabling the systematic development, optimisation, and scale-up of bioprocesses across diverse microbial systems. In this presentation, we will outline how IDEA Bio onboards and delivers projects, from initial scoping and project design through to experimental implementation, data integration, and knowledge transfer. We will highlight our approach to aligning project goals with facility expertise, coordinating infrastructure and staff resources, and ensuring robust data management practices. A case example will illustrate how our structured pipeline supports both academic and industry partners in advancing microbial strain engineering, precision fermentation, and biomanufacturing initiatives.



GARRET DUNLAP, PHD

Associate Director, Policy & International Engagement, Engineering Biology Research Consortium

Dr. Garrett Dunlap joined EBRC as Associate Director of Policy & International Engagement in September 2024. Before this, he was Head of Science and Innovation at the British Consulate-General in New York, fostering UK-US science and tech collaborations. He previously worked as a Graduate Fellow at the Wilson Center, focusing on biosecurity risks from converging technologies, and as a Science Diplomacy Fellow with the Netherlands Innovation Network, exploring deep tech innovation ecosystems. In addition to his current role, Garrett is a Fellow for Ending Bioweapons with the Council on Strategic Risks, and he also participates in working groups for the World Economic Forum and All Tech is Human. He holds a Ph.D. in Biological and Biomedical Sciences from Harvard University and undergraduate degrees in Biology and Political Science from Case Western Reserve University.



ADAM M. FEIST, PHD

Professor of Bioengineering and Group Leader, BRIGHT Biofoundry at the DTU Biosustain (Denmark) & UCSD Biofoundry (USA)

Adam Feist is an Assistant Professor in the Shu Chien-Gene Lay Department of Bioengineering at UC San Diego and a Senior Researcher at the Technical University of Denmark's Center for Biosustainability. He is an expert in microbial adaptive laboratory evolution, systems biology, and computational modeling of metabolic processes. Over the past decade, Dr. Feist has developed and operated a distributed, automation-driven laboratory supporting both internal research and Biofoundry services for academic and industrial partners. His work integrates robotics, large-scale data analysis, and microbial engineering to accelerate the design of microbial strains and uncover emergent properties with applications in biomanufacturing and biomedicine. Dr. Feist has co-authored more than 120 peer-reviewed publications and holds multiple patents. His research excellence has been recognized with the Jay Bailey Young Investigator Award in Metabolic Engineering (2018) and repeated inclusion among the Top 2% of researchers worldwide by PLOS Biology. He earned his Ph.D. (2008) and M.S. (2005) in Bioengineering from UC San Diego, and his B.S. in Chemical Engineering from the University of Nebraska-Lincoln (2003). Dr. Feist also spent two years in a startup environment focused on genome-scale modeling, gaining experience in translating systems biology approaches into applied biotechnology.

Talk Title: The BRIGHT Biofoundry at DTU Biosustain

Abstract: The BRIGHT Biofoundry (DTU) is a dynamic, technology-driven research hub dedicated to accelerating innovation in biotechnology, with a particular focus on the design and development of microbial cell factories and novel food systems. It integrates enabling technologies across computational and molecular biology to transform



large-scale biological data into actionable insights—while adhering to the FAIR (Findable, Accessible, Interoperable, Reusable) data principles. Operating across Technology Readiness Levels (TRL) O to 6-from early-stage concepts to commercially viable spin-offs-the BRIGHT Biofoundry supports bioprocess development from nanoliter to 100-liter scales. To ensure that projects are both economically viable and impactful in advancing biosustainability, it works closely with the Sustainable Innovation Office and the Commercialization and IP Support team. As a vignette of cross-biofoundry collaboration, the BRIGHT Biofoundry includes an automated Adaptive Laboratory Evolution (ALE) platform that is primarily developed at the UC San Diego Biofoundry. This successful transfer involved replicating hardware and software workflows, adapting them to local infrastructure, and training personnel to ensure operational consistency. The process illustrates how biofoundries can exchange mature technologies to accelerate deployment, avoid redundant development, and enable shared innovation across sites. In summary, this presentation will highlight selected projects in chemical and food production, as well as key automation initiatives, illustrating how these capabilities enhance interoperability, reproducibility, and innovation across the DBTL (Design-Build-Test-Learn) cycle.



EMMA FROW, PHD

Associate Professor, Arizona State University

Emma Frow is an associate professor at Arizona State University (ASU). She has graduate degrees in both the natural sciences (biochemistry) and social sciences (science & technology studies), and is an embedded social scientist in the biomedical engineering department at ASU. She has been studying and working with the synthetic biology community for over 15 years, and currently has an NSF CAREER award focused on the design and governance of biofoundries.



PAYAM GHIACI, PHD

RISE Processum of the RISE Research Institutes of Sweden

Payam Ghiaci has been Leader of RISE High-throughput Centre since 2021, as part of the latest investment of the Swedish state in biotechnology testbeds. Complemented with up to 10k L scale-up testbeds, RISE Bioeconomy Arena is home to a full chain of commercialization trials. Lately, Payam has been focused on bioprospecting large and intact microbial collections from distant and exotic environments such as Brazilian Rainforest and West African Sahara, screening for aromatics and lipids with food and personal-care applications. High-throughput screening methods for filamentous fungi is yet another research interest of his.

Talk Title: A Fearless Approach for a Cautious Industry! (Highthroughput techniques for food applications)

Abstract: The food industry is traditionally risk-averse, shaped by stringent safety regulations, consumer expectations, and complex supply chains. Yet, the growing demand for innovation in nutrition, sustainability, and functional ingredients calls for bold, data-driven approaches. This talk explores how high-throughput techniques—once reserved for pharmaceutical and biotech sectors—are now being fearlessly adapted to food applications, offering transformative potential. We take "a step back" to examine the industry's cautious stance toward novel technologies and the barriers to adoption, including sensory and scalability concerns. Then, we move "two steps forward" by showcasing how automation, miniaturization, and multiplexed screening can accelerate discovery and validation of bioactive compounds, microbial strains, and formulation strategies. Case studies will highlight applications in taste and flavor profiling, and microbial bioprospecting for foodrelevant compounds. The presentation will also discuss how integrating omics technologies and machine learning is reshaping food R&D, making it faster and more predictive.



THERESA GOOD, PHD

Directorate Head of Biological Sciences, National Science Foundation

Dr. Theresa Good is currently the Directorate Head of Biological Sciences at the National Science Foundation. Since joining NSF in 2010, she has served in various capacities at NSF managing research in synthetic biology and associated fields and leading first the Division of Molecular and Cellular Biosciences and now the Directorate of Biological Sciences. In her leadership of the NSF Bioeconomy Coordinating Committee, she facilitated



the development of the NSF BioFoundry program, and leveraged resources to enable its funding. As a member of the National Bioeconomy Board Secretariat and of various OSTP subcommittees she has worked across agencies to help coordinate activities across agencies to support the biotechnology. Prior to coming to NSF, Dr. Good was a Professor in Chemical and Biochemical Engineering at the University of Maryland Baltimore County, and before that at Texas A&M. She has been involved in research at the interface of engineering and biological sciences for her entire academic career.



TOMOHISA HASUNUMA, PHD

Professor, Director, Engineering Biology Research Center, Kobe University

Tomohisa Hasunuma is the Director of Engineering Biology Research Center, and concurrently serves as a Professor at the Graduate School of Science, Technology and Innovation at Kobe University, Japan. He earned his B.Sc. (1998), M.Sc. (2000) and PhD (2004) in the Department of Biotechnology at Osaka University, Japan. In 2004, Dr. Hasunuma joined Research Institute of Innovative Technology for the Earth (RITE), before transitioning to Kobe University in 2008. From 2011 to 2014, he held the position of the Researcher for Precursory Research in Embryonic Science and Technology (PRESTO) under the Japan Science and Technology Agency. Dr. Hasunuma has authored over 220 peer-reviewed journal papers and 90 reviews and book chapters. Since 2024, he has served an Associate Editor for ACS Synthetic Biology. His research focuses on engineering biology of microorganisms such as yeast, Escherichia coli, cyanobacteria and microalgae with a particular emphasis on metabolic engineering based on metabolism analysis for the production of biofuels, commodity chemicals and highly functional compounds from renewable biomass and carbon dioxide. Dr. Hasunuma was awarded the Fermentation and Metabolism Research Prize of Japan Bioindustry Association in 2013 and the Biotechnology Encouragement Prize of Biotechnology Society of Japan in 2014.

Talk Title: Data-Driven Engineering Biology for Biomanufacturing

Abstract: Engineering biology is attracting great expectations from society as an academic field that contributes to solving global issues and furthering economic development. The basic concept of engineering biology is the design and construction of biological systems with novel functions, which will lead to a better understanding of the mechanisms of life, but also the realization of valuable industrial applications in fields such as chemistry, energy, medicine, and food. Our research group is developing novel capabilities in the theme of bioengineered cells and systems, applying metabolic engineering of microbes for high-value chemical production, as there is a great deal of industrial interest in biomanufacturing using microorganisms. Recent advances in genome synthesis and engineering, high-throughput technologies, measurement technologies, and computational science have enabled the faster and

Tomohisa Hasunuma / cont

more reliable implementation of increasingly ambitious design strategies. We launched a bio-foundry approach for rapid engineering of model microorganisms, and we have succeeded in developing Escherichia coli and yeast strains that can produce high amounts of useful molecules. Kobe University Engineering Biology Research Center (EGBRC) is working on the development of "Smart Cells," a microbial strain that can produce high amounts of useful substances using computer-designed metabolic pathways and enzymes. In particular, what determines the quality of the design is the experimental data and the analysis and evaluation technology that generates it. Thus, we are developing high-throughput screening technology using supercritical fluids and metabolomics that achieves high reproducibility by automating the pretreatment process. In addition, we have also developed a DBTL platform for enzyme engineering. In this session, I would like to introduce our "Smart Cell Development Platform" incorporating the elemental technologies we developed and look into the future of bioengineering.



KONRAD HERBST, PHD

Head of Facility, Synthetic DNA Accelerator Lab, Center for Synthetic Genomics Heidelberg-Karlsruhe-Mainz, University of Heidelberg

Konrad Herbst is the Head of the Synthetic DNA Accelerator (SynDNA) lab which is part of the newly established Center for Synthetic Genomics Heidelberg-Karlsruhe-Mainz. He studied Molecular Biotechnology at the University of Heidelberg majoring in bioinformatics and molecular biology. During his studies he was part of the 2013 grand prize winning iGEM team were he got inspired by synthetic biology and microbiology. From 2017 to 2021 he did his Ph.D. under the supervision of Prof. Michael Knop at the the Center for Molecular Biology in Heidelberg (ZMBH) developing (among others) novel tools for large scale genetic manipulations in yeast and mammalian cells as well as the respective next-generation sequencing techniques to characterize those manipulations. While doing his Ph.D., Konrad was involved in the first efforts worldwide to establish a LAMP assay as an alternative SARS-CoV-2 diagnostic testing modality using real-world clinical samples. He then went to the US from 2022 to 2024 for a postdoc working with Prof. Daniel Segré at Boston University, where he studied the relationship of different microbes with their environment. Since mid of 2024 he is fully engaged in aiding synthetic genomics efforts by building up the SynDNA Lab. He lives in Heidelberg with his wife and two young children of one and four years.

Talk Title: The Synthetic DNA Accelerator Lab - Enabling the recoding and decoding of life through Synthetic Genomics

Abstract: The Synthetic DNA Accelerator Lab is part of the newly established Center for Synthetic Genomics (Center SynGen) and is located



at the University of Heidelberg in Germany. Our goal is to support other research groups with variant libraries of DNA constructs they need for their Synthetic Genomics endeavors. To this end, we are centralizing and developing infrastructure, workflows, methodologies and know-how for synthetic DNA sequence assembly and diversification. We use in vitro and in vivo molecular cloning methods as well as (semi-)automation to assemble long, complex and varied sequences of DNA. We thrive to accommodate our customer's needs by conducting research and developing technologies tailored to their specific projects. In addition, the lab fosters community building and public outreach to further accelerate the adoption of Synthetic Genomics ideas to better understand sequence-function relationships.



NATHAN HILLSON, PHD

Senior Staff Scientist, Lawrence Berkelev National Lab

After Dr. Hillson earned his Ph.D. in Biophysics from Harvard Medical School, he did his postdoctoral work in Developmental (Micro)Biology at Stanford University School of Medicine. Dr. Hillson's work has spanned the realms of the private (notably as co-founder and Chief Scientific Officer at TeselaGen Biotechnologies, Inc.) and public biotechnology sectors. As Department Head of BioDesign within the Biological Systems & Engineering Division, Dr. Hillson leads scientists and engineers within Lawrence Berkeley National Laboratory whose domain expertise spans synthetic biology, metabolic engineering, microbiology, microbial communities, software engineering, and laboratory automation. As the Lead Principal Investigator of the U.S. DOE Agile Biofoundry, Dr. Hillson leads an even broader group of scientists and engineers distributed across 7 U.S. DOE National Labs towards the development of biomanufacturing tools, processes, and partnerships that enable industrial production of fuels and chemicals for the nation. This complements discovery engines (such as the Joint Genome Institute, to which Dr. Hillson also contributes), by enabling the discovered (yet small scale, low titer/rates/yields) pathways to be more quickly and reliably optimized and scaled. Efforts are supported by DOE-funded entities, including the DOE Agile BioFoundry, DOE Joint BioEnergy Institute, DOE Joint Genome Institute, as well as by industry-sponsored collaborations.

Talk Title: DOE Agile BioFoundry Update

Abstract: This presentation will provide a brief update on changes and developments at the U.S. DOE Agile BioFoundry (ABF). Over the past three years, we have implemented and operated a re-envisioned ABF, with a new vision, mission, goals, and organizational structure. One technical highlight relates to the development of automated strain engineering workflows for the high-throughput genotype/phenotype screening of genome-scale microbial variant libraries.



INDIA HOOK-BARNARD, PHD

Chief Executive Officer, Engineering Biology Research Consortium

India Hook-Barnard is the CEO of the Engineering Biology Research Consortium (EBRC). Her primary interests are in the areas of synthetic biology, precision medicine, responsible innovation, and biosecurity. India enjoys building multidisciplinary collaborations and developing a vision and strategy to address complex challenges. She works with experts and leaders from across academia, industry, and government sectors to identify and shape scientific opportunities, technical feasibility, and policy issues. Her goal is to advance and accelerate engineering biology solutions across all application areas, drive innovation, and grow the bioeconomy for all.

Before joining EBRC, India was Senior Advisor to the Beyond 2020: A Vision and Pathway for NIH Working Group, and Senior Vice President for Patient Outcomes and Experience at the National Marrow Donor Program. She was the Director of Research Strategy and Associate Director for Precision Medicine at the University of California, San Francisco; she helped launch and was the Executive Director of the California Initiative to Advance Precision Medicine. Earlier in her career, India worked at the National Academies of Sciences, Engineering, and Medicine (NASEM), focusing on areas of emerging science and technology, including policy issues of data governance, regulation, bioethics, biodefense, and workforce development. At NASEM, she directed standing committees, workshops, and six consensus reports, including Toward Precision Medicine: Building a Knowledge Network for Biomedical Research and a New Taxonomy of Disease (2011).

As a postdoctoral research fellow at the National Institutes of Health, India studied the regulation of gene expression in bacteria and phage. She earned her Ph.D. in Microbiology-Medicine from the Department of Molecular Microbiology and Immunology at the University of Missouri

Talk Title: Advancing Engineering Biology and the Bioeconomy



COREY HUDSON, PHD

Head of Data, The Align Foundation

Corey M. Hudson, Ph.D., is a computational biologist and Head of Data at The Align Foundation. He specializes in AI-enabled design, genomic security, and scalable biofoundry workflows. He previously led cross-disciplinary teams at Sandia National Laboratories—managing computational biology and wet-lab programs—and served as a Program Manager at DARPA overseeing large, multi-institution efforts in automated molecular design. Dr. Hudson's work spans building open-source tools for genome engineering, digital twins for biomanufacturing, and international capacity-building with partners across Brazil, South Africa, India, and more. He has chaired the advisory board for the Center for Computational



Biology and Genomic Medicine and published widely on retrosynthesis, molecular design, biologically-focused AI and secure bioinformatics.

In his role as Head of Data at The Align Foundation, Dr. Hudson leads data science and engineering teams - building open, Al-ready biological datasets and benchmarks that accelerate discovery across protein and microbial engineering. His work centers on closing the gap between synthetic biology and data science to deliver tools that scale from the bench to production research environments.



DR. FAN JIN

Professor, Chief Engineer of the Shenzhen Infrastructure for Synthetic Biology, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences

Dr. Fan Jin is Professor of Synthetic Biology at Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences (since 2019) and Chief Engineer of the Shenzhen Infrastructure for Synthetic Biology (since 2021). He received a B.S. in Chemistry from the University of Science and Technology of China (2002) and a Ph.D. from The Chinese University of Hong Kong (2007), then pursued postdoctoral training at CUHK, UIUC, and UCLA. His research combines synthetic biology with bacterial motility and biofilm physics to program living cells. The team has created optogenetic circuits that switch Pseudomonas aeruginosa pathogenicity and engineered remotely controllable bacteria for cancer therapy, publishing in National Science Review, ACS Synthetic Biology, and Nature Communications. Dr. Jin currently directs multi-million-RMB national projects on robust genetic circuits and single-cell optogenetic evolution.

Talk Title: Engineering Biology Metrology and Standards in China

Abstract: The Shenzhen Infrastructure for Synthetic Biology represents a major advancement in China's efforts to build modern biofoundries, which became operational in 2024. This facility integrates Design-Build-Test-Learn (DBTL) cycles with standardized operating procedures (SOPs) to enhance reproducibility and efficiency in engineering biology processes. Key components include build platforms like the Synthetic Yeast Foundry, and test platforms for process scale-up, proteomics, metabolomics, and microscopy. Overall, this infrastructure supports China's growing biofoundry landscape, distributed across cities like Hangzhou, Shenzhen, and Tianjin, fostering innovation in synthetic biology.



JÄNTTI JUSSI, PHD

Principal Scientist, Research Team Leader, VTT Technical Research Centre of Finland

Jussi Jantti (PhD 1995 University of Helsinki, Finland) is a Lead in Industrial biotechnology at VTT Technical Research Centre of Finland Ltd, and an adjunct professor in biochemistry at the University of Helsinki. He is a member of the EU-IBISBA infrastructure network, Scientific Advisory board member for the Estonian DigiBio Biofoundry project, Commissioner in the International Commission on Yeasts (ICY), a member of the Board of the European Federation for Biotechnology, Microbial Biotechnology Division, Council member in the Engineering Biology Research Consortium (EBRC, USA), and a Member of the Advisory Board on Biotechnology appointed by the Government of Finland. His recent research has focused on the development of novel genetic engineering tools for microbes for the production of a wide range of end-products.

Talk Title: VTT Biofoundry

Abstract: VTT-Biofoundry focuses on the development of industrially relevant microbial production strains with an emphasis on yeasts and filamentous fungi. To this end, various DNA assembly tools for modular cloning of fungal expression cassettes and toolkits for CRISPR activation/interference tools for industrial, polyploid yeasts and filamentous fungi have been established. Additionally, broadly applicable gene expression tools for yeasts and filamentous fungi have been developed. In addition, computational tools for metabolic modelling, target gene identification and novel AI-based enzyme design have been developed. VTT has a large bioreactor facility up to 1500 liters that can be used for strain validation and scaleup. The translation of phenotypes identified through high-throughput screening is aided by an extensive platform of intermediate size bioreactors as well as state-of-the art analytics. The talk will describe recent VTT-Biofoundry technology developments.



HASEONG KIM, PHD

Head of Infrastructure Division, Korea Biofoundry, Korea Research Institute of Bioscience and Biotechnology (KRIBB)

Dr. Haseong Kim is a synthetic biologist who specializes in lab automation and genome design using statistical and IT technologies. He explores the potential of Al and automation technology at various levels, such as proteins, metabolic pathways, artificial genomes, and cells in synthetic biology research.



Talk Title: High-throughput Combinatorial DNA Assembly Accelerates Metabolic Pathway Optimization

Abstract: Efficient biofoundry workflows require automation-ready DNA assembly. We developed a high-throughput combinatorial strategy based on PCR amplification and bead purification, eliminating transformation and miniaturizing reaction volumes to one microliter. This approach reduced reagent consumption and enabled seamless progression across steps. For reliable screening, culture conditions were optimized for Albased colony color discrimination. As a proof of concept, 2,187 variants of a 16 kb mevalonate pathway were constructed by independently tuning seven enzymes with three RBS strengths. The platform completes a DBTL cycle within one week, and we anticipate that iterative integration of enzyme-level improvements will effectively resolve metabolic bottlenecks, thereby enhancing pathway optimization efficiency.



D.J. KLEINBAUM, PHD

Co-founder, Emerald Cloud Lab

D.J. Kleinbaum, Ph.D. is the Co-founder of Emerald Cloud Lab (ECL), the world's first and largest Cloud Lab. Prior to founding ECL, D.J. co-founded Emerald Therapeutics, which focused on developing a novel antiviral nanotechnology to detect and instruct the apoptosis of infected cells. D.J. holds a Ph.D. in Chemistry from Stanford University, where he studied nucleic acid chemistry under the direction of Professor Eric Kool. He also holds an undergraduate degree in Biological Sciences with concentrations in Computational Biology and Biochemistry from Carnegie Mellon University. He serves on the Advisory Board for the Carnegie Mellon University's Swartz Center for Entrepreneurship.

Talk Title: The what and why (and how) of Cloud Labs

Abstract: What are Cloud Labs? They aren't just automated instruments behind a web interface or CROs with better marketing. They are a new model for doing science: fully programmable, remotely operated facilities that make lab experiments reproducible, shareable, and scalable. This talk cuts through hype and misconceptions to explain what Cloud Labs really are, why they matter for the future of science, and how they complement biofoundries. We'll explore the features that make this model powerful and what it reveals about the hard but necessary work of building robust lab infrastructure.



DR. MICHAEL KÖPKE

Chief Innovation Officer, LanzaTech

Dr. Michael Köpke is the Chief Innovation Officer at LanzaTech (\$LNZA), a public company that uses biology to capture and transform carbon into sustainable products such as fuels, chemicals, proteins, and materials. Michael joined LanzaTech in 2009 and has been instrumental in building up the company's synthetic biology program and computational biology platform. In his current role, Michael oversees the process of innovation and technology partnerships. Michael is a pioneer in synthetic biology of CO2-fixing microbes and sustainable biomanufacturing with over 20 years of experience in the industrial biotech field. Michael holds a Ph.D. in biotechnology from University of Ulm, an inventor of more than 500 patents and author of over 50 peer-reviewed publications. Michael received multiple awards including the Presidential Green Chemistry Challenge Award for Greener Synthetic Pathways and ACS National Award for Team Innovation.

Beyond his role at LanzaTech, Michael is an adjunct faculty at Northwestern University, council member at the Engineering Biology Research Consortium, and in various advisory (International Metabolic Engineering Society, SynBioAfrica, Center for Advanced Bioenergy & Bioproducts Innovation) and editorial boards (Frontiers Microbiology/Bioengineering, Microbial Cell Factories, New Biotechnology).

Michael has provided thought leadership to several community efforts. He co-led the development of a research roadmap on engineering biology for climate and sustainability by a consortium of over 90 experts. Michael also co-initiated the gas fermentation conference series and is co-chairing upcoming Metabolic Engineering and Cell Free Systems international meetings.

Talk Title: C1 Biofoundry: A Commercial Launchpad for Biomanufacturing Sustainable Chemicals & Materials

Abstract: LanzaTech has pioneered and commercialized a novel gas fermentation process. Using carbon-fixing microbes, industrial carbon emissions are captured at source and converted into useful products. LanzaTech's technology is globally licensed with six commercial plants in operation today that abate 500,000 tons CO2 emissions while producing 300,000 tons of sustainable products used in a variety of applications including consumer goods or sustainable aviation fuels.

Building a technology platform around non-model organisms was always an ambitious project and requires specific tools and infrastructure development. Unlike E.coli or yeast, genetic engineering of C1 utilizing microbes is complex and working under anaerobic conditions and with toxic and flammable gases added further complexity. Through 15 years of dedicated development, LanzaTech established a full genetic toolbox and a first fully-integrated C1 biofoundry for automated engineering and prototyping of C1 microbes and other non-model organisms that enabled production of over 100 new molecules.



SHING KWOK, PHD

Program Manager, Biological and Environmental Research (BER), U.S. Department of Energy

Shing Kwok is the Program Manager in the Biological and Environmental Research (BER) program within the Office of Science at DOE. I primarily manage the four Bioenergy Research Centers (BRCs) in BER.



DAEYEON LEE, PHD, MBA

Russell Pearce and Elizabeth Crimian Heuer Professor, University of Pennsylvania

Daeyeon Lee is the Russell Pearce and Elizabeth Crimian Heuer Professor of Chemical and Biomolecular Engineering at the University of Pennsylvania. He received his BS in Chemical Engineering from Seoul National University and his PhD in Chemical Engineering from MIT. His research explores the interactions of soft materials at interfaces, with the goal of developing innovative processes and structures with applications in healthcare and environmental sustainability. He has been recognized for excellence in research with several awards, including the 2010 Victor K. LaMer Award, an NSF CAREER Award, the 2013 3M Nontenured Faculty Award, the 2013 AIChE NSEF Young Investigator Award, the 2014 Unilever Award for Young Investigators in Colloid and Surface Science, the 2017 Soft Matter Lectureship Award, and the 2023 Outstanding Achievement Award in Nanoscience. He has also been acknowledged for his contributions to education with awards such as the Penn CBE Distinguished Teaching Awards and the 2017 S. Reid Warren, Jr. Award, and he held the Evan C. Thompson Endowed Term Chair for Excellence in Teaching from 2020 to 2023. Since 2024, Daeyeon has served as Director of the NSF Artificial Intelligence-Driven RNA BioFoundry (AIRFoundry), an open-access platform that integrates artificial intelligence, automation and microfluidics to advance RNA design, synthesis, and delivery for a broad range of applications.

Talk Title: Artificial Intelligence-driven RNA BioFoundry

Abstract: RNA holds transformative potential due to its ability to store information, produce proteins, and catalyze reactions. However, progress is limited by gaps in RNA design tools, understanding of delivery systems such as lipid nanoparticles, and integration of expertise across the RNA pipeline. AIRFoundry addresses these challenges through an open-access, Al-driven platform for RNA technology. It integrates large-scale microfluidics and automated synthesis to accelerate the design, production, and optimization of RNAs and delivery vehicles. By providing community access to Alcurated knowledge, production technologies, and research-grade

Daeyeon Lee / cont.

materials, AIRFoundry advances both basic science and solutions to global challenges, from health to sustainability, while training the next generation of scientists at the interface of biology, engineering, and AI.



SEUNG-GOO LEE, PHD

Director or Korea BioFoundry, Korea Research Institute of Bioscience and Biotechnology (KRIBB)

Dr. Seung-Goo Lee is a Principal Scientist at the Korea Research Institute of Bioscience and Biotechnology (KRIBB) and a Professor at the University of Science and Technology (UST). He is also an Adjunct Professor at KAIST. In 2025, he was appointed as Director of the Korea National Biofoundry, responsible for establishing and operating national biofoundry infrastructure. He served as Director of the Synthetic Biology and Bioengineering Research Institute at KRIBB from 2022 to 2025 and as Director of the Synthetic Biology Research Center from 2013 to 2021. He founded the K-Biofoundry Beta Lab at KRIBB in 2021. His research focuses on enzyme engineering, high-throughput screening, and synthetic biology. He developed screening methods using gene circuits to support design-build-test-learn (DBTL) workflows.

He has also been active in community building. He was President of the Korean Enzyme Engineering Society (2021–2023) and has served as Administrative Secretary of the Korea Synthetic Biology Association since 2022. Dr. Lee received his PhD in Biological Engineering from KAIST in 1995. He was a postdoctoral fellow at Pennsylvania State University from 2001 to 2003. His awards include the Presidential Medal for Scientists of Korea (2019), the Insan Academic Award (2020), and the CJ Award of the Korean Society for Microbiology and Biotechnology (2023).

Talk Title: Integrating Infrastructure, Ecosystems, and Standards— The Korea National Biofoundry Initiative

Abstract: The Korea National Biofoundry, launched in 2025 as part of the National Synthetic Biology Strategy announced in 2022, represents a major step toward strengthening research hubs, establishing competitive biofoundry infrastructure, and fostering a sustainable ecosystem. The initiative progresses along two axes: building a centralized hub and cultivating an open ecosystem. The hub is designed to provide advanced infrastructure, automated Design-Build-Test-Learn (DBTL) workflows, digital management systems, and skilled manpower. It begins with a set of essential workflows and a ready-to-use microbial chassis bank, enabling applications in gene circuits, therapeutic microbes, metabolic bioconversion, and enzyme engineering. In parallel, the ecosystem, coordinated by the Korea Synthetic Biology Association, advances regulatory frameworks, social acceptance studies, workforce training, and



collaborative networks to ensure long-term sustainability. The initiative is guided by a public, open, cooperative, and standards-based (POCS) strategy. Public investment ensures non-exclusive development and equitable benefit-sharing; openness emphasizes transparency and data sharing; cooperation promotes cross-sector and global collaboration; and standards support interoperability and reproducibility across workflows and facilities. By integrating infrastructure with ecosystem building, the Korea National Biofoundry aims to bridge fundamental research and industrial application, reduce barriers to biodesign, and accelerate translational biotechnology. Its long-term vision is to nurture startups, expand innovation capacity, and establish Korea as an active contributor to the global biofoundry network and the growing bioeconomy.



STÉPHANE LEMAIRE, PHD

Director Biofoundry Sorbonne University, Chief Innovation Officer & Co-founder Biomemory, Directeur de Recherche CNRS, Department of Computational, Quantitative and Synthetic Biology, Sorbonne Université, Paris, France

Dr. Stéphane Lemaire, a recognized expert of synthetic biology, photosynthesis and microalgae, is the founder and Director of Sorbonne University Biofoundry and leader of the Paris Biofoundry consortium. This innovative infrastructure is dedicated to automated high-throughput bioengineering of microorganisms (bacteria, yeast, microalgae), mammalian cells and cell free systems. It aims at answering fundamental biological questions and creating artificial systems with broad biotechnological impact. He heads the Synthetic and Systems Biology of Microalgae research group at the Department of Computational, Quantitative and Synthetic Biology (CQSB) at Sorbonne University. Additionally, he is the Chief Innovation Officer and Co-founder of Biomemory, a pioneering start-up company aiming to revolutionize digital storage harnessing DNA as a sustainable, high-capacity storage medium.

Talk Title: Paris Biofoundry

Abstract: The Paris Biofoundry is a distributed research platform that unites the expertise of leading institutions in the Paris region, including Sorbonne and Paris-Saclay Universities, the Micalis and Curie Institutes, the Genopole cluster, and national research institutions including CNRS, INSERM, and INRAE. Its mission is to accelerate the development of synthetic biology by providing state-of-the-art facilities to design and test biological systems at unprecedented scales. The Paris Biofoundry also aims to be at the forefront of the bioconvergence revolution, integrating biological engineering with data science and artificial intelligence to address pressing global challenges. This distributed biofoundry, spread

Stéphane Lemaire / cont.

across four sites in the Paris region, provides laboratories and companies with access to cutting-edge technologies to accelerate fundamental, applied and translational research, as well as industrial development and innovation. The Paris Biofoundry is centered around high-throughput DNA assembly and microbial engineering, particularly focusing on bacteria, yeasts, and microalgae (Sorbonne Université), mammalian cell engineering (Institut Curie), cell-free systems (Institut Micalis), industrial scale-up and downstream processes (Genopole). By combining these capabilities, the Paris Biofoundry enables versatile applications for both academic and industrial research, driving innovation across diverse fields including health, energy, materials and the environment. Paris Biofoundry will also develop and distribute new tools, methods and processes to the community including novel technologies, standardized DNA parts as well as automated and Al-driven engineering methods.



BRIARDO LLORENTE, PHD

Chief Scientist, Group Leader, Associate Professor, Australian Genome Foundry, ARC Centre of Excellence in Synthetic Biology, School of Natural Sciences, Macquarie University, Australia

Briardo is the Chief Scientist of the Australian Genome Foundry (AGF), Group Leader at the Australian Research Council Centre of Excellence in Synthetic Biology (CoESB), and an Associate Professor at Macquarie University in Sydney, Australia. Briardo is interested in tackling major challenges through synthetic biology while pushing the boundaries of genomic, metabolic, and intercellular engineering. His team engages in diverse research areas, ranging from re-engineering symbiosis and genomes to enhancing biomanufacturing and developing improved crops and medicines. Before joining the AGF and CoESB, Briardo was a CSIRO Synthetic Biology Future Science Fellow. He also served as a Marie Curie Fellow and a Juan de la Cierva Fellow at Barcelona's CRAG and worked as a visiting researcher at the University of Aarhus in Denmark and the Salk Institute in California. Briardo completed his PhD at the INGEBI and the University of Buenos Aires, Argentina.

Talk Title: Synthetic Genomics: From Bacteria to Yeast and Plants

Abstract: The Australian Genome Foundry (AGF) is a state-of-the-art, robotics-accelerated synthetic biology facility at Macquarie University in Sydney, Australia. This talk will provide an overview of the AGF and showcase our recent advancements in synthetic genomics across bacteria, yeast, and plants.



CEDRIC MEYER, PHD CANDIDATE

Institute of Biochemical Engineering, University of Stuttgart

Cedric Meyer is a doctoral researcher at the Institute of Biochemical Engineering at the University of Stuttgart. His research interests are the study of biochemical reaction networks, systems metabolic engineering, and bioprocess development. His current research focuses on strain optimization by leveraging mechanistic models and machine learning as design tools. Cedric studied Technical Biology at the University of Stuttgart where he obtained his Bachelor's and Master's degree working on metabolic analysis of Arabidopsis thaliana mutants as well as on mechanistic models to deepen the systems level understanding of the cell death pathway apoptosis. Cedric seeks to use computational models to uncover knowledge gaps in the understanding of microbial production systems, while using these models to guide efficient bioprocess development.

Talk Title: Model guided design of E. coli strains for the heterologous production of dopamine

Abstract: For optimal flux towards the product, heterologous pathways must be ideally designed. The flux depends on the availability of metabolic resources, on the in vivo concentration of heterologous enzymes and on their processivity. While the expression of native enzymes is typically controlled by translation initiation, control can shift to translation elongation when using heterologous enzymes, e.g. under control of strong promoters. Then protein expression rate is not only determined by the growth dependent composition of the transcription and translation machinery but also specific to the codon sequence. Here, we apply a sequence specific mechanistic model of transcription and translation as a design tool to optimize the heterologous dopamine pathway in E. coli. The model estimates protein expression rates, identifies slow sequence parts that can be codon optimized and calculates the usage of metabolic resources for heterologous protein production. For model evaluation, strain variants that were previously generated by ribosomal binding site engineering were recreated in silico. Comparing model predictions to experimental measurements pointed to blind spots in the previous engineering strategy. By estimating protein concentrations while providing detailed mechanistic information this model lays the foundation for efficient optimization of the dopamine pathway.



WATARU MIZUNASHI, PHD

Deputy Senior Manager, Frontier & Open Innovation Division, Mitsubishi Chemical Corporation

Wataru Mizunashi is Deputy Senior Manager, Frontier & Open Innovation Division, Mitsubishi Chemical Corporation. He is also serving as Fellow, Technology and Innovation Strategy Center (TSC), New Energy and Industrial Technology Development Organization (NEDO), and Guest Professor Engineering Biology Research Center, Kobe University. He received his M.S. degree from Okayama University, and he joined to company. While working for the company, he was assigned as an invited researcher at the Laboratory of Fermentation Microbiology at the University of Tokyo and completed his Ph.D. at Okayama University in Industrial Microbiology. His interest is the commercialization of products using bioconversion, enzyme engineering, and metabolic engineering. He has been working in industry for over 30 years in R&D and Business creation in the fields of biotransformation and healthcare (Vice President at Mitsubishi Rayon America, General Manager of Biotechnology Laboratory at Mitsubishi Chemical Corporation, etc.). He is serving as a member of the International Advisory Council on Global Bioeconomy, and a member of the Global Future Council on Generative Biology and Bioeconomy initiative in the World Economic Forum.



LARS NIELSON, PHD

Professor, Chair of Biological Engineering at University of Queensland; Senior Group Leader, Australian Institute for Bioengineering & Nanotechnology (AIBN); Scientific Director, Novo Nordisk Foundation Center for Biosustainability, DTU, Denmark

Prof Nielsen is Professor and Chair of Biological Engineering at UQ, Senior Group Leader at the Australian Institute for Bioengineering & Nanotechnology (AIBN), and Scientific Director at the Novo Nordisk Foundation Center for Biosustainability, DTU, Denmark. At the Australian Institute for Bioengineering and Nanotechnology (AIBN), Prof Nielsen established a world class environment for a team of 50+ staff and students working in dedicated facilities for industrial biotechnology. Working with colleagues in Amyris, he led the establishment of a public Biofoundry at AIBN in 2016, now supported by Bioplatforms Australia as IDEA Bio. In 2015, he was awarded the prestigious Novo Nordisk Foundation Laureate Research Grant to establish a group at the NNF Center for Biosustainability (CFB) in Denmark. At CFB, he was Chief Scientific Officer during a renewal bid (2019-2021) and Chief Technology Officer during the Biofoundry establishment (2021-2023). He recently co-authored the successful NNF BRIGHT application (2025-2032), which continues the focus on sustainability and automated science through AI driven biofoundries. Professor Nielsen is the current Chair of the Global Biofoundry Association, a collaboration between 40+ biofoundries across the world.



STEPHAN NOACK, PHD

Jülich Biofoundry, Forschungszentrum Jülich GmbH

Stephan Noack is an experienced Bioprocess Engineer and, since 2010, Head of the "Quantitative Microbial Phenotyping" group at the IBG-1: Biotechnology, Forschungszentrum Jülich, Germany. His core expertise lies in developing and applying automation technologies for targeted and untargeted strain engineering, quantitative omics analytics for metabolic modeling, and lab-scale bioprocess development using tailor-made biocatalysts. After earning his Master's degree in Bioprocess Engineering from the Technical University of Dresden, he obtained his doctoral degree (Dr.-Ing.) from the University of Siegen in 2009. He subsequently worked as a postdoctoral fellow in "Fermentation Technology" at Forschungszentrum Jülich and served as a Visiting Scientist at the Novo Nordisk Foundation Center for Biosustainability in Denmark in 2014. Noack is co-manager of the "Jülich Biofoundry" and has coordinated several (inter)national projects with academic and industry partners, including the "AutoBioTech" innovation lab, the BioSC FocusLab "HyImPAct", and the Helmholtz Innovation Lab "MiBioLab". Noack is co-author in more than 100 publications and his scientific standing is reflected by appointments to the editorial boards of renowned journals, including Current Opinion in Biotechnology, Microbial Cell Factories, and Engineering in Life Sciences. For his contributions, he has received several awards, such as the BioSC Supervision Award (2019), the Labvolution Award (2019), the Innovation Plus Award of Forschungszentrum Jülich (2018), and the Karl-Schügerl Research Award of Biotechnology (2007).

Talk Title: Biotechnological pigment production using integrated strain and bioprocess development at the Jülich biofoundry

Abstract: Novel biotechnological production processes are expected to replace many of their petrochemical counterparts in the future, but the development of strains and bioprocesses is very labor-intensive. One notable example is the production of pigments for the textile industry, which often relies on by-products from fossil fuels. Indigoidin, a blue pigment, could be a sustainable alternative to conventional indigo if economically viable bioprocesses are developed. Recently, we established automated rational engineering workflows for the industrial organism Corynebacterium glutamicum on our AutoBioTech platform. This enables the flexible generation of strain libraries with plasmid-based modules to study the expression of gene variants for selected enzymes. The resulting libraries can be rapidly characterized using the Mini Pilot Plant technology, which is another integral part of the Jülich biofoundry. In this talk, I will present how we successfully integrated these technologies to create and test a novel library of indigoidine-producing C. glutamicum strains. Specifically, we created a DNA library with parts following the MoClo syntax to modulate the expression levels of relevant genes. After transforming these biobricks into C. glutamicum via automated electroporation, single clones from each combinatorial variant were picked and further characterized under controlled conditions in microbioreactors. Based on the resulting performance indicators, we selected the most promising indigoidine production strains to enter bioprocess development and an initial scale-up from microtiter plates to lab-scale bioreactors. This work demonstrates how standardized, miniaturized, and automated workflows lead to more efficient strain and bioprocess development and enable faster development cycles for novel bio-based value chains.



CHUEH LOO POH, PHD

Associate Professor, Director of NUS Biofoundry, Department of Biomedical Engineering, NUS Synthetic Biology for Clinical and Technological Innovation (SynCTI), National University of Singapore

Dr. Chueh Loo POH is an Associate Professor with the Department of Biomedical Engineering, College of Desing and Engineering, at National University of Singapore (NUS). He is Director of NUS Biofoundry and a Team PI at National Centre for Engineering Biology (NCEB), Singapore. He is also deputy director of SINERGY, Singapore consortium for Synthetic Biology. His research interests in Synthetic Biology focuses on reprogramming microbes for health and sustainability. He is the founding president of the Society of Synthetic Biology, Singapore (SynBioSG), vice-chair of the Global Biofoundry Alliance (GBA) steering committee and co-Editor-in-Chief of Wiley/IET Engineering Biology journal. He also serves as member in OECD Expert working group in Engineering Biology.

Talk Title: Data-driven solutions and innovation at Singapore Biofoundry at NUS

Abstract: The emergence of biofoundries which utilize automation, high-throughput equipment and software tools have enabled engineering biology at scale, allowing many designs to be built and tested in each Design-Built-Test-Learn (DBTL) cycle. This enables rapid prototyping of the desired engineered biological systems. However, the processes involved are resource intensive and can be inefficient. We still lack means to predict the performance of different biological designs well.

In recent years, there has been great interest in the use of machine learning / artificial intelligence (AI) in engineering biology to enable the engineering of biology to be more predictive, overcoming the resource intensive trial-and-error approach. The convergence of engineering biology, machine learning / Al and automation offers an exciting opportunity to develop novel "intelligent" technological platforms that could accelerate the engineering of biological systems and advance our understanding of the underlying biological processes and design principles. Ultimately, this could enable us to create engineering biology solutions that can tackle challenges (e.g., climate change, sustainability, and planetary health) more efficiently. However, data driven machine learning / AI requires massive amount of biodata to realize predictive models. To address this challenge, advancing biofoundries which is well poised for large data generation would be vital. In this talk, we will present an update on the development we have made at Singapore Biofoundry at NUS, including the development of data management system and biosensors enabled ultra-high throughput sorting systems.



SRIDHAR RAGHAVACHARI, PHD

Program Director, Biological Sciences Directorate at the National Science Foundation.

Dr. Sridhar Raghavachari is a Program Director in the Biological Sciences Directorate at the National Science Foundation. Since joining NSF in 2013, he has served in various capacities at NSF, initially managing research in sensory and motor neuroscience and various NSF programs under the BRAIN Initiative as well as the Midscale research infrastructure programs. He developed the NSF BioFoundry program and currently manages the four funded BioFoundries. Prior to coming to NSF, Dr. Raghavachari was on the faculty of the Department of Neurobiology at Duke University Medical Center, where his research was on developing mathematical models of synaptic plasticity and working memory.



DR. PAUL RATERRON

Program Director, National Science Foundation (NSF)

Dr. Raterron joined NSF in 2018 as a Program Director in the Geophysics Program. Since then, he has been involved in other programs and cross-directorate activities. He joined the Office of International Science and Engineering (OISE) in 2022 where he manages NSF Global Centers Program as well as several countries' portfolios. Prior to coming to NSF, Dr. Raterron had a 30-year academic career in France (Centre National de la Recherche Scientifique) and the U.S. (Stony Brook University and Brown University). He has extensive experience in the study of geologic materials at extreme conditions of pressure and temperature. His research work has implications for understanding the dynamics and seismic properties of Earth's deep interior.



GENE E. ROBINSON, PHD

Director, Carl R. Woese Institute for Genomic Biology (IGB)

Gene E. Robinson (Ph.D., Cornell University, 1986) joined the faculty of the University of Illinois Urbana-Champaign in 1989. He holds a University Swanlund Chair and Center for Advanced Study Professorship, is director of the Carl R. Woese Institute for Genomic Biology

Gene E. Robinson / cont.

(IGB), and former director of the University's Neuroscience Program. Robinson pioneered the application of genomics to the study of social behavior, has been honored with the Wolf Prize in Agriculture, and is a member of the American Academy of Arts & Sciences, National Academy of Sciences, National Academy of Medicine, and American Philosophical Society.



DAVID ROSS, PHD

Project Leader, NIST Living Measurement Systems Foundry

David Ross is a physicist and project leader at the National Institute of Standards and Technology, where he currently leads the Living Measurement Systems Foundry. David's current work focuses on the development of large-scale measurements and machine-learning approaches to enable more predictive engineering of biological systems. David received a B.S. in physics from Caltech in 1992 and a PhD in physics from the University of California, Irvine in 1996. After a postdoctoral stint at the École Normale Supérieure in Paris, David took a position as a postdoctoral fellow at the National Institute of Standards and Technology (NIST) in 1999. He has remained at NIST since and is now a senior scientist and project leader.

Talk Title: Biofoundries as Large-Scale Data Generation Centers: Reproducible, Meaningful Data to Solve the Protein Function Problem

Abstract: The success of AlphaFold2 and similar AI models in predicting protein structure from sequence has demonstrated the potential revolutionary impact of AI applied to biotechnology. A key ingredient in that success was the protein structure data in the PDB. So, many funders and researchers in the biotechnology space are exploring ways to create the "next PDB" that will enable AI models with similar revolutionary impact. However, the data in the PDB cost over \$10B and took over four decades to collect. Plus, that data's utility for training cutting-edge Al models was more of a fortunate accident rather than an intentional outcome. So, although we can use the PDB as an inspiration, we need new models for data generation to replicate its success and to enable future high-impact Bio-Al models (in less than 40 years). Because of the scale and reproducibility offered by modern laboratory automation, there is an opportunity for the growing network of biofoundries to play a significant role in the generation of future large Al-ready biological datasets. In this talk, we will discuss strategies for scale-up of Al-ready data generation across multiple biofoundries, drawing upon examples from a collaboration between NIST and The Align Foundation to collect large datasets to enable a solution to the Protein Function Problem. The key aspects of that strategy include: a clear specification of the AI prediction task that data will underpin, the use of shared laboratory automation



protocols and calibration standards to enable quantitatively reproducible measurements with distributed data collection at multiple biofoundries, and the development of standards for reporting on data quality.



MAX RYADNOV, PHD

NPL Fellow in Biometrology and Professor of Biophysics, Head, Engineering Biology, Director, Reference Biofoundary, National Physical Laboratory (UK)

Max leads Engineering Biology at NPL. He is an NPL Fellow in biometrology, Professor of biophysics and holds a PhD in Chemistry. In his role Max is responsible for pre-normative research for standardisation in biology delivered with global metrology organisations such as VAMAS where he chairs a technical working area supporting the industry uptake of life sciences innovations. Max has worked with over 100 companies at different TRLs, and collaborates extensively in the UK and internationally, with a substantial grant portfolio from UKRI, ISCF, EURAMET, STFC and industry. He has authored over 150 publications, two books in biodesign and is the editor of several book series. His work continues to promote science beyond the bench and is regularly covered in industry-oriented magazines and by the mainstream media.

Talk Title: Towards Engineering Biology Metrology and Standards

Abstract: Engineering principles applied to harness biology seed technologies accessing goods and products limited only by imagination. The extent to which the principles themselves can be harnessed are limited by the reproducibility of their application to biological systems and processes. An ultimate advantage of linking engineering and biology is that of traceability. Here paths between the two, being probed in the UK's National Physical Laboratory, with examples from research and industry are discussed.



MARIA SAVINO, PHD

Global Segment Development Manager, Beckman Coulter Life Sciences

Maria Savino holds a Ph.D. in Cellular and Molecular Biology complemented by a Master in Business Administration. She has been sales manager for biotechnology companies within an international scope for more than 10 years, and since she joined Beckman Coulter Life Sciences after the acquisition of Labcyte Inc. in 2019, she has occupied roles in marketing and business development. Today she's focused on driving biomanufacturing activity and developing a workflow solution showing the value of all Beckman solutions in this field.

Talk Title: Tools to Drive DBTL Efficiently, De-Risk Scale-Up, and Prioritize High-Quality Data (Enabling smarter biomanufacturing decisions through automation, precision, and robust data integrity)

Abstract: Efficient execution of the Design-Build-Test-Learn (DBTL) cycle is essential for accelerating biomanufacturing and reducing risks during scale-up. Key enablers include automation of DNA assembly, microbial transformation, and colony selection, as well as high-throughput strain screening and real-time data integration. Technologies such as acoustic liquid handling, flow cytometry, and microbioreactors support precise and scalable workflows. Advanced scheduling and data management systems ensure reproducibility and traceability across iterative cycles. Together, these tools streamline development, improve decision-making, and help bridge the gap between lab-scale innovation and industrial-scale production.



DR. CLEMENT SCIPION

Scientist, Biotransformation and Engineering, A*STAR Singapore Institute of Food and Biotechnology Innovation (A*STAR SIFBI)

Clement Scipion is a Scientist at A*STAR's Singapore Institute of Food and Biotechnology Innovation (SIFBI), where he contributes to the development of walk-away biofoundry automation and enzyme engineering. His research focuses on accelerating metabolic engineering using medium- to high-throughput robotic systems, data-driven design, and Al-guided enzyme optimization. Clement holds an M.Eng. from École Centrale Marseille, a Ph.D. from the National University of Singapore, and completed postdoctoral training at the University of Pennsylvania. Prior to joining SIFBI, he worked in biotechnology start-ups.

Talk Title: Towards Walk-Away Automation: Engineering Terpene Synthases with the SPARROW Biofoundry



Abstract: The SPARROW biofoundry (SIFBI Parallel Robotic Workstation) is designed for fully integrated, walk-away automation of synthetic biology workflows. From DNA assembly to microbial production and metabolite analysis, our goal is to eliminate manual intervention, enabling faster and more reproducible engineering cycles. SPARROW has been deployed to scale enzyme engineering efforts, notably in the production of high-value terpenes. In our latest project, we cloned and screened 228 mutants of Citrus sinensis limonene synthase (tCsLS) using SPARROW, leading to the identification of a high-performing mutant (Q8K). Under optimized conditions, this variant produced the highest (+)-limonene titer reported to date (4.9 g/L). This work demonstrates how modular automation, mediumto-high-throughput screening, and data-driven design can accelerate both discovery and scale-up. Looking ahead, we aim to incorporate Al-guided mutagenesis and real-time analytics to further streamline the design-build-test-learn loop.



WILL SERBER

VP and General Manager, Automation, Ginkgo Bioworks

Will Serber is General Manager of Automation at Ginkgo Bioworks and leads a team of ~70 people across commercial, scientific, and engineering disciplines. Together, they are responsible for designing, developing, and commercializing new automation technologies. Will came to Ginkgo via Zymergen, which he joined early enough to help grow from 4 to ~1000 employees over 10 years. He led the group that created the proprietary modular automation technologies currently being offered by Ginkgo's Automation Business Unit (RACs & Catalyst Software). He has degrees from Columbia University and Princeton University in astrophysics.

Talk Title: The future of Biofoundries in the world of AI

Abstract: Ginkgo Bioworks has spent over a decade building one of the world's most automated biofoundries. Today, we're asking: how does the model change when Al isn't just an add-on, but a core collaborator? This talk will explore how agent-based interfaces and closed-loop capabilities are beginning to reshape not only how workflows are executed, but how scientific questions are asked and answered. By combining flexible and scalable automation hardware, constraint-based scheduling, and Al agents capable of planning, monitoring, and interpreting scientific experiments, we're creating systems that transform the usefulness of automation and the potential of the biofoundry for scientific discovery.



KRISTEN SHELDON

Senior Laboratory Technologist, Boston University

Kristen Sheldon is an experienced molecular biologist and synthetic biology researcher focused on integrating automation and high-throughput genomics into complex experimental workflows. At Boston University's DAMP Lab, she designs and implements robotic pipelines for molecular cloning and next-generation sequencing, enabling rapid microbial engineering and genome analysis. Her work incorporates scalable molecular protocols, automated liquid handling, and streamlined data generation to accelerate discovery. Prior to joining the DAMP Lab, Kristen contributed to large-scale COVID-19 diagnostics at BU, supporting high-throughput testing during the height of the pandemic

Talk Title: Engineering Biology at Scale: From Concept to Function in an Academic Biofoundry

Abstract: The DAMP Lab is a synthetic biology core facility at Boston University advancing high-throughput molecular workflows, automation, and next-generation sequencing. Its mission is to equip researchers with scalable, reproducible tools for designing, building, and analyzing complex biological systems. Over the past year, the lab has advanced projects in microbial engineering, clinical assay development, and functional variant screening, leveraging integrated robotic platforms and genomics pipelines. Operating within an academic environment presents unique technical, cultural, and financial challenges alongside opportunities for collaboration. This presentation will highlight the lab's capabilities, showcase representative projects, and share key lessons in managing and evolving a cutting-edge synthetic biology core.



VOLKER SIEBER, PHD

Chair, Professor of Chemistry of Biogenic ResourcesProfessor, SynBiofoundryTUM, TU Muenchen

Volker Sieber studied chemistry at the University of Bayreuth and the University of Delaware. After obtaining his doctorate, he conducted postdoctoral research at the California Institute of Technology in the lab of Prof. Frances Arnold. Between 2001 and 2008, he held several positions in the chemical industry, including roles at Degussa and Süd-Chemie. Since late 2008, he has served as a full professor at TUM. He is the Founding Rector of the TUM Campus Straubing for Biotechnology and Sustainability, where TUM concentrates its research and teaching in the field of bioeconomy. Starting in 2009 he built up an institute branch of the Fraunhofer Society on the topic of bio- chemo- and electrocatalysis. Prof. Sieber has been a founding member of the Bioeconomy Council for the Bavarian government and until this year served as the first spokesperson for the Bavarian Innovation Cluster for Industrial



Biotechnology. In 2017 he initiated the Global Bioeconomy Alliance, of which he is currently the chairman. He is Honorary Professor of the University of Queensland since 2017. Volker Sieber's research focuses on designing and developing synthetic enzyme cascades, also in combination with chemical catalysis for the sustainable production of chemicals and feed compounds from biomass and CO2. Notable examples of his work include the development of a four-enzyme, ATP-free glycolysis pathway and the production of amino acids from methanol. He also explores the use of non-natural cofactors and engineers enzymes to better utilize these novel systems. As part of the TUM International Future Lab (REDEFINE H2), his research group achieved to produce green hydrogen from biogenic materials such as sugars using engineered hydrogenases. In addition, his lab develops methodologies in microfluidic-based ultra-high-throughput (UHT) screening, synthetic biology tools for protein expression, metabolic engineering approaches for non-model microorganisms as well as novel biogenic polymers to reduce microplastics accumulation.

Talk Title: SynBiofoundry@TUM - Synthetic Biology for Sustainability and Clean Tech

Abstract: The SynBiofoundry@TUM is the synthetic biology platform at the Technical University of Munich, purpose-built to accelerate the design-buildtest-learn (DBTL) cycle in metabolic engineering, enzyme engineering, and cell factory development with a focus on sustainability and clean tech processes. Leveraging state-of-the-art robotics, high-throughput analytics, and advanced computational design, the facility enables rapid prototyping and systematic optimization of engineered biological systems. Its integration with TUM's dedicated internal and via partner available upscaling facilities of a multipurpose pilot plant (up to 30 m3), it provides a seamless pipeline from microscale strain development to bioreactor validation, ensuring that promising concepts can be efficiently translated into industrially relevant processes. Beyond technical capabilities, the SynBiofoundry@TUM is embedded in TUM's strong innovation ecosystem, actively supporting venture creation and entrepreneurial development. Located close to Munich—one of Europe's leading hotspots for biotechnology startups—it acts as a catalyst for transforming cutting-edge synthetic biology research into viable, scalable, and investment-ready solutions. This talk will present recent development examples, outline the core technological competencies of the SynBiofoundry@TUM, its role within the Germany's biomanufacturing terface of academic research, landscape, and its unique position industrial application, and str

NILMANI SINGH, PHD

Automation Engineer, NSF iBioFoundry, Institute for Genomic Biology, University of Illinois Urbana-Champaign (UIUC)

Dr Nilmani Singh is an Automation Engineer at the NSF iBioFoundry at the University of Illinois Urbana-Champaign (UIUC). His work focuses on designing and implementing automation to advance synthetic biology, protein engineering, and metabolic engineering, with the broader goal of developing a robust, end-to-end autonomous biofoundry platform. He has developed automation workflows for diverse applications, including plasmid assembly, machine learning-

Nilmani Singh / cont.

guided protein engineering, and natural product discovery. His recent work integrated AI/ML tools with biofoundry to develop an autonomous enzyme engineering platform. This platform requires only an input protein sequence and a quantifiable way to measure fitness and can be applied to engineer a wide array of proteins. He has played a central role in the conceptualization, design, and construction of the NSF iBioFoundry and is leading efforts to establish core biofoundry workflows and services to be offered to the broader research community as part of the iBioFoundry user program. A major focus of his work at the NSF iBioFoundry is integrating emerging AI/ML tools with robotics and automation to create robust automated pipelines for the advancement of synthetic biology. He holds a Ph.D. in Cell and Developmental Biology from UIUC, where his research explored protein-lipid interactions using single-molecule microscopy, applied probabilistic modeling to predict such interactions, and investigated the regulation of muscle regeneration by cytokines.



MARKO STORCH, PHD

Director Biofoundry Operations, Co-director Imperial Drug Discovery Hub, London Biofoundry, Imperial College London

Following single molecule studies of enzymes responsible for successful cell division during his PhD in biophysics at the Max Planck Institute in Dresden, Marko joined the Synthetic Biology Centre at Imperial College London as research fellow. At Imperial he developed highly accurate and automated DNA assembly methods to overcome bottlenecks in engineering biology by constructing large libraries of plasmids encoding metabolic pathways and genetic circuits. His projects also included work on directed evolution systems and tech-transfer.

In 2019, he joined the London Biofoundry as Head of Synthetic Biology and Automation leading on the integration of workflows, platform expansion and Covid-19 rapid response projects in diagnostics and sequencing. Since 2024 Marko is Director of Biofoundry Operations overseeing a project portfolio including platform development, strain engineering campaigns, consortia projects and work with start-ups and industry partners. He supports the Imperial Drug Discovery Hub as Co-director leveraging biofoundry capabilities for small molecule screens in targeted and phenotypic assays.

Marko is interested in collaboratively advancing high-throughput engineering biology methods for molecules and cells, creating integrated and highly productive biofoundry platforms. He also supports entrepreneurship opportunities in biofoundry ecosystems to accelerate research progress towards real-world impact.

Talk Title: London Biofoundry Update

Abstract: We will share updates on platform and capability development, including DNA assembly, strain engineering and scale-up workflows. We are also interested in new collaborations to develop integrated multi-omics approaches supporting strain development and adaptive laboratory evolution workflows.

Following successful automated genetic engineering campaigns for bacteria and yeast, the team now works on automating tissue culturebased assays. We are testing a beta version of a novel integrated cell



culture automation system in collaboration with the manufacturer to feed into high-throughput microscopy assays and omics platforms.

Additionally, we'll share an overview of how our biofoundry enables and supports an ecosystem of ambitious projects in human functional genomics, antimicrobial resistance research, sustainable protein development through the new Bezos Centre at Imperial and compound screening at the Imperial Drug Discovery Hub.

We are especially excited to advance biofoundry capabilities and adoption with the GBA through new international initiatives including the flagship NSF Global Centre for Biofoundry applications program and a new Engineering Biology collaboration between communities in the UK and South Korea.



DR. HILLE TEKOTTE

Senior Product Applications Specialist, Thermo Fisher Scientific

Dr. Tekotte is a proficient biologist with over 20 years of experience in cutting-edge research laboratories. Throughout her career, she has worked with a variety of model organisms and mastered numerous scientific protocols, excelling in cell biology, molecular biology, and synthetic biology. Recognizing the importance of laboratory automation, Dr. Tekotte became the Manager at the Edinburgh Genome Foundry, where she was instrumental in automating synthetic biology workflows. Eager to expand these approaches, Dr. Tekotte joined Thermo Fisher Scientific as an Applications Specialist, focusing on developing advanced, automated platforms. She specializes in translating complex laboratory protocols into automated workflows, enhancing efficiency and innovation in drug discovery, biologics development, analytical characterization, and synthetic biology.

Talk Title: Innovative Lab Automation Technologies Advancing Synthetic Biology

Abstract: Thermo Scientific's innovative lab automation solutions are transforming the landscape of synthetic biology. Discover how our state-of-the-art systems, featuring integrated robotics and smart workflow scheduling software, enhance assay consistency and quality while significantly boosting testing throughput by eliminating manual input and process deviations. Experience the power of end-to-end robotic assay execution with dynamic, data-driven workflows that offer real-time, bi-directional connectivity with your existing technology stack, including LIMS, eLNs, and ML/Al tools. These innovations streamline the Design-Build-Test-Learn cycles essential for automated synthetic biology foundries. By harnessing the latest technological advancements, researchers are enabled to break new ground in scientific discovery. Our cutting-edge automation tools are driving progress in synthetic biology and beyond.



VALLO VARIK, PHD

Director of the Estonian Biofoundry, Faculty of Science and Technology, Institute of Bioengineering,
Estonian Biofoundry, University of Tartu

Dr. Tufvegren Borgstrom completed her PhD in Applied Microbiology working with yeast for production of bioethanol from hemicellulosic biomass at Lund University, Sweden, in 2021. She then joined the Mahadevan lab at the University of Toronto, Canada, to work on metabolic engineering for production of value-added compounds from sustainable substrate streams. She soon started doing more lab and project management work, including project management of projects supported by Genome Canada, Ontario Genomics, and DARPA. She has experience in writing grant applications, interacting with both industry and government stakeholders, and managing research work.

Talk Title: From strain engineering to drug discovery

Abstract: At the Estonian Biofoundry, we have started three pilot workflows. First, we use randomized strain engineering to adjust cofactor use in key metabolic steps of an oleaginous yeast, with the aim of easing redox bottlenecks and improving carbon efficiency. Second, we are building a cell-free prototyping platform to quickly screen genetic parts and multi-gene pathways, starting in a model organism and then moving the same approach to gas-fermenting microbes. Third, we are advancing protein engineering to broaden catalytic functions that support bioprocess intensification and biomass valorization. In parallel, we are launching an early-discovery track in drug development with two broad paths. One path builds a platform to identify, validate, and optimize RNA-dependent RNA polymerase variants for self- or trans-amplifying RNA technologies. The other path runs microscopy-based screens for antimicrobials against intracellular pathogens, with a focus on host-modulating mechanisms. Both paths rely on machinelearning pipelines for feature extraction, classification, and exploration of the design space. Together, these pilots build local expertise in automated protein and strain engineering, speed up part and pathway prototyping, and position the Biofoundry to deliver flexible services—from industrial biotechnology to early therapeutic discovery—while we train personnel and create reusable methods for the regional community.



IAN WHEELDON, PHD

Professor Chemical and Environmental Engineering, Co-Director of the ExFAB Biofoundry,
Director of the Center for Industrial Biotechnology, University of California, Riverside

Dr. Wheeldon is a Professor, the Director of the Center for Industrial Biotechnology at the University of California, Riverside, and the co-Director of the ExFAB Biofoundry. He is He



received his PhD in Chemical Engineering from Columbia University in 2009 and completed two years of postdoctoral training at Harvard Medical School and the Wyss Institute for Biologically Inspired Engineering at Harvard University. Dr. Wheeldon received a Master's of Applied Science from the Royal Military College of Canada (2003), and a Bachelor's of Applied Science (1999) from Queen's University, Canada. His research is focused on synthetic biology for chemical synthesis.

Talk Title: The ExFAB Biofoundry: Accelerating Biotechnology from Extreme & Exceptional Microorganisms

Abstract: Biofoundries enable breakthroughs in biological understanding and prototyping by eliminating throughput bottlenecks – namely by automating biological "unit operations" that researchers would otherwise perform in low-throughput and at high-expense at the bench. While countless parts, circuits, and workflows have emerged from the designbuild-test-learn cycle, many biofoundries typically handle microorganisms that are domesticated—easy to grow and that proliferate under laboratory conditions. To realize the promise of synthetic biology, there is a critical need for user platforms that are dedicated to a new generation of synthetic biology, one that focuses on discovering, phenotyping, and engineering new environmental isolates, microbial communities, and microbes with extreme phenotypes. With this motivation, a collaborative team from UC-Santa Barbara, UC-Riverside, and CalPoly-Pomona have established the BioFoundry for Extreme & Exceptional Fungi, Archaea and Bacteria (Ex-FAB). ExFAB's uniqueness lies in its focus on accommodating nature's more unusual microorganisms - what we refer to as "extreme" in that they do not conform to standard growth habits and culture conditions, and "exceptional" in that they defy our current understanding of biology.



LANCE WELLS, PHD

Professor of Biochemistry & Molecular Biology, Associate Director of the Complex Carbohydrate Research Center, PI of BioF:GREAT, Georgia Institute of Technology

Dr. Lance Wells received his B.S. in Chemistry from the Georgia Institute of Technology and his Ph.D. In Biochemistry & Molecular Biology from the Emory School of Medicine. Following an NIH F32 supported Post-Doctoral fellowship in Biological Chemistry at the Johns Hopkins School of Medicine, he joined the Complex Carbohydrate Research Center (CCRC) and the Department of Biochemistry & Moleculer Biology at the University of Georgia as a tenure-track assistant Professor in 2003. He has risen through the ranks and is currently a Distinguished Research Professor, a Georgia Research Alliance Endowed Distinguished Investigator, and the Associate Director of the CCRC. Dr. Wells has graduated 20 Ph.D. students and published over 150 manuscripts that have been cited more than 16,500 times (h-index: 64). His laboratory has been continuously extramurally funded included grants from the NIH, American Heart Association, Bill and Melinda Gates Foundation, W.M. Keck Foundation, and most recently as the PI of an \$18 million BioFoundry

Lance Wells / cont.

focused on glycobiology. He has served on NIH study section, serves on editorial boards of multiple journals, has served as a guest editor for special issues for multiple journals, has been an ASBMB Special Meeting organizer and theme organizer of the Annual meeting, has been a founder of two start-up companies, was the 2024 President of the Society for Glycobiology, and is the 2027 Chair of the Gordon Research Conference on Glycobiology.

Talk Title: BioF:GREAT, Democratizing Glycobiology

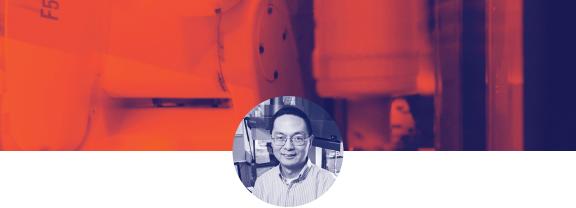
Abstract: BioF:GREAT aims to resolve the issue that glycans, despite being one of the 4 basic building blocks of life and present in all living organisms, are undertaught in the classroom and understudied at the research bench. BioF:GREAT will take major steps towards addressing these deficiencies by developing new research, technologies, and instructional experiences that span across the tree of life to democratize alycoscience and bring it into mainstream life science research and education. By providing equitable access to advanced infrastructure and resources in glycoscience through its user facility, BioF:GREAT will advance scientific inquiry and education in biosciences across all kingdoms of life. BioF:GREAT's synergistic efforts in research, technology development, platform sharing, teaching, and training will lead to discoveries and deliverables that catalyze commercial applications in bioenergy, bioengineering, biomaterials, and biomedicine and have farreaching impacts on academic, government, and industry ecosystems as well as catalyzing new instructional experiences and startup development.



KEN-ICHI YOSHIDA, PHD

Professor of Applied Microbiology, Kobe University

After obtaining a Master of Science in Agriculture at Kyoto University in 1989, he got an Assistant professor position at Fukuyama University in 1990. He was given a PhD at Kyoto University in 1993 and served as a Postdoc fellow at INRA, France, in 1996-97. He moved to Kobe University in 2004 as an Associate professor and became a Full professor of Applied Microbiology in 2009. He received the prize for Encouragement of Young Scientists (2002) and twice for Excellent papers from the Japan Society for Bioscience, Biotechnology, and Agrochemistry (2008 and 2014). He received the Fermentation and Metabolism Research Award (2006) from the Japan Bioindustry Association (JBA) and a prize from the NAGASE Science Technology Foundation (2009). He received the Hyogo Science Prize (2023). He has served in the Research Promotion Bureau in the Ministry of Education, Culture, Sports, Science and Technology, Japan (MEXT) (2005-2007). He has acted as an honourable FEMS Ambassador since 2019 to date. He served at Kobe University Brussels European Centre as one of the directors (2013-2019 and 2022-2023) and as Executive Director of the Centre for EU Academic Collaboration/Office for International Strategic Planning, Head of the Europe & Africa Division (2019 to 2023). Currently, he is Deputy Dean of the Graduate School of Science, technology and Innovation (2024-date).



HUIMIN ZHAO, PHD

Departments of Chemical and Biomolecular Engineering, Chemistry, Biochemistry, and Bioengineering, Carl R. Woese Institute for Genomic Biology, DOE Center for Advanced Bioenergy and Bioproducts Innovation, NSF Molecule Maker Lab Institute, NSF iBioFoundry, NSF Global Center for Biofoundry Applications; University of Illinois Urbana-Champaign

Dr. Huimin Zhao is the Steven L. Miller Chair of chemical and biomolecular engineering and professor of chemistry, biochemistry, and bioengineering at the University of Illinois Urbana-Champaian (UIUC), director of NSF AI Institute for Molecule Synthesis (moleculemaker. org), NSF iBioFoundry (ibiofoundry.illinois.edu), and NSF Global Center for Biofoundry Applications, and Editor in Chief of ACS Synthetic Biology. He received his B.S. degree in Biology from the University of Science and Technology of China in 1992 and his Ph.D. degree in Chemistry from the California Institute of Technology in 1998 under the guidance of Nobel Laureate Dr. Frances Arnold. Prior to joining UIUC in 2000, he was a project leader at the Industrial Biotechnology Laboratory of the Dow Chemical Company. He was promoted to full professor in 2008. Dr. Zhao has authored and co-authored over 460 research articles and over 30 issued and pending patent applications. In addition, he has given over 540 plenary, keynote, or invited lectures. Thirty-eight (38) of his former graduate students and postdocs became professors or principal investigators around the world. Dr. Zhao received numerous research and teaching awards and honors such as SIMB Charles Scott Award, AIChE Daniel I.C. Wang Award, AIChE FP&B Division Award, ECI Enzyme Engineering Award, ACS Marvin Johnson Award, SIMB Charles Thom Award, and NSF CAREER Award. His primary research interests are in the development and applications of synthetic biology, machine learning, and laboratory automation tools to address society's most daunting challenges in health, energy, and sustainability.

Talk Title: NSF iBioFoundry for Basic and Applied Biology

Abstract: Naturally occurring or engineered biological systems such as protein machines, genetic circuits, and microbial cell factories have promised to solve many grand challenges of modern society. However, the traditional research and development process is slow, expensive, and inconsistent, representing a major challenge in basic and applied biological research. To address this challenge, we have established a next-generation biofoundry at the University of Illinois Urbana-Champaign—Illinois BioFoundry (iBioFoundry) with funding support from NSF. This iBioFoundry is dedicated to developing new capabilities for biofoundries through an integrated and synergistic in-house research program and community-engaged program (user program) and providing the broader research community with unrestricted access to the research resources, training, education, and outreach activities developed in the center. Our overarching goal is to develop a cloud biofoundry that integrates synthetic biology, artificial intelligence/machine learning (AI/ML), and laboratory automation to democratize basic and applied biological research. Such biofoundry will revolutionize biology and the biotechnology industry similar to what computers did to computing and the microelectronics industry.



