Organized by Cambridge Healthtech Institute

Celebrating 25 Years

PepTalk

The Protein Science and Production Week

January 19-22, 2026
Hilton Bayfront San Diego, CA + Virtual

2026 PROGRAMS

- EXPRESSION & PRODUCTION
- HIGHER THROUGHPUT & INNOVATION
- ANALYTICS & PREFORMULATION
- PEPTIDE EXPRESSION & DEVELOPMENT - NEW
- ANTIBODY ENGINEERING & THERAPEUTICS

KEYNOTE PANEL

The PepTalk Legacy: 25 Years of Science, and the Next Era of Protein Research

MODERATOR:
Dominic Esposito, PhD
Senior Director, Protein Sciences, Septerna

PANELISTS:
Henry C. Chiou, PhD
Thermo Fisher Scientific (Retired)

Nicola Burgess-Brown, PhD
Structural Genomics Consortium

Ian Hunt, PhD
Novartis Pharma AG

Deborah Moore-Lai, PhD
ProFound Therapeutics

David W. Wood, PhD
Ohio State University

RESERVE YOUR SPOT TODAY!

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Includes Access to
BioLogic SUMMIT 2026
Harnessing ML/AI for the Design & Optimization of Biotherapeutics

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ABOUT THE EVENT

Join a vibrant community of scientists, trailblazers, and industry leaders at PepTalk 2026, as as we mark 25 years of accelerating breakthroughs in biotherapeutic discovery and development. Renowned as one of the most influential events in protein science, PepTalk where fresh ideas ignite, collaborations flourish, and next-generation solutions take shape.

This year's expanded agenda features symposia and conference tracks covering protein expression, production platforms, lab automation for higher throughput, analytical characterization and preformulation strategies for novel modalities, antibody discovery and development, and new this year - expression and development therapeutic peptides and miniproteins.

Gain insights from expert speakers, engage with a dedicated community, and leave with tools and strategies to move research forward. Experience four days of focused learning, expert-led sessions, poster presentations, keynotes, roundtables, panel discussions, exhibitions, and networking opportunities.

CONFERENCE PROGRAMS feature keynote presentations, case studies, and new unpublished data from influential leaders in academia and industry.

SYMPOSIA align with the overarching pipeline theme, are led by esteemed researchers and thought leaders, and will offer an invaluable opportunity to delve into technical nuances often overlooked, and feature interactive discussions, panel talks, and podium presentations.

BUZZ SESSION BREAKOUT GROUPS initiate discussions about current research and trends.

EXHIBIT HALL provides face-to-face networking with technology & service providers ready to share their latest products and services.

POSTER SESSIONS showcase cutting-edge, ongoing research—over 100 posters will be presented!

MEET UPS create opportunities for attendees to broaden their network, expand skillsets, and meet fellow attendees at dedicated gatherings for Young Scientists, Women-in-Science, Speed Networking, Linked-In Skills Workshop etc.

ON-DEMAND ARCHIVE of presentations to access on your own time.

PepTalk Celebrating 25 Years

JANUARY 19-22, 2026 | HILTON BAYFRONT SAN DIEGO, CA + VIRTUAL

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#CHIPepTalk

CONFERENCE PROGRAMS

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SYMPOSIUM: (Re)Discovering Protein Expression Platforms

- Recombinant Protein Production - Part 1
- Recombinant Protein Production - Part 2

HIGHER THROUGHPUT & INNOVATION

SYMPOSIUM: Predictive Protein Production

- Automation in Protein Discovery
- Advanced Tools for Purification and Quality

ANALYTICS & PREFORMULATION

SYMPOSIUM: AI/ML Approaches in Immunogenicity Prediction

- Analytical Strategies for Novel Biologics
- Biotherapeutics Aggregation and Preformulation Strategies

PEPTIDE EXPRESSION & DEVELOPMENT NEW

SYMPOSIUM: Peptide Drug Hunting 101: The Life of a Peptide

- Peptide Targets: Discovery, Expression, and Validation
- Peptide Therapeutics: Accelerating Discovery and Development

ANTIBODY ENGINEERING & THERAPEUTICS

SYMPOSIUM: Engineering Multispecifics: Oncology and Beyond

- Novel Formats and New Antibody Approaches
- Advancing Multispecific Engineering to the Clinic

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CONFERENCE PROGRAMS

Bridging Biotherapeutic Discovery and Development

	JANUARY 19 | SYMPOSIA	JANUARY 20-21	JANUARY 21-22
PROTEIN EXPRESSION & PRODUCTION	(Re)Discovering Expression Platforms	Recombinant Protein Production Part 1	Recombinant Protein Production Part 2
HIGHER THROUGHPUT & INNOVATION	Predictive Protein Production	Automation in Protein Discovery	Advanced Tools for Purification and Quality
ANALYTICS & PREFORMULATION	AI/ML Approaches in Immunogenicity Prediction	Analytical Strategies for Novel Biologics	Biotherapeutics Aggregation and Preformulation Strategies
PEPTIDE EXPRESSION & DEVELOPMENT - NEW	Peptide Drug Hunting 101: The Life of a Peptide	Peptide Targets: Discovery Expression and Validation	Peptide Therapeutics: Accelerating Discovery and Development
ANTIBODY ENGINEERING & THERAPEUTICS	Engineering Multispecifics: Oncology and Beyond	Novel Formats and New Antibody Approaches	Advancing Multispecific Engineering to theClinic

BuzZ sessions

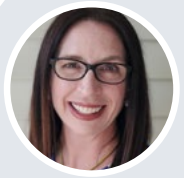
PepTalk BuzZ Sessions are focused, stimulating discussions in which delegates discuss important and interesting topics related to upstream protein expression and production through downstream scale-up and manufacturing. These are moderated discussions with brainstorming and interactive problem-solving among scientists from diverse areas who share a common interest in the discussion topic.
Continue to check the event website for detailed discussion topics and moderators.

PepTalk
The Protein Science and Production Week

PLENARY SESSIONS

TUESDAY - 4:30-5:40 PM

Trends and Innovation Driving the Future of Biotherapeutics



Deborah Moore-Lai, PhD

Yves Fomekong Nanfack, PhD

Lieza Danan, PhD

Aline de Almeida Oliveira, PhD

4:30 Welcome Remarks
Mimi Langley, Executive Director, Conferences, Cambridge Healthtech Institute

4:35 Chairperson's Remarks
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 – 4:50 Building an AI-Native Platform for Accelerated Biologics Discovery at Sanofi
Yves Fomekong Nanfack, PhD, Executive Director & Head, End-to-End AI Foundations, Large Molecules Research Platform, Sanofi

4:50 – 5:00 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing
Lieza Danan, PhD, Founder & CEO, LiVeritas

5:00 – 5:10 Technological Trends Shaping the Landscape of Biopharmaceuticals
Aline de Almeida Oliveira, PhD, Competitive Intelligence Advisor (AICOM), Bio-Manguinhos/Fiocruz, Brazil

5:10 – 5:40 PLENARY FIRESIDE CHAT
Moderator: John K. Kawooya, PhD, Private Consultant, Robotics-Plate-Based-Ultra-HT Biologics Purification
Panelists:
Yves Fomekong Nanfack, PhD, Executive Director & Head, End-to-End AI Foundations, Large Molecules Research Platform, Sanofi
Lieza Danan, PhD, Founder & CEO, LiVeritas
Aline de Almeida Oliveira, PhD, Competitive Intelligence Advisor (AICOM), Bio-Manguinhos/Fiocruz, Brazil

THURSDAY - 8:25 - 9:30 AM

8:25 Welcome Remarks
Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

8:30 Plenary Keynote Introduction
Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 – 9:30 PLENARY FIRESIDE CHAT: End-to-End *in silico*-Designed Biologics
Moderator:
Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.
Panelists:
Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)
Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

Andrew Nixon, PhD

Stephanie Truhlar, PhD

Charlotte M. Deane, PhD

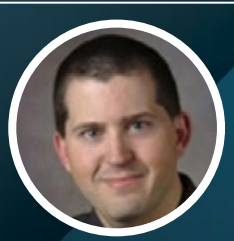
Garegin Papoian, PhD

Celebrating 25 Years

PEPTALK KEYNOTE PANEL

WEDNESDAY - 1:10-1:45 PM

MODERATOR:



DOMINIC ESPOSITO, PHD
Senior Director, Protein Sciences, Septerna

The PepTalk Legacy:

25 Years of Science, and the Next Era of Protein Research

Join us for a keynote panel as we celebrate 25 years of PepTalk - a gathering place for the global protein science community. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

PANELISTS

HENRY C. CHIOU, PHD
Senior Director General Manager, Biosciences, Thermo Fisher Scientific (Recently Retired)

NICOLA BURGESS-BROWN, PHD
Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium

IAN HUNT, PHD
Global Head of Scientific Engagement Strategy, Novartis Pharma AG

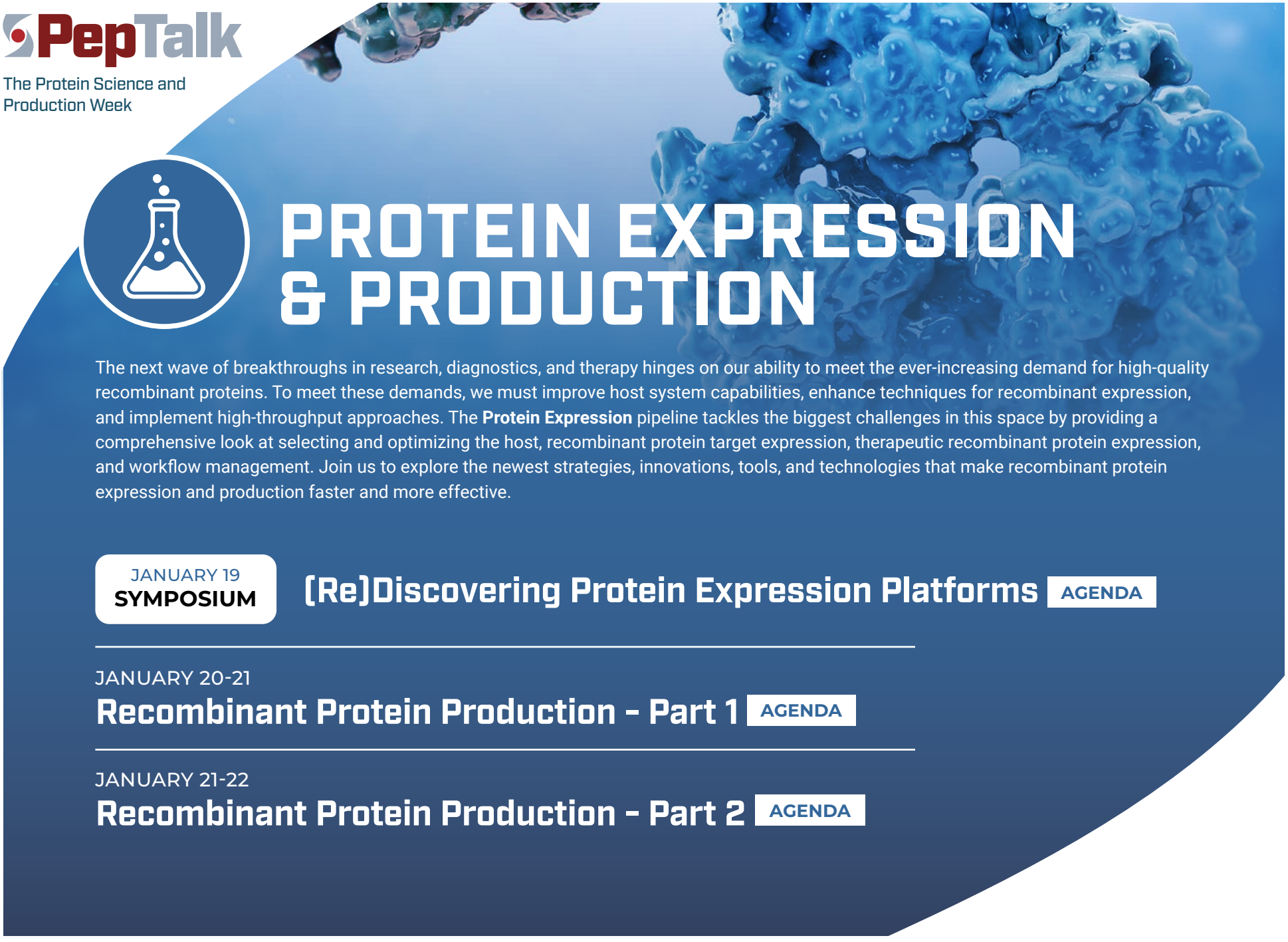
DEBORAH MOORE-LAI, PHD
Vice President, Protein Sciences, ProFound Therapeutics

DAVID W. WOOD, PHD
Professor, Chemical & Biomolecular Engineering, Ohio State University

Join us in celebrating our 25-year milestone at the cake cutting in the Exhibit Hall immediately following the Keynote Panel, 1:45–2:15PM

PepTalk

The Protein Science and Production Week



PROTEIN EXPRESSION & PRODUCTION

The next wave of breakthroughs in research, diagnostics, and therapy hinges on our ability to meet the ever-increasing demand for high-quality recombinant proteins. To meet these demands, we must improve host system capabilities, enhance techniques for recombinant expression, and implement high-throughput approaches. The **Protein Expression** pipeline tackles the biggest challenges in this space by providing a comprehensive look at selecting and optimizing the host, recombinant protein target expression, therapeutic recombinant protein expression, and workflow management. Join us to explore the newest strategies, innovations, tools, and technologies that make recombinant protein expression and production faster and more effective.

JANUARY 19
SYMPOSIUM

(Re)Discovering Protein Expression Platforms AGENDA

JANUARY 20-21

Recombinant Protein Production – Part 1 AGENDA

JANUARY 21-22

Recombinant Protein Production – Part 2 AGENDA

(Re)Discovering Protein Expression Platforms

Roadmaps for Rapid, Reliable, Resource-Efficient Recombinant Protein Production

SYMPOSIUM

EXPRESSION & PRODUCTION

MONDAY, JANUARY 19

8:00 am Registration and Morning Coffee

THE SCIENCE OF THE HOST SELECTION PROCESS

8:45 Organizer's Welcome Remarks

Mary Ann Brown, Executive Director, Conferences; Team Lead, PepTalk, Cambridge Healthtech Institute

8:50 Chairperson's Remarks

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

9:00 KEYNOTE PRESENTATION: Host with the Most: Choosing the Right System for Optimal Protein Expression

Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium

The SGC has been expressing and purifying proteins for more than 20 years for structural and functional studies, and has gained insights into which expression host is most suitable for a particular target. This lecture will summarize our high-throughput screening processes (using *E. coli*, insect, and mammalian cells) for a range of protein types (intracellular, secreted, and integral membrane proteins) and provide case studies on tackling new projects.

9:30 Like a Moth to a Flame: How Insect Cells Can Blaze the Trail to Better Recombinant Protein Production

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

In use for over four decades now, insect cell protein expression has produced thousands of high-quality proteins for drug discovery, X-ray crystallography, and vaccine development. Technological developments in the last decade have increased the value of this system and broadened the scope of its use to numerous new areas, including the production of multiprotein complexes and cryo-EM. We will discuss the numerous advantages of insect cells for producing high-value recombinant proteins.

10:00 Beyond the Periplasm: High-Purity Recombinant Protein Secretion in a Novel Bacterial Expression Host

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

Protein production in bacteria is limited by downstream processing (DSP), as purification accounts for most of the time and cost of protein manufacturing. Opera Bioscience has developed the type 3 secretion system (T3SS) in a novel bacterial expression platform to achieve single-step secretion of heterologous proteins, achieving up to 90% purity while bypassing the periplasm and cell lysis. This enables efficient fermentation to manufacture proteins for reagents, enzymes, and therapeutics.

10:30 Promoting Protein Expression in *Pichia*

Iskandar Dib, Principal Scientist, VALIDOGEN GmbH

Promoters drive transcription—the crucial first step in recombinant protein production. Transcriptional strength, however, often needs to be balanced with cellular processing capacity downstream. Thus, fine-tuning promoter strength is key to an optimal flow through the process of expression, folding, and secretion. This talk highlights VALIDOGEN's latest development—new promoter variants, methanol-induced and, in particular, methanol-free—and their synergy with other expression-enhancing elements from the "UNLOCK PICHIA" toolbox to maximize protein yields.

11:00 Networking Coffee Break

11:15 A Novel Cytochrome P450 Protein Expression System Based on the Unicellular Kinetoplast Protozoan *Leishmania tarentolae*

Jed Lampe, PhD, Associate Professor, Pharmaceutical Sciences, University of Colorado

Expression of mammalian proteins can often be a significant challenge due to membrane integration, post-translational modifications, and prosthetic cofactor integration. This is particularly true for the human cytochrome (CYP) P450 enzymes, a large family of xenobiotic-detoxifying oxidoreductases. In this presentation, we will describe our efforts to develop a CYP expression system using the unicellular kinetoplast protozoan *Leishmania tarentolae* as a novel and highly advantageous host for CYP expression.

11:45 Cost-Effective and Customizable Production of Pharmaceutical Proteins in *Trichoderma reesei*

Antti Aalto, PhD, Research Team Leader, Protein Production, VTT Technical Research Center of Finland

Trichoderma reesei is a filamentous fungus known for its high productivity and extensive use in the enzyme and food industries. Our research shows it is also an attractive platform for pharmaceutical proteins. We generated strains with high-expression levels of an IgA-Fc fragment and a model monoclonal antibody, secreted into the extracellular medium. Glycoengineering modifies the fungal N-glycans into mammalian types. Technoeconomic assessment indicates lower manufacturing costs compared to mammalian cells.

12:15 pm LUNCHEON PRESENTATION: Quick 'n' Clean - Innovative HTP BsAb Production for Optimal Pairing Screening at Discovery Stage

Jiansheng Wu, Senior Vice President, WuXi Biologics USA LLC

Production of bsAbs remains challenging, especially for bsAbs with two distinct light chains, as chain mispairing constrains throughput, yield, and purity. We introduce Quick 'n' Clean, an HTP platform for producing diverse bsAb formats, automating steps from expression to purification. The platform rapidly generates bsAbs in both double-tag and tagless formats with high purity and yield. Tagless bsAbs suit ADC conjugation, *in vitro* assays, and *in vivo* studies. Quick 'n' Clean enables rapid optimal pairing screening and streamlines downstream workflows, establishing a next-gen platform for bsAb R&D.

12:45 Session Break

EXPLORING, ENGINEERING & ENHANCING EXPRESSION PLATFORMS

1:15 Chairperson's Remarks

Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific

1:20 Everything the Light Touches Is Yours to Express: Overcoming Limitations of Constitutive Expression Using the Power of Optogenetics

Maximilian Hoerner, Head, Optogenetics, Prolific Machines

Prolific Machines' photomolecular platform uses molecular optogenetics to dynamically control gene expression in mammalian

cell lines using light. The unique features of Prolific's platform enable novel solutions for the production of next-generation, complex biologics. This presentation will describe the platform, demonstrate its application in the expression of therapeutic proteins in CHO cells, and explain how it enables a new level of performance and control while leveraging a proven mammalian production architecture.

1:45 Engineering *E. coli* Hosts for Advanced Protein Production Using a Systems Approach

Romel Menacho-Melgar, PhD, CSO, Roke Biotechnologies

We present a systems engineering approach to modifying *E. coli* for scalable, efficient protein production. By decoupling growth from expression, we implement strain modifications that are incompatible with growth but enable high-titer production of challenging proteins. This includes strain engineering to ease scale-up and dynamic modulation of protease and reductase activity to express nanobodies and degradation-prone proteins. We also demonstrate genetically programmed in-Bioreactor purification, greatly simplifying downstream processing.

2:10 Identification of Loci with High Transgene Expression in CHO Cells

Ipek Tasan, PhD, Senior Scientist, Arc Institute; Former Postdoc, Amgen

Targeted integration (TI) of therapeutic protein-encoding transgenes into predetermined high and stably expressing transcriptional hotspots in CHO cells can simplify CLD processes for biologics. We used TRIP (Thousands of Reporters Integrated in Parallel) technology to identify transcriptional hotspots in CHO cells through randomly integrated barcoded reporters tracked by sequencing. TRIP-identified hotspots achieved 9.4-fold higher mRNA levels and 5.6-fold increased protein titers compared to controls, providing a powerful functional screening method.

2:35 Pfast Protein Expression: A Rapid, Robust Solution for Accelerating Antibody Screening

primrose bio

Diane Retallack, President & COO, Primrose Bio

P. fluorescens-based Pfenex Expression Technology® transforms protein production through combinatorial screening to identify robust strains. With >20 years of development and 6 marketed products, Pfenex excels where others fail. Launched in 2024, Pfast™ offers an affordable 10 day evaluation of protein titer and quality. Tested on >30 partner proteins, Pfast significantly improved productivity challenges, improving pipeline management with seamless integration.

3:05 Networking Refreshment Break

3:30 Bispecific Antibody Production Using Split Selectable Markers through mRNA Trans-Splicing

Yiting Lim, PhD, Senior Scientist II, Cell Line Development, Just Evotec Biologics

To overcome challenges in multi-chain and bispecific antibody expression, we created a new stable expression system using only the auxotrophic glutamine synthetase (GS) selection marker. Up to four different antibody chains can be stably expressed in GS-KO CHO-K1 cells using two plasmids in our split GS vector system through mRNA trans-splicing, a post-transcriptional event whereby exons from two separate RNAs join to produce a chimeric RNA.

4:00 Multi-Protein Complex—Try Baculovirus (Even with Mammalian Cells)

Robert M. Petrovich, PhD, Protein Expression Director, Genome Integrity & Structural Biology Lab, NIH NIEHS

As a protein expression core, we focus on hard-to-express targets for structure–function studies. Our current targets include multi-protein transmembrane complexes. These target proteins require co-expression of chaperone proteins as well. I will focus my talk on two targets: the Alpha 7 nicotinic receptor (which requires co-expression of a chaperone) and the ghrelin GPCR complex (four proteins, a chaperone, and a nanobody to help stabilize the complex).

4:30 Beyond the Cell: Streamlining Biologics Discovery and Commercial-Scale Manufacturing with Cell-Free Protein Synthesis

Jacquelyn Blake-Hedges, PhD, Senior Scientist, Protein Biochemistry, Sutro Biopharma

Cell-free protein synthesis unlocks high-throughput biologics discovery and machine learning–driven protein engineering. By decoupling cell growth from protein production, it enables rapid expression in just 5–8 hours using preprepared, stable extracts. Unlike cell-based systems, this open system offers precise control, efficient incorporation of non-natural amino acids, and production of complex molecules from diverse scaffolds—all with a single extract. Moreover, this cutting-edge platform is fully scalable from benchtop to commercial manufacturing.

5:00 Close of (Re)Discovering Protein Expression Platforms Symposium

TUESDAY, JANUARY 20

7:30 am Registration and Morning Coffee

PRODUCING CHALLENGING PROTEINS: MEMBRANE AND DIFFICULT-TO-EXPRESS TARGETS

8:30 Organizer's Opening Remarks

Nikki Cerniuk, Conference Producer, Cambridge Healthtech Institute

8:35 Chairperson's Opening Remarks

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

8:40 Optimizing Target Protein Production: Host Selection's Impact On Quality

Erika Orban, PhD, Principal Scientist, Protein Discovery and Bioanalytics, Zoetis Inc.

Zoetis is working with a canine cytokine, which is important in the disease of interest, but its expression is challenging. The protein was expressed in different hosts, but none of them produced functionally active cytokine. For this reason, three cell-free expression systems were tested. Two of the proteins showed binding, but only one was functionally active. Choosing the best expression system is critical and is key for antibody screening.

9:10 Cell-Free Refolding of Challenging Membrane Proteins into SMALP Nanodiscs for Enhanced Stability and Functionality

Matthew A. Coleman, PhD, Senior Scientist & Group Leader, Biosciences and Biotechnology Division, Lawrence Livermore National Laboratory

We will discuss cell-free methods using various forms of nanodisc such as apolipoportei, telodendrimers, and SMALPs to support and refold challenging membrane proteins, including large mammalian proteins over 200 kDa. This includes protein porins, CAR T receptors, voltage-gated ion channels, and SARS-CoV-2 RBD, which were all expressed in *E. coli* lysates and solubilized in synthetic or natural lipids. These approaches enhance stability and functionality, streamlining membrane protein production.

9:40 CHS-114, a Highly Selective, Cytolytic Antibody Targeting Intratumor CCR8+Tregs: A Case Study in Overcoming Challenges in Developing Anti-GPCR Antibodies Without Off-Target Binding

Narendiran Rajasekaran, PhD, Director, Cellular Immunology, Coherus Biosciences

G protein-coupled receptors (GPCRs) regulate important physiological processes and are attractive targets for drug development. Generation of selective antibodies against GPCRs is challenging due to their structural complexities and low immunogenicity. CHS-114 is a human afucosylated IgG1 monoclonal antibody targeting CCR8 that preferentially depletes intratumor CCR8+Tregs. CHS-114 is a differentiated antibody with no off-target binding and in clinical studies demonstrates acceptable safety profile to date, anti-tumor activity, and immune activation.

10:10 Expi293 PRO Expression System: Higher Titers and Faster Time to Protein in an Easily Automated Format

Jonathan Zmuda, Sr Director, R&D, Protein & Viral Vector Expression Systems, Thermo Fisher Scientific Inc

Producing increasingly complex proteins with higher yields and higher throughput is critical to accelerating protein research and therapeutic drug development. Here, we introduce the Expi293 PRO Expression System, a next-generation transient expression system designed to meet the rigorous demands of protein expression scientists from the milliliter to multi-liter scale. We highlight the ability of the Expi293 PRO system to achieve gram-per-liter titers in as little as 48 hours, while also possessing an easily automatable protocol to maximize throughput.

10:40 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

11:20 Strategies for Expressing Complex Multi-Pass Protein Targets

Puneet Khandelwal, PhD, Associate Director, Biologics Discovery-Therapeutic Discovery, Johnson & Johnson Innovative Medicine

Complex multi-pass membrane proteins are targets for many potential therapeutic antibodies. However, producing these proteins in a native-like state for antibody discovery and development presents a significant challenge. Presently, there is no single expression system or immunogen that can consistently support antibody discovery strategies and thus requires a diversified repertoire to efficiently target these complex membrane protein targets. This presentation will present key challenges and solutions for these complex targets.

11:50 Unlocking Complex Targets: Efficient Production of Multi-Protein Assemblies in Mammalian Cells via MultiBacMam

Robert M. Petrovich, PhD, Protein Expression Director, Genome Integrity & Structural Biology Lab, NIH NIEHS

Client groups are now asking for harder-and-harder-to-express-and-purify protein targets. These include multi-protein complexes and transmembrane protein complexes. Many of these target proteins require co-expression of chaperone proteins as well. I will focus my talk on two targets: the Alpha 7 nicotinic receptor (requires co-expression of a chaperone) and the Ghrelin GPCR complex (4 proteins, a chaperone, and a nanobody to help stabilize the complex).

12:20 pm Transition to Lunch

12:30 LUNCHEON PRESENTATION: Future Fields' EntoEngine™: From Sequence to Scale in Seven Months with Transgenic Drosophila

Matt Anderson-Baron, Co Founder & CEO, Future Fields

Future Fields produces custom proteins at scale in transgenic Drosophila melanogaster. Conventional systems struggle with manufacturing challenging proteins; our novel platform, the EntoEngine™, overcomes issues with PTMs, host toxicity, insolubility, and protein folding, all while seamlessly scaling functional proteins for commercial use. Highlighting multiple case studies, including a key client success, we demonstrate how our transgenic system circumvents recombinant protein expression difficulties associated with conventional systems and brings a sequence to scale in seven months.

1:00 Refreshment Break in the Exhibit Hall with Poster Viewing

LINKEDIN SKILLS WORKSHOP

Meet the Moderator at the Plaza in the Exhibit Hall

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

PRODUCING CHALLENGING PROTEINS: MEMBRANE AND DIFFICULT-TO-EXPRESS TARGETS *(CONT.)*

1:30 Chairperson's Remarks

Christopher Cooper, DPhil, Founder, Protein Sciences, Enzymogen Consulting

1:35 Recombinant Membrane Protein Production and Subsequent *in vitro* Glycosylation: Overcoming the Challenges of Producing Membrane Proteins with Complex Post-Translational Modifications

Gabriel A. Cook, PhD, Assistant Professor, Department of Chemistry, Oklahoma State University

Glycoproteins take part in nearly every biological process and, when not properly maintained, can lead to disease states. Glycosylation of these important proteins has been shown to influence protein structure, dynamics, protein-protein interactions, and recognition by host immunity. In order to study these affects, full-length recombinantly expressed membrane proteins that contain *N*-glycosylation consensus sequences have been glycosylated *in vitro* by *N*-glycosyltransferase in the presence of membrane mimetic environments.

2:05 High-Yield Production of C-Terminally Processed KRAS4a, HRAS, and NRAS for Biophysical Study

Simon A. Messing, PhD, Scientist II, Frederick National Lab & Protein Expression Lab, Leidos Biomedical Research, Inc.

The RAS family consists of four isoforms (KRAS4b, HRAS, KRAS4a, NRAS), and mutations are involved in many human cancers. HRAS, KRAS4a, and NRAS activation is linked to localization to the plasma membrane by addition of a lipid tail, post-translationally. Using our insect cell expression platform, we describe a protocol that leads to milligram quantities of protein. Production of these three proteins is important to novel drug-screening campaigns.

2:35 Evaluation of Codon Optimization Strategies for Human and Murine Glycoproteins

Rob Meijers, PhD, Head, Biological Discovery, Institute for Protein Innovation

Efficient biologics development depends on optimal protein expression in mammalian cells. We evaluated five codon usage strategies for 21 human and murine glycoproteins expressed from our open-source pTipi2.1 vector in HEK293 cells. Small-scale screens revealed no benefit of codon optimization over native sequences, while RNA stability-focused schemes reduced yields. In large-scale production, biased codon usage occasionally improved yields. Thus, codon optimization is non-essential, but exploring multiple strategies can enhance consistency.

3:05 Advanced vector platforms for enhanced biotherapeutic protein expression

Peter O'Callaghan, Senior Director, Head Expression Systems Sciences, Licensing, Lonza

In the fast-paced world of recombinant protein manufacturing using GS-CHO cells it's crucial to start the process with an optimised expression vector that is delivered into the host cell line at transfection. The design of the expression vector has many variables that can influence the final product titre, product quality, as well as long-term expression stability, and in particular, the choice of promoter driving transcription of the product genes is key. In this presentation I will describe the development of Lonza's new expression vector platform GSquad® Pro, and its engineered high-performance promoter LHP-1, which delivers significant benefits to key biomanufacturing performance metrics. I will also give some scientific insights into how Lonza is building industry-leading datasets on gene expression control in CHO cells, and taking learnings from this work to inform further improvements to DNA vector design.

3:35 Refreshment Break in the Exhibit Hall with Poster Viewing

PLENARY KEYNOTE SESSION: TRENDS AND INNOVATION DRIVING THE FUTURE OF BIOTHERAPEUTICS

4:30 Welcome Remarks

Mimi Langley, Executive Director, Life Sciences, Cambridge Healthtech Institute

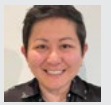
4:35 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 From Targets to Biologics: AI Powering the Next Leap in Discovery at Takeda

Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

Takeda's AI/ML strategy is redefining the path from targets to biologics, using advanced models to identify and validate novel targets, decode complex biology, and design the next generation of high-quality therapeutic molecules. By integrating agentic, generative, and large language model–driven approaches, AI is powering the next leap in discovery at Takeda.



4:50 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing

Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences

As biotherapeutics become more complex, automation of traditional testing labs falls short of delivering the insights needed for regulatory success. This talk introduces a GxP-native, full-stack AI platform designed to orchestrate and optimize mass spectrometry-based testing workflows across CMC, bioanalysis, and regulatory reporting. Rooted in regenerative system design, this infrastructure enables scalable, adaptive, and compliant operations, empowering biopharma teams to accelerate product development with confidence, clarity, and scientific precision.

5:00 Technological Trends Shaping the Landscape of Biopharmaceuticals

Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/ Fiocruz, Brazil

Currently, the biopharmaceutical industry is undergoing rapid technological advancements that are revolutionizing development and production of biopharmaceuticals. Consequently, new therapeutic categories are gaining prominence, such as antibody-drug conjugates, bispecific antibodies, advanced therapies, among others. This rapid evolution requires constant vigilance to identify breakthroughs and guiding strategic decision-making in this dynamic field. The aim of this strategic foresight analysis is to discuss technological trends for the future of biopharmaceuticals.

5:10 PLENARY FIRESIDE CHAT

Moderator: Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

Kicking off with three focused 10-minute presentations, the Fireside Chat transitions into an engaging 30-minute fireside discussion. Panelists will delve into cutting-edge topics, including the role of AI/ML in biologics discovery, advancements in next-generation analytics and tools, entrepreneurial trends and investment landscapes, and emerging therapeutic modalities. In tribute to Dr. King's legacy, this session will also highlight the importance of fostering diversity, equity, and inclusion within the biotech innovation ecosystem.

Panelists:
Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences
Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil
Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

5:40 Networking Reception in the Exhibit Hall with Poster Viewing

YOUNG SCIENTIST MEET-UP

Meet the Moderator at the Plaza in the Exhibit Hall

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

6:40 Close of Day

WEDNESDAY, JANUARY 21

7:15 am Registration Open

BuzZ Sessions

7:30 BuzZ Session with Continental Breakfast

BuzZ Sessions are informal, moderated discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the BuzZ Sessions page on the conference website for a complete listing of topics and descriptions.

BuzZ Table 1: Recent Developments in Tools for Protein Production: What's Hot and What Have We Not Got (but Need)

Christopher Cooper, DPhil, Founder, Protein Sciences, Enzymogen Consulting

- Alternative proteases for fusion tag removal
- Cost-effective reagent-based QC methods
- Protein-labeling technologies
- Up-and-coming fusion tags and promising expression systems
- Is there one hypothetical reagent that would be transformational to your protein production efforts?

BuzZ Table 2: Revisiting Construct Design, Cloning Strategies, and Expression Systems

Rob Meijers, PhD, Head, Biological Discovery, Institute for Protein Innovation

- What is the use of codon optimization? Revisiting gene synthesis
- HTP cloning methods; Golden gate assembly, Gibson cloning, etc
- Expression systems revisited (Old and up and coming)
- Expression chaperones, fusion proteins
- Open source cell lines, vectors and media

LEVERAGING COMPUTATIONAL TOOLS

8:15 Chairperson's Remarks

Erika Orban, PhD, Principal Scientist, Protein Discovery and Bioanalytics, Zoetis Inc.

8:20 Boosting Recombinant Protein Titers with Metabolic Modelling, and Harmonizing Metabolomics Datasets for Cross-Study Integration

Hardik Dodia, PhD, Postdoctoral Scholar, Shu Chien-Gene Lay Department of Bioengineering, University of California San Diego

Efficient recombinant protein production requires strategies that enhance yield while reducing experimental trials. This work demonstrates how metabolomics and dynamic flux balance analysis accelerate process optimization. By mapping substrate utilization and identifying metabolic hubs, targeted supplementation boosted protein productivity by 12-fold. This approach enables rapid, cost-effective bioprocess development. We also present a novel framework to harmonize metabolomics datasets from repositories such as Metabolomics Workbench, enabling broader comparative analyses across studies.

8:50 Smart Production: Leveraging AI for Efficient Recombinant GPCR Expression

Alex Blanco, PhD, Scientist, Nabla Bio

AI-driven design is accelerating the development of novel antibodies and antigen mimics, but translating these into functional proteins requires robust expression strategies. We describe our workflow for producing and screening AI-designed proteins, including solubilized multi-pass membrane protein mimics (solMPMPs). By integrating design with high-throughput recombinant production, we highlight challenges in expression and manufacturability—and demonstrate how iterative feedback improves the success of computationally engineered biologics.

9:20 Membrane Protein Targets Reengineered for Soluble Expression

Alexander Taguchi, PhD, Director of Machine Learning, iBio Inc.

Membrane protein targets are recombinantly expressed in a soluble, native-like conformation using a machine learning-guided scaffolding approach. These membrane protein surrogates are experimentally validated to retain native ligand binding and are expressed in human cells to support post-translational modifications. This strategy enables soluble production of previously intractable targets and has led to the successful discovery of highly specific antibodies against challenging membrane proteins.

9:50 AI-Accelerated Advancements to Cell Line Development: Integrating Sequence Mining, ASR, and ML-Stability Models

Demeetra

Corey Brizzee, Dir Gene Editing, Gene Editing, Demeetra

Demeetra's strategy for applying computational design to enhance stable cell line expression includes the re-architecting of Cas-CLOVER targeted nuclease, and unique codon optimization of transposases. Our workflow integrates enzyme functional mining, ancestral sequence reconstruction (ASR), and AI-based sequence prediction. By iterating computational design with experimental validation, we are beginning to construct a next-generation gene-

editing platform shaped by computational in conjunction with biological evolution.

10:05 "inGenius® Bioprocessing: Reducing Risk, Boosting Titre with ML-Driven Protein Production"

Ian Fotheringham, President & Founder, Ingenza Ltd

Optimising recombinant protein production remains a stubbornly unpredictable process, frequently requiring time-consuming and costly iteration of gene sequences and genetic constructs. To overcome this persistent manufacturing limitation, Ingenza has developed codABLE®, a groundbreaking machine-learning algorithm being deployed across bacterial, yeast and mammalian protein production hosts. codABLE® aligns gene sequence design with tuneable host-specific gene expression, for optimal recombinant protein production first time. Its use, alongside novel, orthogonal gene regulators, AI-optimised protein secretion and innovative antibiotic-free gene maintenance, within Ingenza's "inGenius®" platform, results in more predictable routes to maximise production of biologics, biocatalysts and any other protein target.

10:20 Coffee Break in the Exhibit Hall with Poster Viewing

SPEED NETWORKING

Meet the Moderator at the Plaza in the Exhibit Hall

Kevin Brawley, Project Manager, Production Operations & Communications, Cambridge Innovation Institute

ADVANCEMENTS IN TARGET-PEPTIDE PRODUCTION

11:00 Recombinant Expression and Characterization of Histatin-Derived Peptides

Robert M. Hughes, PhD, Associate Professor, Chemistry, East Carolina University

Histatins comprise a family of ~12 histidine-rich peptides naturally present in human saliva. Their antimicrobial properties have attracted significant interest as potential therapeutics for combating oral infections. Recombinant expression of histatin peptides with *E. coli* has traditionally used cyanogen bromide to cleave the desired peptide sequence from a fusion protein. This talk will present an immobilized enzyme approach for obtaining histatin peptides that obviates the need for cyanogen bromide.

11:30 Engineering Cell-Free Glycosylation Systems for Immune-Optimized Vaccines

Zachary Shaver, Research Scientist, Michael Jewett Laboratory, Northwestern University

We developed a cell-free workflow combining gene expression and AlphaLISA to rapidly engineer and characterize post-translational modifications, including glycosylation, for conjugate vaccine production. Using this method, we optimized oligosaccharyltransferases and identified protein sites enabling efficient glycosylation. This approach supports scalable *in vitro* vaccine production and accelerates the development of more immunogenic conjugate vaccines through improved enzyme and carrier protein design.

12:00 pm KEYNOTE PRESENTATION: Yeast-Based Expression and Enzymatic Cyclization of Disulfide-Rich Cyclic Peptide Scaffolds for Drug Development

David J. Craik, PhD, Professor & UQ Laureate Fellow, The University of Queensland

Macrocyclic, disulfide-rich peptides are valuable in drug development, but traditional solid-phase peptide synthesis is environmentally harmful. We present a sustainable platform using yeast to secrete peptide precursors, which are matured *in vitro* via asparaginyl endopeptidases. Three peptide classes were produced, including the first recombinant α-conotoxin in native form. Yields reached 85–97 mg/L in bioreactors—surpassing prior methods—offering an eco-friendly, scalable alternative for cyclic peptide production.

12:30 Transition to Lunch

12:40 LUNCHEON PRESENTATION: Accelerating Membrane Protein Purification: Innovations with Nuclera

Wenguang Liang, Sr Scientist, Molecular & Cell Sciences, Bayer CropScience

Membrane proteins are crucial for various cellular processes and serve as key targets in drug discovery as well as trait development in crop science. However, their purification presents significant challenges due to their hydrophobic nature and complex structural requirements. This talk will delve into recent innovations we have adapted using Nuclera that are transforming the landscape of membrane protein purification. We will discuss high-throughput screening methods that expedite optimization processes, followed by advanced expression systems and novel extraction techniques that enhance both yield and stability. By integrating these innovative approaches, researchers can effectively overcome traditional barriers in membrane protein purification, thereby facilitating more effective studies and accelerating product development. Join us to discover how these advancements can lead to breakthroughs in both drug discovery and agricultural biotechnology.

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:

Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

2:15 Close of Conference

WEDNESDAY, JANUARY 21

1:00 pm Registration Open

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

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1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

ACCELERATING ANTIBODY-BASED PRODUCTION

2:15 Chairperson's Opening Remarks

Diana Freire, M.Sc, Competitive Intelligence Office, Bio-Manguinhos/ Fiocruz, Brazil

2:20 Accelerating Recombinant-Antibody Fragment Production Using Bacterial and Mammalian Cell-Free Protein-Synthesis Platforms

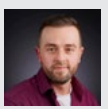
Shakiba Nikfarjam, PhD, Postdoc, Lawrence Livermore National Lab

We present a hybrid cell-free protein synthesis platform using *E. coli* and mammalian lysates to enable rapid, on-demand production of recombinant antibody fragments within hours. Coupled with fluorescence correlation spectroscopy for direct, purification-free KD measurements, this workflow accelerates screening, reduces material requirements, and supports high-throughput antibody engineering. Our approach offers a fast, flexible alternative to cell-based expression for next-generation recombinant protein development.

2:50 Exploiting High-Throughput Capabilities to Produce Optimal Humanized Antibodies

Kathryn Armour, PhD, Principal Scientist, Biologics Discovery & Development, LifeArc

Humanization of conventional and single-domain antibodies to produce stable, developable molecules is critical for clinical use. Our design process generates an array of humanized versions for each parent variable region, and high-throughput capabilities allow efficient expression and assaying of the hundreds of heavy-light combinations. Interrogating a variant matrix can improve on parental properties through optimization of binding, function, developability, and human identity, thus pinpointing lead candidates suitable for the clinic.



3:20 FEATURED PRESENTATION: Repressing Expression of Difficult-to-Express Recombinant Proteins During the Selection Process Increases Productivity of CHO Stable Pools

Jean-Sebastien Maltais, PhD, Research Officer, Medical Devices, National Research Council Canada

Many next-generation therapeutics remain intrinsically challenging to produce in CHO cells. We exploited a cumate-inducible CHO platform allowing reduced expression of various classes of r-proteins during selection of stable pools. Fed-batch productions showed that pools generated without cumate (OFF-pools) were significantly more productive. Using an inducible system to minimize r-protein expression during pool selection can contribute to reducing cellular stresses, including ER stress and metabolic burden, leading to improved productivity.

3:50 Talk title: Enabling Targeted *in vivo* Gene Therapy: The Critical Role of Recombinant Proteins in LNP-Based Therapeutics

WACKER

Moira Monika Schuler, Global CMC & Tech Bus Dev Mgr, Wacker Biotech

In vivo gene therapy utilizing targeted lipid nanoparticle (LNP) systems represents a transformative approach in the development of advanced therapies. The success of these targeted LNP-based therapies is fundamentally dependent on the availability of high-quality antibodies and antibody fragments, which serve as essential moieties for precise delivery and targeting. Manufacturing of these antibodies is central to the success of this strategy.

4:20 Refreshment Break in the Exhibit Hall with Poster Viewing

CONSIDERATIONS FOR THERAPEUTIC PEPTIDE PRODUCTION

4:50 Dermal Peptide Solutions: Unique Challenges for Actives and Delivery

Jay Sarkar, PhD, Co-Founder, reThink64 Bionetworks

Peptide actives are gaining traction, not just for internal medicine, also for topical usage. The challenges for dermal delivery, however, puts constraints on the types of peptide solutions that can be produced so far. Pushing the boundaries with longer sequences with more diversified targets necessitates the tandem evolution of large-molecule delivery solutions. This talk will review existing solutions as well as introduce novel modalities for dermal peptide products.

5:20 Applying Biologic CMC Principles to Peptide Production: From Discovery to Development

Steven Bowen, PhD, Principal Consultant, ELIQUENT Life Sciences

This talk explores how biologic CMC (Chemistry, Manufacturing, and Controls) principles can be effectively applied to peptide production across the discovery-to-development continuum. By leveraging established frameworks from biologics, we demonstrate strategies to enhance peptide quality and regulatory readiness. Key topics include process development, analytical characterization,

and quality control, emphasizing a streamlined approach to accelerate peptide therapeutics toward clinical success.

5:50 Close of Day

THURSDAY, JANUARY 22

8:00 am Registration Open

PLENARY KEYNOTE SESSION: End-to-End *in silico*-Designed Biologics

8:25 Welcome Remarks

Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

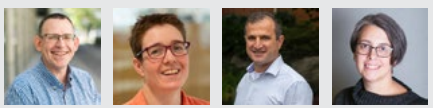
8:30 Plenary Keynote Introduction

Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 PLENARY FIRESIDE CHAT: End-to-End *in silico*–Designed Biologics



Moderator: Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

- How is the path to drug development different with ML/AI?
- How far off is *de novo* design for biologics? For antibodies?
- How is ML/AI used for target selection?
- How do you accelerate DMTA cycles?
- Data standardization—how to incorporate historical data?
- Federated learning—how do you ensure you have enough data to build a model?
- Promoting change management

Panelists:
Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)
Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:30 Coffee Break in the Exhibit Hall with Poster Viewing

WOMEN IN SCIENCE MEET-UP

Meet the Moderators at the Plaza in the Exhibit Hall

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

OBSTACLES AND INNOVATIONS IN THERAPEUTIC PROTEIN PRODUCTION

10:20 Chairperson's Remarks

Kathryn Armour, PhD, Principal Scientist, Biologics Discovery & Development, LifeArc

10:25 Advances and Challenges in Plant-Based Expression Systems for Therapeutic Proteins

Diana Freire, M.Sc, Competitive Intelligence Office, Bio-Manguinhos/ Fiocruz, Brazil

Plant-based expression platforms have emerged as a promising biotechnological alternative for producing therapeutic recombinant proteins that require complex post-translational modifications. This work will present the current landscape and key advantages and challenges of this platform, discuss emerging technologies designed to overcome these obstacles, and highlight recent advances and opportunities that improve the viability of plant-based systems for the development of innovative, effective, and affordable biopharmaceuticals.

10:55 Metabolome Profiling Reveals Host Factors Driving Soluble Expression of Disulfide Rich Proteins in ***E. coli***

Snehal Ganjave, PhD, Specialist, Pharmaceutical Chemistry, University of California- San Francisco

Recombinant production of disulfide rich proteins in E. coli is hindered by host redox imbalance, misfolding and aggregation. In our study, we combined untargeted metabolomics of two E. coli strains (BL21 (DE3) and SHuffle) with manipulation of fusion tags (thioredoxin) and induction temperature to identify metabolic signatures associated with soluble vs insoluble expression. Our findings reveal actionable metabolome based indicators of host performance and provide a roadmap for rational expression platform design.

11:25 High-Throughput Reagent Production to Enable Biotherapeutics Discovery

Holly Schmidt, Senior Principal Scientist, Bristol Myers Squibb

Supporting biologics drug discovery for a large organization requires high-throughput techniques for expression, purification, and characterization of reagents to enable candidate exploration. High-quality extracellular domains of target proteins or chaperones are useful for many applications, including hydrogen-deuterium exchange, structural efforts, and direct binding analysis of biotherapeutics to targets by SPR. Enabling workflows, including chaperone selection and modified multi-step ÄKTA systems to produce mg-scale reagents, will be discussed.

11:55 Accelerating Discovery: Applications of Cell-Free Protein Expression Technology

nuclera

Judy Ronau, Sr Scientist II, Small Molecule Therapeutics & Platform Technology, AbbVie Inc

At AbbVie, the discovery and development of innovative therapies relies on our ability to rapidly access and characterize proteins that are central to disease biology. In this talk, I will discuss the pivotal role that proteins play in our drug discovery efforts and explain how adopting cell-free protein expression technology has enhanced efficiency beyond conventional cell-based systems. After outlining the core methodology, I will share some internal case studies that demonstrate the impact of this technology in early discovery and expanding our scientific capabilities.

12:25 pm Transition to Lunch

12:30 LUNCHEON PRESENTATION: Advancing Chromatography Techniques with the NGC Chromatography System. BIO-RAD

Philip Chapman, Sr Product & Marketing Mgr, Protein Purification, Bio Rad Labs

This workshop, led by Marketing Manager, Philip Chapman, will provide insight into Bio-Rad's evolution of chromatography and purification products, along with outlining the rationale behind the design of the NGC™ chromatography system. We will discuss how the system was developed to support a range of purification needs, from basic laboratory workflows to more advanced applications. Key topics will include the flexible hardware design, software features, and system configurations that allow users to perform manual purification, automated methods, and continuous chromatography on the same platform. The workshop will focus on practical considerations for implementing and transitioning between different purification approaches using a single chromatography system. We hope you can join us! Lunch will be provided.

1:00 Ice Cream & Cookie Break in the Exhibit Hall with Last Chance for Poster Viewing

WORKFLOW MAKEOVERS: REINVENTING PIPELINES FOR CONSISTENCY, SPEED, AND SCALE

1:40 Chairperson's Remarks

Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

1:45 Advancements in Protein-Expression Workflows for Drug Discovery

Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

This presentation will explore how advancements in protein-expression workflows are revolutionizing drug discovery. We will focus on how new expression technologies—including Bacmam, cell-free systems, and automated high-throughput platforms—enable the rapid and parallelized production of a vast number of protein variants. These integrated workflows provide a robust, efficient, and scalable foundation for the development and characterization of next-generation therapeutic proteins, significantly accelerating the entire drug discovery process.

2:10 Building a Better Pipeline: Setting Up Recombinant Protein Workflows in a New Research Environment

Christopher A. Wassif, PhD, Director, Molecular Engineering & Antibody Technologies, AstraZeneca

Building the laboratory of the future involves space planning, integrating advanced automation, digital data management, and artificial intelligence to accelerate scientific discovery and streamline workflows. Emphasizing modular design and high-throughput capabilities, such laboratories enable seamless collaboration and rapid adaptability to evolving research needs. Enhanced connectivity, real-time data analysis, and scalable infrastructure ensure reproducibility and efficiency, positioning the lab as a dynamic hub for innovation in both foundational and translational science.

2:35 Next-Generation Shake Flasks: Can We Reach Bioreactor-Level Performance?

Vikash Kumar, Senior Scientist, Biologics Process Research and Development, Merck

The Aero-Yield breathable flask replaces traditional polycarbonate flasks. Fabricated with gas-permeable silicone, it enables full-wall-surface O2/CO2 exchange. This improves oxygen flux 58-fold and boosts kLa by 40–100%. Cultures of *E. coli* and *Pichia pastoris* showed 40–66% biomass and 41–115% protein yield gains. With an O2-enriched gas jacket, gains reached 156% in biomass and 140% in recombinant titer, matching bioreactor growth rates. Aero-Yield offers scalable, affordable, bioreactor-like performance for early-stage bioprocessing.

3:00 Harnessing the Power of Incremental Innovation in a Protein-Biochemistry Lab

Christa Cortesio, PhD, Director, Protein Biochemistry & Analytics Core, Kite, a Gilead Company

This presentation will focus on incremental innovations implemented in our small but mighty protein-biochemistry group, highlighting both individual- and group-driven initiatives that have positively influenced productivity and scientific impact. Through this approach, our group has been able to streamline processes, enhance efficiency, and contribute to the development of novel CAR T cell therapies, demonstrating the significant impact that small, iterative improvements can have in a laboratory setting.

3:25 PANEL DISCUSSION: The Evolving Lab: From New Workflows to Scalable Discovery Pipelines

Moderator: Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

Laboratory workflows are central to advancing drug discovery, yet they face increasing demands for speed, reproducibility, and scalability. This closing panel explores the methodologies, technologies, and strategies reshaping how labs operate today. Panelists will highlight ways to streamline processes, enhance reliability, and build resilient workflows capable of meeting tomorrow's scientific challenges.

Panelists:

Oleg Brodsky, MBA, Senior Principal Scientist, Structural Biology & Protein Sciences, Pfizer Inc.

Christopher Cooper, DPhil, Founder, Protein Sciences, Enzymogen Consulting

Christa Cortesio, PhD, Director, Protein Biochemistry & Analytics Core, Kite, a Gilead Company

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Vikash Kumar, Senior Scientist, Biologics Process Research and Development, Merck

Christopher A. Wassif, PhD, Director, Molecular Engineering & Antibody Technologies, AstraZeneca

4:15 Close of Conference

PepTalk

The Protein Science and Production Week

HIGHER THROUGHPUT & INNOVATION

The demand for high-quality proteins continues to accelerate across research, diagnostics, and therapeutic applications. Scientists are expanding the protein landscape by integrating advanced workflows, automation, high-throughput screening, real-time analytics, next-generation purification strategies, robust quality control, and data-informed decision-making. The Higher Throughput & Innovation pipeline brings together innovators and leaders in biopharmaceutical process development to tackle bottlenecks, spotlight emerging technologies, and share practical, scalable solutions. Join us to learn how automation, AI, and integrated platforms are shaping the future of protein science.

JANUARY 19
SYMPOSIUM

Predictive Protein Production AGENDA

JANUARY 20-21

Automation in Protein Discovery AGENDA

JANUARY 21-22

Advanced Tools for Purification and Quality AGENDA

MONDAY, JANUARY 19

8:00 am Registration and Morning Coffee

ENGINEERING DISCOVERY: AI-POWERED DESIGN AND ANTIBODY PRODUCTION AT SCALE

8:50 Organizer's Remarks

Lynn Brainard, Conference Producer, Cambridge Healthtech Institute

8:55 Chairperson's Remarks

Cheemeng Tan, PhD, Chancellor's Fellow; Professor, Department of Biomedical Engineering, University of California, Davis

9:00 Innovating Hit Discovery through Open Data: Insights from Target 2035's Protein Platform

Rachel J. Harding, Assistant Professor, University of Toronto

The Target 2035 initiative is transforming early drug discovery through open, collaborative protein science. Co-led by the SGC, this project advances open science by integrating protein production, high-throughput screening, and public data sharing. Central to this is the Protein Donation Program, enabling global contributions for ligand discovery screening. A co-developed roadmap outlines how FAIR data practices improve scalability, reproducibility, and access, accelerating hit discovery and target validation through shared infrastructure.

9:30 ML-Guided Synthesis of Proteins on Synthetic and Extracellular Vesicles

Cheemeng Tan, PhD, Chancellor's Fellow; Professor, Department of Biomedical Engineering, University of California, Davis

Artificial nanovesicles and extracellular vesicles need surface proteins to target cells and deliver drugs. Existing engineering takes weeks, handles few proteins, and yields mixed products. Here, we showcase EV-PRIME (EV-Protein Rapid Insertion by cell-free Membrane Engraftment). The one-pot, machine-learning-guided system uses cell-free synthesis to express and embed proteins onto vesicles within hours. It represents the first high-throughput, ML-directed platform for engineering protein-enhanced vesicles.

10:00 Single-Walled Carbon Nanotube Probes for Protease Characterization Directly in Cell-Free Expression Reactions

Sepehr Hejazi, Ph.D. Candidate, Iowa State University

Cell free expression is a powerful technique for rapidly prototyping protein candidates in a discovery program. Gene templates are directly added to cell lysate yielding assayable quantities of proteins in a few hours. This talk covers our recent efforts in designing functional assays (protein binding and activity) that can be conducted directly in cell lysate, removing the need to purify the protein, thereby increasing data throughput for predictive models.

10:30 Days, Not Weeks: Unlocking AI Design + Lab-in-the-Loop with ALiCE® HTPE for Target Discovery

Jonathan Fauerbach, Head of R&D, LenioBio GmbH

What if a single platform could express full-length mAbs, intractable antigens like GPCRs, and therapeutic mini-binders (nanobodies, VHHs, peptides)—all in days, not weeks or months? LenioBio's ALiCE® HTPE cell-free eukaryotic platform reimagines target discovery by integrating AI-driven *de novo* design with lab-in-the-loop high-throughput expression and screening. This unified workflow bypasses cell-based limitations, enabling native-folding production of diverse modalities from DNA templates at unprecedented scale.
The result is a collapsed Design–Build–Test–Learn cycle that powers parallel validation across vast sequence spaces, unlocking previously inaccessible targets and accelerating next-generation biologics discovery.

11:00 Networking Coffee Break

11:15 Chai-2: Zero-Shot Antibody Design in a 24-Well Plate

Nathan Rollins, Founding Scientist, Chai Discovery

We present a novel antibody discovery approach enabling precise epitope specification and rapid timelines achieving sequence identification in 24 hours and KD determination within two weeks. Using the generative AI model Chai-2, we achieved a 16% hit rate in *de novo* antibody design, a 100-fold improvement over prior methods. In a single round, Chai-2 produced binders for 50% of 52 diverse targets, highlighting AI's transformative potential in biologics discovery.

11:45 Predicting Purification Process Fit of Monoclonal Antibodies Using Machine Learning

Andrew J. Maier, Principal Engineer, Purification Development, Genentech, Inc.

This presentation describes a modeling strategy for antibody purification process fit assessment. Principal Component Analysis is applied to extract a one-dimensional basis for comparison of molecular chromatographic binding behavior from high-throughput screens. Ridge Regression is used to predict the principal component for new molecular sequences. This workflow is demonstrated with 97 monoclonal antibodies for five chromatography resins. Model development benchmarks four descriptor sets from biophysical descriptors and protein-language models.

12:15 pm Enjoy Lunch on Your Own

PREDICTING EXPRESSION: CRACKING COMPLEX PROTEINS WITH SMARTER SYSTEMS

1:30 Chairperson's Remarks

Matthew A. Coleman, PhD, Senior Scientist & Group Leader, Biosciences and Biotechnology Division, Lawrence Livermore National Laboratory

1:35 Decoding Protein Expression Landscapes via Massive Screening and Machine Learning over Combinatorial Libraries

Haotian Guo, PhD, Founder & CEO, Ailurus Bio

To unravel the complex genetic grammar of protein expression, we developed a systematic approach for the construction of a gigantic parallel assay of combinatorial libraries, characterizing expression across hundreds of millions of genetic contexts. Leveraging a premade library of all *E. coli* regulatory elements, we generate high-resolution, ultra-high-throughput datasets of sequence-to-expression relationships, ready for machine learning, offering a powerful framework for data-driven protein engineering.

2:05 High-Throughput Viscosity Screening Enables AI-Driven Structure Modeling for Biotherapeutic Design

Alayna George Thompson, PhD, Associate Director, Drug Product Development, AbbVie

Viscosity is a crucial parameter for biotherapeutic development, but traditional measurements consume large sample amounts. AbbVie developed the iBEACON to enable viscosity screening early in drug discovery; it measures viscosity vs. concentration curves up to 150 mg/mL with 100 micrograms of protein. This novel instrument allows us to collect data on ~10-fold more molecules per program. We are using these large data sets to build next-generation models of viscosity.

2:35 PUREfrex: The Rebuilt Protein Factory

Takashi Ebihara, COO, GeneFrontier Corporation

PUREfrex is a rebuilt cell-free protein expression system that transforms how proteins are produced and explored. Its modular design enables precise molecular control and broad adaptability—from expressing challenging biologics to supporting high-throughput workflows. PUREfrex serves as a flexible foundation for therapeutic protein development, synthetic biology, and AI/ML-driven innovation.

2:50 Selected Poster Presentation: High-Throughput Wet-Lab Validation and Rich SPR Data Generation for RL and SFT of AI Models

Engin Yapici, Phd, VP of Business Development, SPOC Biosciences

AI-driven protein and antibody design is constrained by slow, low-throughput experimental validation, and SPOC® overcomes this bottleneck by enabling on-chip synthesis and full kinetic screening of 192–1152 candidates to generate AI-ready, low-picomolar–resolution datasets in just 3–4 weeks. Using this platform, we profiled ~700 anti-HER2 scFv variants across multiple pH conditions, producing rich sequence–function kinetics matrices that directly support model training, active learning, and the rapid optimization of next-generation biologics.

3:05 Networking Refreshment Break

3:30 Predictive Discovery of VHH Antibodies Targeting CCR8: A Case Study in GPCR Therapeutics

Alexander Alexandrov, PhD, Director of Protein and Antibody Sciences, Abilita Therapeutics

This presentation will detail the discovery of VHH antibodies targeting the membrane protein CCR8, a GPCR selectively expressed on tumor-infiltrating regulatory T cells. We will walk through the end-to-end workflow—from antigen preparation and immunization to panning, humanization, affinity maturation, and developability optimization—leveraging miniaturized screening assays to guide candidate selection. The talk culminates in the structural elucidation of the antibody-antigen complex, demonstrating the power of predictive approaches in membrane protein targeting.

4:00 Cell-Free Refolding of Challenging Membrane Proteins into SMALP Nanodiscs for Enhanced Stability and Functionality

Matthew A. Coleman, PhD, Senior Scientist & Group Leader, Biosciences and Biotechnology Division, Lawrence Livermore National Laboratory

We will discuss cell-free methods using various forms of nanodisc such as apolipoprotein, telodendrimers, and SMALPs to support and refold challenging membrane proteins, including large mammalian proteins over 200 kDa. This includes proteins like MOMP, CAR T receptors, voltage-gated ion channels, and SARS-CoV-2 RBD that were all expressed in *E. coli* lysates and solubilized in synthetic or natural lipids. These approaches enhance stability and functionality, streamlining membrane protein production.

4:30 Orthogonal Mammalian Selection Systems: Mining Data and Nature

Hooman Hefzi, PhD, Associate Professor, Advanced Mammalian Cell Engineering Group, Biotechnology and Biomedicine, Technical University of Denmark

Selection systems such glutamine synthetase (Gs) and dihydrofolate reductase (Dhfr) have been used for decades to generate highly productive CHO cell lines. Using high-throughput CRISPR screens we identified asparaginase as a novel selectable marker that can be used alongside Gs in glutamine dropout media to generate cell lines with higher specific productivity and titer. Separately, we will share preliminary data on using essential amino acid biosynthesis as a selection system.

5:00 Close of Predictive Protein Production Symposium

TUESDAY, JANUARY 20

7:30 am Registration and Morning Coffee

PRECISION PEPTIDE ENGINEERING: AT-SCALE FOR FUTURE THERAPEUTICS

8:30 Organizer's Remarks

Lynn Brainard, Conference Producer, Cambridge Healthtech Institute

8:35 Chairperson's Remarks

Wenshe Ray Liu, PhD, Harry E. Bovay, Jr. Endowed Chair, Professor in Chemistry, Texas A&M University

8:40 Next-Generation Libraries of Peptide Macrocycles for mRNA Display

Albert A. Bowers, PhD, Professor, Division of Chemical Biology and Medicinal Chemistry, University of North Carolina Chapel Hill

mRNA display allows production and selection of vast macrocyclic peptide libraries. We present a strategy for making target class-selective mRNA display libraries by using N-terminal selective cyclization chemistry to allow post-translational chemical derivatization of internal cysteines. We thus install analogs of dimethyl lysine (KMe2) in selections against epigenetic targets UHRF1 and RBBP7. We further combine this methodology with late-stage barcoding strategy for rapid preparation of focused libraries for hit-to-lead optimization.

9:10 Beyond Binding Affinity: Optimizing Peptide Discovery for Targeted Therapeutics

Mette Soendergaard, PhD, Co-Founder & CSO, Cell Origins LLC

Phage display has become a cornerstone of peptide discovery, enabling the identification of high-affinity binders against a wide array of targets. However, binding affinity alone is not a reliable predictor of therapeutic success. Enhancing the translational potential of peptides requires addressing critical factors such as off-target effects, biodistribution, and pharmacokinetics in the discovery process. By employing selection strategies under physiologically relevant conditions, we can prioritize candidates with optimized therapeutic profiles.

9:40 Using Phage Display Methods for Rapid Identification of Covalent Cyclic Peptides Targeting Diverse Proteins

Matthew Bogyo, PhD, Professor, Department of Pathology, Stanford University School of Medicine

Hydrolases are enzymes that often play pathogenic roles in diseases such as cancer, asthma, arthritis, atherosclerosis, and infection by pathogens. Probes that allow dynamic monitoring of their activity can be used as diagnostic and imaging agents, as well as for identification of enzymes as drug leads. I will describe efforts using phage display, mRNA display, and high-throughput fragment screening to identify selective covalent-binding probes for diverse protein targets.

10:10 Accelerating Bioprocess Development with AI + Automation

GenScript

Justin Byers, President & CEO, Axio Biopharma

Bioprocess development faces increasing challenges from accelerated timelines, fragmented data, and process variability, leading to delayed patient access. This presentation explores how AI and high-quality data generation can address these challenges, introducing Axio's federated approach to secure, collaborative learning. A case study featuring the GenScript Quatro ProAb 1300 highlights how automated purification accelerates antibody discovery and development through AI-powered workflows.

10:40 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

11:20 Phage-Assisted Active Site-Directed Ligand Evolution of Peptide Ligands for Epigenetic Drug Targets

Wenshe Ray Liu, PhD, Harry E. Bovay, Jr. Endowed Chair, Professor in Chemistry, Texas A&M University

The conventional phage display technique, while a powerful tool for drug discovery, is limited by its reliance on the 20 genetically encoded amino acids. To increase the versatility of the technique, we have integrated both chemical cyclization and genetically incorporated noncanonical amino acids into phage display. Unique applications afforded by new technology platforms in drug discovery have been demonstrated on multiple epigenetic drug targets, including SIRT2, HDAC8, ENL, and BRD9.

11:50 Accurate Sequence-to-Affinity Models from High-Throughput Peptide Binding Assays

Harmen J. Bussemaker, PhD, Professor, Biological Sciences & Systems Biology, Columbia University

Affinity selection on random peptide libraries, coupled with next-generation sequencing, yields high-throughput yet sparse data, which we use to train biophysical models that predict SH2 domain binding free energy and c-Src kinase efficiency over the full theoretical sequence space. Our model predictions are validated against biophysical measurements of synthesized peptides. This unbiased approach enables scalable, accurate prediction of protein functional properties, supporting more effective identification and optimization of drug candidates.

12:20 pm Transition to Lunch

12:30 LUNCHEON PRESENTATION: Automate Your Protein Chromatography Workflows: Strategies For Increasing Throughput

cytiva

Akemi Kunibe, Field Application Scientist, Cytiva

1:00 Refreshment Break in the Exhibit Hall with Poster Viewing

LINKEDIN SKILLS WORKSHOP

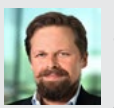
Meet the Moderator at the Plaza in the Exhibit Hall

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

AUTOMATE TO INNOVATE: POWERING HIGH-THROUGHPUT BIOLOGICS WITH SCALABLE PLATFORMS

1:30 Chairperson's Remarks

Christopher A. Wassif, PhD, Director, Molecular Engineering & Antibody Technologies, AstraZeneca



1:35 KEYNOTE PRESENTATION: Automation for Rapid Large-Scale Data Generation of Biologics

James D. Love, PhD, Vice President, Cross Modality Workflows, Novo Nordisk AS

Science has always required the generation of high quality data. To leverage developments in AI/ML, matching the computational power that is available to us, we are actively generating even larger data sets that are missing to train models relevant to biologics drugs, especially developability parameters. This talk will focus on the large scale automation and high throughput approaches we are taking to achieve this goal.

2:05 From Gene to Protein, Uninterrupted: The Power of Workcell Automation in Accelerating Discovery

Pei-Hsuan Chu, Associate Director, AstraZeneca

Automation enables scalable workflows that produce hundreds of antibodies weekly, transforming biotherapeutic discovery with greater speed and reproducibility. Advances in automated cloning and next-generation sequencing allow efficient, parallel construction and validation of expression vectors. Combined with automated protein production, these methods establish robust, high-throughput pipelines. This work presents integrated workflows from cloning to purification, highlighting the transition from modular tools to end-to-end solutions advancing biologics research and supporting AI-driven discovery.

2:35 Deploying a Fleet: Scalable Automation for an Antibody Discovery and Validation Platform

Curtis Walton, PhD, Director of Automation and Process Optimization, Institute for Protein Innovation

At the Institute for Protein Innovation, we've developed a scalable antibody discovery platform capable of identifying and validating antibodies against hundreds of protein targets annually. Traditional automation approaches often become bottlenecks that are rigid, over-specialized, or single points of failure. In this talk, we introduce our fleet-based automation strategy, designed to provide flexibility, built-in redundancy, and rapid deployment across discovery and validation workflows.

3:05 Blow past biologics formulation and stability hurdles with Aunty

UNCHAINED LABS

Andre Mueller, Sr. Product Manager, Aunty & Honeybun, Unchained Labs

Stability screening of proteins is like an obstacle course, especially when testing many candidates and conditions. Most lab tools are either inflexible one-hit wonders that don't give the full stability picture or seriously low-throughput, creating major bottlenecks. Aunty breaks out of the pack by combining full-spectrum DSF, SLS, and DLS with a standard format 96-well quartz plate and full integration readiness. Aunty's speed and resolution let you power through melting & aggregation experiments – with just 8 µL of each sample. Capture conformational and colloidal stability info of the whole plate every minute of your experiment. Join my presentation to see how Aunty characterizes mAbs and ADCs in different formulations and how excipients tune protein stability.

3:35 Refreshment Break in the Exhibit Hall with Poster Viewing

PLENARY KEYNOTE SESSION: TRENDS AND INNOVATION DRIVING THE FUTURE OF BIOTHERAPEUTICS

4:30 Welcome Remarks

Mimi Langley, Executive Director, Life Sciences, Cambridge Healthtech Institute

4:35 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 From Targets to Biologics: AI Powering the Next Leap in Discovery at Takeda

Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

Takeda's AI/ML strategy is redefining the path from targets to biologics, using advanced models to identify and validate novel targets, decode complex biology, and design the next generation of high-quality therapeutic molecules. By integrating agentic, generative, and large language model–driven approaches, AI is powering the next leap in discovery at Takeda.

4:50 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing

Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences

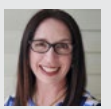
As biotherapeutics become more complex, automation of traditional testing labs falls short of delivering the insights needed for regulatory success. This talk introduces a GxP-native, full-stack AI platform designed to orchestrate and optimize mass spectrometry-based testing workflows across CMC, bioanalysis, and regulatory reporting. Rooted in regenerative system design, this infrastructure enables scalable, adaptive, and compliant operations, empowering biopharma teams to accelerate product development with confidence, clarity, and scientific precision.

5:00 Technological Trends Shaping the Landscape of Biopharmaceuticals

Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/ Fiocruz, Brazil

Currently, the biopharmaceutical industry is undergoing rapid technological advancements that are revolutionizing development and production of biopharmaceuticals. Consequently, new therapeutic categories are gaining prominence, such as antibody-drug conjugates, bispecific antibodies, advanced therapies, among others. This rapid evolution requires constant vigilance to identify breakthroughs and guiding strategic decision-making in this dynamic field. The aim of this strategic foresight analysis is to discuss technological trends for the future of biopharmaceuticals.

5:10 PLENARY FIRESIDE CHAT




Moderator: Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

Kicking off with three focused 10-minute presentations, the Fireside Chat transitions into an engaging 30-minute fireside discussion. Panelists will delve into cutting-edge topics, including the role of AI/ML in biologics discovery, advancements in next-generation analytics and tools, entrepreneurial trends and investment landscapes, and emerging therapeutic modalities. In tribute to Dr. King's legacy, this session will also highlight the importance of fostering diversity, equity, and inclusion within the biotech innovation ecosystem.

Panelists:
Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences
Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil
Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

5:40 Networking Reception in the Exhibit Hall with Poster Viewing

YOUNG SCIENTIST MEET-UP

Meet the Moderator at the Plaza in the Exhibit Hall

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

6:40 Close of Day

WEDNESDAY, JANUARY 21

7:15 am Registration Open

BuzZ Sessions

7:30 BuzZ Session with Continental Breakfast

BuzZ Sessions are informal, moderated discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the BuzZ Sessions page on the conference website for a complete listing of topics and descriptions.

BuzZ Table 3: Expanding the bsAb Toolbox through Automated Workflows

Alexandra Cabatingan, Resin Specialist, Cytiva

- How MabSelect Mild Elution enables streamlined and reproducible platforms
- Using MagSepharose for high-throughput screening
- Automated downstream applications using AKTA chromatography systems and their impact on workflow efficiency

BuzZ Table 4: Challenges Developing High-Throughput Production Workflows for Complex Biologics

Ayla Sessions, Associate Director, AstraZeneca

REDEFINING DISCOVERY: AUTOMATION FOR FUNCTION, PRODUCTION, AND SCALE

8:15 Chairperson's Remarks

Iman Farasat, PhD, Director, Biologics Discovery, Johnson & Johnson Innovative Medicine

8:20 When Automation Meets Native Membrane Proteins – A Cube Biotech Story

Jan Kubicek, CSO & Co Founder, Cube Biotech GmbH

The introduction of automation in soluble protein research has fundamentally changed the approach to biological complexity, transforming manual, experience-based workflows into standardized and scalable processes. These advances significantly accelerated discovery while reducing trial-and-error. Native membrane protein research faces similar challenges—low yields, instability, condition dependency, and limited reproducibility—further complicated by the inherent complexity of lipid–protein interactions. As demonstrated by the evolution of soluble protein workflows, such limitations are often procedural rather than biological. Applying automation to native membrane protein research therefore represents a logical next step. Systematic, controlled screening approaches enable a shift from artisanal experimentation toward data-driven optimization, with the potential to make native membrane proteins accessible as routine, reproducible research targets without compromising their functional integrity.

8:50 Scaling Discovery: High-Throughput Protein Science at the SGC to Enable Success for Challenging Drug-Discovery Targets

Rachel J. Harding, Assistant Professor, University of Toronto

Targeting sperm-specific proteins for non-hormonal contraception poses unique protein science challenges due to poor annotation, a lack of close homologs, and a scarcity of model systems. We sought to address this with high-throughput protein production using bacterial, insect, and mammalian systems. Our scalable workflow includes parallel construct design, tiered purification, real-time QC, and ongoing AI and automation integration, advancing best practices for tackling difficult drug-discovery targets.

9:20 Accelerating Multispecific Antibody Production and Analytics: Integrating Mini-Scale Affinity Chromatography into High-Throughput uHPLC Workflows

Nicholas Santos, Senior Associate Scientist, Large Molecule Research, Sanofi

Multispecific antibodies present challenges in production due to product-related impurities. Large Molecule Research has developed a uHPLC workflow that enables high-throughput characterization of molecules using 1mL or less of supernatant. The automated process delivers accurate, purification-based titer measurements and integrated product quality data. This multi-dimensional analysis enables the development of downstream processing methods based on analytical-scale HIC and IEX chromatography prior to harvesting, saving significant time and resources.

9:50 Precision antibody engineering: tailored services for accelerated development

Claudia Chiocchini, Mgr Protein R&D, R&D, Thermo Fisher Scientific Inc

In the rapidly evolving field of antibody discovery, whether employing traditional methods or AI-assisted design, the need for rapid and reliable data generation is paramount. Strategies for accelerating the process are especially important early in development. In this presentation, we introduce the latest advancements to our comprehensive high-throughput gene and protein synthesis platforms. From a high-throughput expression and purification platform with single sample traceability to the highly efficient ExpiCHO and Expi293 PRO expression systems, our services are designed to accelerate antibody optimization efforts by enhancing both speed and reliability.

10:20 Coffee Break in the Exhibit Hall with Poster Viewing

SPEED NETWORKING

Meet the Moderator at the Plaza in the Exhibit Hall

Kevin Brawley, Project Manager, Production Operations & Communications, Cambridge Innovation Institute

11:00 Automation of Biochemical Assays Using an Open-Sourced, Inexpensive Robotic Liquid Handler

George Moukarzel, PhD, Senior Scientist, Merck & Co., Inc.

High-throughput Screening uses robotic liquid handlers, but traditional systems are costly and complex. Opentrons' OT-2 is a low-cost (<$10,000), medium-throughput, Python-based alternative. Two assays (PicoGreen and Bradford) showed OT-2's accuracy to be comparable to Tecan EVO systems. Despite lacking a 96-channel pipette, crash detection, and having limited deck space, OT-2 is a cost-effective, open-source tool ideal for early-stage development and method transfer.

11:30 Ada: An Integrated Robotics Work Cell for High-Throughput Functional Assessment of Complex Biologics

Jennifer Houtmann, Senior Assay and Automation Scientist, Biologics Engineering, AstraZeneca

Comprising a robotic arm, ten unique instruments, and a purpose-built, safety-focused enclosure, the Ada work cell enables functional testing of large molecules spanning a breadth of modalities. Leveraging customized software and real-time LIMS integration, the work cell supports advanced ADC and T cell engager mediated cytotoxicity and immunophenotyping assays. This innovative platform accelerates discovery and drives advancements at the forefront of complex biologics research and development.

12:00 pm Building the Lab of the Future for Protein Production in the Age of AI and Automation

Iman Farasat, PhD, Director, Biologics Discovery, Johnson & Johnson Innovative Medicine

The complexity of mammalian cell culture and the heterogeneity of large molecule products have historically limited the application of robotic automation platforms in production and characterization to mainly either early stages for small-quantity, stage-gate quality material, or later stages for industrializing specific task accomplishments. Here, we reveal our next-generation automation strategy to bridge the gap and prepare large-quantity of high-quality material, solving an essential need for more complex biologics modalities.

12:30 Transition to Lunch

12:40 LUNCHEON PRESENTATION: New Biotage® PhyPrep: The Only Walkaway System for Automated Maxi to Giga Scale, Transfection-Grade DNA Plasmid Purification

Biotage

Chris Suh, Regional Market Segment Manager, Biotage

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:

Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

2:15 Close of Conference

WEDNESDAY, JANUARY 21

1:00 pm Registration Open

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

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David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

DRIVING INNOVATION IN PURIFICATION: NOVEL TOOLS FOR COMPLEX BIOLOGICS

2:15 Chairperson's Remarks

David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

2:20 Rapid Affinity-Based Purification of Multispecific Antibodies Using Kappa Select and Protein L

David J. Reczek, PhD, Head of US Biologics Research, Large Molecules Platform, Sanofi

We have designed and engineered a set of purification-enabling mutations into specific regions of multispecific antibody chains which enables a highly effective, rapid and high-throughput, all affinity-based purification scheme for many different formats. This innovation can help accelerate the early identification of lead candidate molecules in research by allowing simple and fast isolation of highly pure material from mixtures of product-related impurities.

2:50 Self-Removing Tags on a Magnetic Bead: Case Studies on Difficult Target Optimization

David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

Magnetic beads have become a common tool for the rapid affinity purification of a wide range of target proteins. We have now combined our self-removing affinity tag with a magnetic core to provide a highly effective platform for quickly purifying tagless proteins. This talk will cover several case studies on the purification of difficult protein targets by optimization of the tag and buffer components for optimal expression and stability.

3:20 High-Throughput Multi-Dimensional Chromatography Configuration for Purification of Large Molecule Therapeutics at Research Scale

Ian Scott, Scientist, Protein Therapeutics, Gilead Sciences

Large-molecule biologics, such as monoclonal and multispecific antibodies, are often desired as potential therapeutics for many indications. Recent advances in automation have increased expression throughput for therapeutic candidates at research scale, but increasing purification throughput for high-quality samples remains a challenge, particularly for asymmetrical multispecific antibody formats. To address this challenge, a multi-dimensional chromatography system was configured to automate 2- and 3-step purification processes using the latest chromatography resins.

3:50 Solving Purification Challenges for Antibody Variants Already in the Capture Step

cytiva

Mahafuzur Rahman, PhD, Scientist, Cytiva R&D

The expanding diversity of antibody-derived therapeutics—including bispecific antibodies and antibody fragments—poses significant challenges for downstream purification. Bispecific antibodies, in particular, are prone to aggregation, exhibit elevated levels of product-related impurities, and often present with lower expression titers compared to conventional monoclonal antibodies (mAbs). These factors complicate process development and necessitate tailored purification strategies to ensure product quality, safety, and manufacturing efficiency.
We will explore how process conditions—such as pH and buffer composition—can impact molecular stability and contribute to impurity formation, including acid-induced aggregation. We will present strategies for the selective removal of product-related impurities during the purification of asymmetric bispecific antibodies (bsAbs) and the use of MabSelect™ mild elution resins in purifying diverse antibody formats.

4:20 Refreshment Break in the Exhibit Hall with Poster Viewing

4:50 Accelerating Multispecific Antibody Production and Purification: Novel Technologies and Automation for High-Throughput, Multi-Milligram Yields

Ayla Sessions, Associate Director, AstraZeneca

Novel labware, integrated automation, and optimized workflows now enable efficient, high-throughput production and purification of multispecific antibodies at multi-milligram scales. Recent advances remove long-standing bottlenecks in harvesting and purifying challenging antibody formats from midscale cultures, supporting seamless, end-to-end automation. These innovations accelerate discovery and development pipelines, advancing the automated manufacture of complex biologics previously limited by labor-intensive manual processes.

5:20 Expanding and Optimizing Purification and Analytical Capabilities for High-Throughput Screening

Daniel Yoo, Scientific Associate Director, Large Molecule Discovery & Research Data Science, Amgen, Inc.

5:50 Close of Day

THURSDAY, JANUARY 22

8:00 am Registration Open

PLENARY KEYNOTE SESSION: End-to-End *in silico*-Designed Biologics

8:25 Welcome Remarks

Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

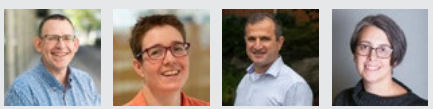
8:30 Plenary Keynote Introduction

Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 PLENARY FIRESIDE CHAT: End-to-End *in silico*–Designed Biologics



Moderator: Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

- How is the path to drug development different with ML/AI?
- How far off is *de novo* design for biologics? For antibodies?
- How is ML/AI used for target selection?
- How do you accelerate DMTA cycles?
- Data standardization—how to incorporate historical data?
- Federated learning—how do you ensure you have enough data to build a model?
- Promoting change management

Panelists:

Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)

Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:30 Coffee Break in the Exhibit Hall with Poster Viewing

WOMEN IN SCIENCE MEET-UP

Meet the Moderators at the Plaza in the Exhibit Hall

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

OPTIMIZING QUALITY AND EFFICIENCY WITH NEXT-GENERATION PROCESS STRATEGIES

10:20 Chairperson's Remarks

David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

10:25 Using Short Solubility-Controlling Peptide Tags for Protein-Biologics Purification

Yutaka KURODA, PhD, Professor, Life Science & Biotechnology, Tokyo University of Agriculture & Technology

Our Ni^{2+}-induced selective precipitation technique enables rapid, high-yield purification of His-tagged proteins. We also developed 5-7-residue short solubility-controlling peptide tags to promote protein solubilization or oligomerization for production and purification. These methods can also be used to enhance the immunogenicity of viral proteins, supporting subunit vaccine development without adjuvants or complex delivery systems. We illustrate this approach using proteins from Japanese encephalitis virus and coronaviruses.

10:55 Early High-Throughput Optimization of Expression Conditions Enabling Streamlined Purification Processes

Cristian Alberto, Senior Associate Scientist, Bristol Myers Squibb

Our strategy focuses on improving product quality during the expression phase to mitigate the contaminant profiles entering the purification stage. By employing mild elution Fc binding resin, we successfully reduced the purification process of complex antibodies from three steps to one, selectively eluting contaminants at different pH values. This optimized approach increases efficiency and ensures high product quality to enable rapid downstream characterization in supporting early discovery research.

11:25 Rethinking Biologics Purification in the Lab of the Future

Sidharth Mohan, PhD, Senior Principal Scientist, High-Throughput Expression Sciences, Biologics Discovery, Johnson & Johnson Innovative Medicine

The purification of Ab-based therapeutics has been simplified by protein-A and other affinity-based methods. Their increasing complexity necessitates downstream polishing steps via manual, customized, and labor-intensive processes to remove product-related contaminants that obfuscate assay execution and triaging. We describe a high-throughput purification platform to effect the production of 10+mgs of high-quality material, automating all aspects of chromatography, liquid-handling, and informatics for delivering >95% purity of material for 100+ molecules/week.

11:55 PANEL DISCUSSION: From Expression to Characterization: High-Throughput Purification Strategies for Multispecific Antibodies

Moderator: David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

As multispecific antibody formats increase in complexity, purfication speed and material quality have become critical bottlenecks in early discovery. In this focused panel, learn from experts as they share practical strategies spanning expression optimization, affinity-based capture, and automated multi-dimensional chromatography. Attendees will gain insights into how integrated purification strategies can accelerate workflows and deliver molecules ready for advanced characterization.

Panelists:

Cristian Alberto, Senior Associate Scientist, Bristol Myers Squibb

Sidharth Mohan, PhD, Senior Principal Scientist, High-Throughput Expression Sciences, Biologics Discovery, Johnson & Johnson Innovative Medicine

David J. Reczek, PhD, Head of US Biologics Research, Large Molecules Platform, Sanofi

Ian Scott, Scientist, Protein Therapeutics, Gilead Sciences

12:25 pm Transition to Lunch

12:30 LUNCHEON PRESENTATION: Tips and Tricks in speeding up Transient HEK293 and Transient/Stable CHO from 96 well, 24 well, 6 well, 125mL-7L Optimum Growth flasks

Sam Ellis, CEO, Thomson Instrument Co

The conditions for Plasmids, Transient HEK293 and Transient/Stable CHO from 96 well, 24 well, 6 well, 125mL-7L Optimum Growth flasks need to be maintained at small scale. Data will be presented on techniques and technology that allow for getting high amounts of protein in smaller volumes with fast techniques from 1mL-3L. This allows teams to get to IND molecules quickly. All of these techniques are proven technologies for protein production, structural biology, and can lead to successful clinical candidates.

1:00 Ice Cream & Cookie Break in the Exhibit Hall with Last Chance for Poster Viewing

WORKFLOW MAKEOVERS: REINVENTING PIPELINES FOR CONSISTENCY, SPEED, AND SCALE

1:40 Chairperson's Remarks

Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

1:45 Advancements in Protein-Expression Workflows for Drug Discovery

Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

This presentation will explore how advancements in protein-expression workflows are revolutionizing drug discovery. We will focus on how new expression technologies—including Bacmam, cell-free systems, and automated high-throughput platforms—enable the rapid and parallelized production of a vast number of protein variants. These integrated workflows provide a robust, efficient, and scalable foundation for the development and characterization of next-generation therapeutic proteins, significantly accelerating the entire drug discovery process.

2:10 Building a Better Pipeline: Setting Up Recombinant Protein Workflows in a New Research Environment

Christopher A. Wassif, PhD, Director, Molecular Engineering & Antibody Technologies, AstraZeneca

Building the laboratory of the future involves space planning, integrating advanced automation, digital data management, and artificial intelligence to accelerate scientific discovery and streamline workflows. Emphasizing modular design and high-throughput capabilities, such laboratories enable seamless collaboration and rapid adaptability to evolving research needs. Enhanced connectivity, real-time data analysis, and scalable infrastructure ensure reproducibility and efficiency, positioning the lab as a dynamic hub for innovation in both foundational and translational science.

2:35 Next-Generation Shake Flasks: Can We Reach Bioreactor-Level Performance?

Vikash Kumar, Senior Scientist, Biologics Process Research and Development, Merck

The Aero-Yield breathable flask replaces traditional polycarbonate flasks. Fabricated with gas-permeable silicone, it enables full-wall-surface O2/CO2 exchange. This improves oxygen flux 58-fold and boosts kLa by 40–100%. Cultures of *E. coli* and *Pichia pastoris* showed 40–66% biomass and 41–115% protein yield gains. With an O2-enriched gas jacket, gains reached 156% in biomass and 140% in recombinant titer, matching bioreactor growth rates. Aero-Yield offers scalable, affordable, bioreactor-like performance for early-stage bioprocessing.

3:00 Harnessing the Power of Incremental Innovation in a Protein-Biochemistry Lab

Christa Cortesio, PhD, Director, Protein Biochemistry & Analytics Core, Kite, a Gilead Company

This presentation will focus on incremental innovations implemented in our small but mighty protein-biochemistry group, highlighting both individual- and group-driven initiatives that have positively influenced productivity and scientific impact. Through this approach, our group has been able to streamline processes, enhance efficiency, and contribute to the development of novel CAR T cell therapies, demonstrating the significant impact that small, iterative improvements can have in a laboratory setting.

3:25 PANEL DISCUSSION: The Evolving Lab: From New Workflows to Scalable Discovery Pipelines

Moderator: Kanika Bajaj Pahuja, PhD, Senior Scientific Manager, Protein Sciences, Genentech

Laboratory workflows are central to advancing drug discovery, yet they face increasing demands for speed, reproducibility, and scalability. This closing panel explores the methodologies, technologies, and strategies reshaping how labs operate today. Panelists will highlight ways to streamline processes, enhance reliability, and build resilient workflows capable of meeting tomorrow's scientific challenges.

Panelists:

Oleg Brodsky, MBA, Senior Principal Scientist, Structural Biology & Protein Sciences, Pfizer Inc.

Christopher Cooper, DPhil, Founder, Protein Sciences, Enzymogen Consulting

Christa Cortesio, PhD, Director, Protein Biochemistry & Analytics Core, Kite, a Gilead Company

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

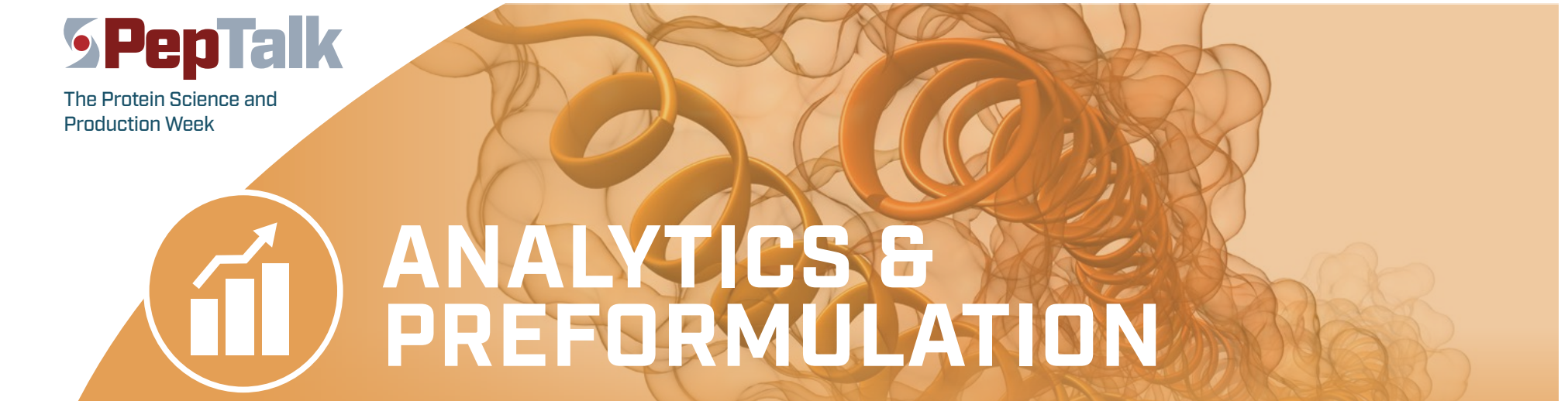
Vikash Kumar, Senior Scientist, Biologics Process Research and Development, Merck

Christopher A. Wassif, PhD, Director, Molecular Engineering & Antibody Technologies, AstraZeneca

4:15 Close of Conference

PepTalk

The Protein Science and Production Week



ANALYTICS & PREFORMULATION

This Analytics & Preformulation pipeline explores the intersection of predictive modeling, formulation science, and analytical innovation in the early development of novel biologics. As the complexity and diversity of biotherapeutic modalities expand, the integration of artificial intelligence, strategic formulation, and robust analytical platforms has become essential for accelerating development timelines and ensuring clinical success. AI/ML Approaches in Immunogenicity Prediction will showcase cutting-edge tools for predicting specific immune responses in early-stage development. The Analytical Strategies for Novel Biologics conference will explore the evolving analytical landscape for next-generation biologics, including modalities of bispecifics, ADCs, fusion proteins, peptides, and RNA-based therapeutics; the Biotherapeutics Aggregation and Preformulation Strategies conference focuses on predicting and mitigating aggregation risk using strategies for early aggregation screening and biophysical characterization while assessing preformulation challenges for novel modalities and high-concentration biologics.

JANUARY 19
SYMPOSIUM

AI/ML Approaches in Immunogenicity Prediction AGENDA

JANUARY 20-21

Analytical Strategies for Novel Biologics AGENDA

JANUARY 21-22

Biotherapeutics Aggregation and Preformulation Strategies AGENDA

AI/ML Approaches in Immunogenicity Prediction

Accelerating Insights with AI/ML Precision

SYMPOSIUM

ANALYTICS & PREFORMULATION

MONDAY, JANUARY 19

8:00 am Registration and Morning Coffee

8:50 Organizer's Welcome Remarks

Julie Sullivan, Associate Producer, Conferences, Cambridge Healthtech Institute

8:55 Chairperson's Remarks

Alessandro Sette, PhD, Professor, Co-Director, Center for Vaccine Innovation, La Jolla Institute for Immunology

9:00 Integrating Computational and *In Vitro* Tools for Comprehensive Immunogenicity Risk Assessment: A Case Study on FLT3L-Fc

Yinyin Li, PhD, Principal Scientist, Biochemical & Cellular Pharmacology, Genentech, Inc.

Immunogenicity risk is a critical consideration in the development of biotherapeutics, particularly during the lead selection phase. To enhance our ability to predict, manage, and mitigate the potential immunogenicity of therapeutic candidates, we have developed a robust strategy that integrates computational and *in vitro* tools for comprehensive risk assessment. This approach enables us to evaluate clinical tolerance risks and optimize drug candidates more effectively.

9:30 Immunogenicity and Sequence Conservation as a Tool to Prepare against Future Possible Pandemics

Alessandro Sette, PhD, Professor, Co-Director, Center for Vaccine Innovation, La Jolla Institute for Immunology

We developed an integrated pipeline to predict and experimentally verify the immunogenic targets recognized by human T cells in viral family of potential pandemic concern. The approach is based on integration of published data curated in the IEDB, bioinformatic predictions and *in vitro* primary immunogenicity assay utilizing human T cells. The immunogenicity data is then integrated with sequence conservation across relevant phylogenetic spaces; and further integrated with AI-based immunogenic design.

10:00 Advancing Preclinical Immunogenicity Prediction: Machine Learning on Clinical Data and Pathogen Cross-Reactivity Integration

Olga Obrezanova, PhD, AI Principal Scientist, Biologics Engineering, Oncology R&D, AstraZeneca

Unwanted immunogenicity presents significant challenges to the safety and efficacy of biological drugs, and current computational and *in vitro* prediction tools have limited clinical relevance. Here, we introduce ImmunoScreen, an *in silico* tool for immunogenicity assessment, integrated within AstraZeneca's lead selection and optimization workflows. We highlight novel approaches aimed at improving prediction accuracy, with a focus on identifying T cell epitopes that are cross-reactive with pathogen sequences.

10:30 Analyzing and Decreasing the Immunogenicity Potential of Biotherapeutics Using *in Silico* Approaches

Michael Gutknecht, PhD, Principal Scientist II, Novartis

Immunogenicity potential assessment should be started as early as possible in the biotherapeutic development process to inform de-immunization approaches and to avoid resources spending on candidates with a high inherent immunogenicity potential. Oftentimes, this is only possible using *in silico* tools. In my presentation, I would like to introduce the audience to the *in silico*-based workflow we implemented to analyze and decrease the immunogenicity potential of biotherapeutics in early development.

11:00 Networking Coffee Break

11:15 Combining Artificial and Human Intelligence to Develop Safer Biotherapeutics

Guilhem Richard, PhD, CTO, EpiVax Inc.

EpiVax has developed the ISPRI platform for assessing the immunogenic risk of biotherapeutics. New AI/ML models have been integrated into ISPRI, leading to enhanced prediction of tolerated epitopes and estimation of ADA responses. These updates have improved characterization of epitopes within biotherapeutic molecules and enabled a six-fold increase in the correlation between predicted and observed ADAs over existing approaches, with over 80% of accurately predicted ADAs.

11:45 Strategic Immunogenicity Risk Assessment of T Cell Engagers: Integrating *in silico*, Proteomics, and *in vitro* Approaches

Daron Forman, PhD, Senior Principal Scientist, Discovery Biotherapeutics, Bristol Myers Squibb

Evaluating the immunogenicity risk of T cell engagers poses distinct challenges, particularly due to the proliferative effects of the CD3-binding arm. This presentation outlines a comprehensive strategy that integrates *in silico* prediction algorithms, the MHC-associated peptide proteomics (MAPPs) assay, and a dendritic cell–PBMC co-culture proliferation model to characterize potential immunogenicity. A case study is presented to demonstrate how these tools collectively inform risk mitigation during development of T cell engagers.

12:15 pm Enjoy Lunch on Your Own

1:30 Chairperson's Remarks

Yuri Iozzo, PhD, Head of Digital Biology, Biologics Drug Discovery, ModeX Therapeutics

1:35 FEATURED PRESENTATION: Application and Opportunities for AI/ML in Immunogenicity Risk Prediction

Timothy Hickling, PhD, Consultant, Quasor Ltd.

AI/ML offers powerful tools for predicting immunogenicity risk in therapeutic development. These approaches enhance early risk assessment, reduce late-stage failures, and guide safer drug design. Opportunities include personalized predictions, improved regulatory confidence, and accelerating translation of biologics, peptides, and novel modalities into the clinic with minimized immunogenicity concerns.

2:05 Cytokine-Informed Machine-Learning Approach to Predict Protein Immunogenicity

Yuri Iozzo, PhD, Head of Digital Biology, Biologics Drug Discovery, ModeX Therapeutics

Understanding and predicting protein immunogenicity remains a central challenge in both therapeutic development and immunological research. We offer a fresh perspective by directly leveraging experimental immune response data combined with machine learning. This approach moves beyond traditional reliance on MHC binding predictions and on the Treg concept. This presentation will highlight the conceptual foundation and emerging applications of cytokine-informed models, emphasizing their potential as complementary tools in immunogenicity prediction.

2:35 Immunological Principles from *in silico* to In Patients

Maurizio Zanetti, PhD, Professor, Principal Investigator, Tumor Immunology Lab, University of California San Diego

This presentation discusses immunological principles to guide AI/ML epitope selection in cancer. I will cover the limitations of current vaccine trials and what we can do in the future.

3:05 Networking Refreshment Break

3:30 Reverse Translation: Using Clinical Insights to Guide Preclinical Risk-Assessment Machine-Learning Models

Daniel Leventhal, PhD, Principal Consultant, Tactyl

By analyzing real-world patient outcomes, adverse events, and biomarker responses, AI/ML can identify patterns and mechanistic insights that guide safer drug design. This approach improves predictive accuracy, reduces late-stage failures, and aligns preclinical testing with clinical realities, enabling more efficient development of therapeutics and facilitating targeted strategies for safety, efficacy, and personalized medicine.

4:00 Emerging Opportunities for More Multimodal Precision in the Emerging NeuroSymbolic and Agentic Models of Machine Learning

John Mattison, MD, Scholar-in-Residence, Responsible AI and Advanced Technologies, University of California San Diego

LLMs and related chatbots have accelerated adoption of machine learning technologies, but fall far short in modeling the complexities of homeostatic human physiology or incorporating more human-curated approaches. RAG architectures are helpful, but full exploitation of neurosymbolic learning and agentic approaches in concert will drive the next generation of discovery.

4:30 PANEL DISCUSSION: Next-Gen Immunogenicity: Harnessing AI and Machine Learning

Moderator: Timothy Hickling, PhD, Consultant, Quasor Ltd.

- What does the future of immunogenicity look like?
- What are the impacts on safety, efficacy, and clinical success?
- How can we drive the future of AI and Machine Learning for Immunogenicity?

Panelists:

Yuri Iozzo, PhD, Head of Digital Biology, Biologics Drug Discovery, ModeX Therapeutics

Guilhem Richard, PhD, CTO, EpiVax Inc.

TUESDAY, JANUARY 20

7:30 am Registration and Morning Coffee

CHARACTERIZING NOVEL BIOLOGICS

8:30 Organizer's Remarks

Julie Sullivan, Associate Producer, Conferences, Cambridge Healthtech Institute

8:35 Chairperson's Remarks

Philip White, PhD, Project Head, Global Research, Sanofi

8:40 Applicability of Hydrophobic Interaction Chromatography for Determining Drug-to-Antibody Ratio of Antibody-Drug Conjugates

Masahiro Mimura, PhD, Analytical Researcher, Analytical Research Labs

Hydrophobic interaction chromatography (HIC) is widely used to determine drug-to-antibody ratio (DAR), a critical quality attribute of ADCs. However, some ADCs present challenges in DAR determination by HIC due to poor peak separation of DAR variants, with the root causes remaining unclear. We investigated which ADC properties impact peak separation in HIC and identified linker length as one of the structural features significantly affecting the peak separation.

9:10 Driving Bioanalytical Method Development

Javier Aguilera, PhD, Senior Scientist, Bioanalytical & Molecular Assays, Moderna

Driving bioanalytical method development is crucial for advancing drug discovery and development. Robust methods ensure accurate measurement of therapeutic candidates, metabolites, and biomarkers in complex biologics. Continuous innovation and optimization drive efficiency, accelerate timelines, and enhance data quality, ultimately enabling safer and more effective therapies.

9:40 Analytical Characterization Strategies for Delivery of High-Quality mRNA Vaccines

Gautam Sanyal, PhD, Principal Consultant, Vaccine Analytics, LLC

Structural integrity of an mRNA construct encoding the antigenic protein is key to potency of an mRNA vaccine. Additionally, for vaccines delivered in lipid nanoparticle (LNP) formulations, physicochemical properties of LNPs impact cellular and translation of mRNA to deliver the encoded protein antigen. Measurements of structural and biophysical properties of the mRNA payload and the LNPs can be correlated to protein-expression efficiency (potency) *in vitro* and immunogenicity *in vivo*.

10:10 High Throughput Characterization of Biologics and Their Stability via Cuvette Based Dialysis and Automatic Continuous Dilution

Curt Jarand, PhD, Research Assistant Professor, Physics & Engineering Physics, Tulane University

This recent cuvette-based technology allows characterizing of biologics and their stability, critical for formulation optimization, including avoidance of aggregation. It encompasses two technologies; i) monitoring the effects on biologics, including their reversibility, as agents are dialyzed in or out; these latter include electrolytes, surfactants, denaturants, and other excipients, and ii) measuring Molecular Weight, virial coefficients (A2, B22), kD for diffusion coefficients, CMC, and dissolution rates using automatic continuous dilution.

10:10 Presentation to be Announced

QUARTZY

10:40 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

11:20 NMR Toolkit Development for Structural Fingerprinting of Short Oligonucleotide Therapeutics

Robert G. Brinson, PhD, Research Chemist, IBBR, NIST

Short oligonucleotides are an emerging platform for rare diseases, offering high specificity and ease of design. Their chemical modifications impact important molecular attributes, yet low-resolution methods often provide insufficient characterization. Here, we present NMR techniques for structural fingerprinting and compare these results to other analytical methods. We employ statistical tools, enabling the detection of subtle molecular variations. Our work establishes NMR for fingerprinting of important quality attributes of oligonucleotide therapeutics.

11:50 FEATURED PRESENTATION: Advancing mRNA Platform Technologies: Integrating Analytics, Manufacturing, and Regulatory Strategies

Philip White, PhD, Project Head, Global Research, Sanofi

The presentation will cover mRNA-LNP technology as a flexible platform for vaccine development, focusing on standardized manufacturing processes and analytical methods in CMC. Benefits of this approach, including accelerated timelines and streamlined submissions, will be discussed. The speaker will address industry efforts to establish mRNA-LNP as a recognized platform technology and present a comprehensive framework for evaluating changes to platform components while maintaining quality and consistency across products.

12:20 pm Transition to Lunch

12:30 Enjoy Lunch on Your Own

1:00 Refreshment Break in the Exhibit Hall with Poster Viewing

LINKEDIN SKILLS WORKSHOP

Meet the Moderator at the Plaza in the Exhibit Hall

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

BIOANALYTICAL METHOD DEVELOPMENT AND AAV ASSESSMENT

1:30 Chairperson's Remarks

JiMin Lee, PhD, Professor, KAIST

1:35 Navigating Developability in Novel Antibody Formats: Lessons from Antibodies with Extended Hypervariable Loops

Marcel Passon, PhD Researcher, Biopharmaceutical Technology, Ghent University / Technical University of Munich

Developability guidelines primarily reflect conventional antibody architectures, leaving innovative formats with extended CDR loops underexplored. Antibodies bearing long or ultra-long CDR-H3 regions – particularly those forming autonomous antigen-binding domains known as picobodies – offer new therapeutic opportunities but remain poorly characterized from a biophysical standpoint. We examine their developability profiles, defining principles for identifying format-specific liabilities and guide engineering strategies that expand current frameworks for unconventional antibody formats

2:05 Assessment of Adeno-Associated Virus (AAV) Purity by Capillary Electrophoresis-Based Western

Julyana Acevedo, PhD, Scientist II, Analytical Development, Sangamo Therapeutics, Inc.

In the development of AAV-based gene therapies, it is important to obtain a drug product with high purity. CE-Western assays enable increased throughput and automated workflows for the analytical assessment of AAV, such as assays to quantify the relative stoichiometry of viral proteins (VP). We demonstrated that CE-Western can be used as a high-throughput platform to assess the identity, composition, and purity of rAAV drug products.

MOLECULAR INTERACTION CHARACTERIZATION

2:30 Chairperson's Remarks

Xiangdan Wang, PhD, Senior Principal Scientist, BioAnalytical Sciences, Genentech, Inc.

2:35 Rapid Development of Dual-specific Antibody Therapeutics Using AI-driven Design with High-Throughput Cell-based Binding and SPR Analyses

Jack Hu, PhD, Director, Aureka Bio

The rapid development of dual-specific antibody therapeutics is being revolutionized by AI-driven design combined with high-throughput cell binding technologies. AI accelerates candidate prediction, optimizing binding affinity and specificity for dual targets. High-throughput screening enables efficient evaluation of thousands of antibody variants against cell populations. Together, these innovations significantly reduce development timelines and enhance precision.

3:05 Biosensor to Bedside: Tuned Fc Receptor Kinetics Enhances *ex vivo* Immune Activation in Rilvegostomig

Thomas Moon, PhD, Associate Director, Lead, Biomolecular Interactions Team, AstraZeneca

3:35 Refreshment Break in the Exhibit Hall with Poster Viewing

PLENARY KEYNOTE SESSION: TRENDS AND INNOVATION DRIVING THE FUTURE OF BIOTHERAPEUTICS

4:30 Welcome Remarks

Mimi Langley, Executive Director, Life Sciences, Cambridge Healthtech Institute

4:35 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 From Targets to Biologics: AI Powering the Next Leap in Discovery at Takeda

Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

Takeda's AI/ML strategy is redefining the path from targets to biologics, using advanced models to identify and validate novel targets, decode complex biology, and design the next generation of high-quality therapeutic molecules. By integrating agentic, generative, and large language model–driven approaches, AI is powering the next leap in discovery at Takeda.

4:50 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing

Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences

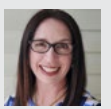
As biotherapeutics become more complex, automation of traditional testing labs falls short of delivering the insights needed for regulatory success. This talk introduces a GxP-native, full-stack AI platform designed to orchestrate and optimize mass spectrometry-based testing workflows across CMC, bioanalysis, and regulatory reporting. Rooted in regenerative system design, this infrastructure enables scalable, adaptive, and compliant operations, empowering biopharma teams to accelerate product development with confidence, clarity, and scientific precision.

5:00 Technological Trends Shaping the Landscape of Biopharmaceuticals

Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil

Currently, the biopharmaceutical industry is undergoing rapid technological advancements that are revolutionizing development and production of biopharmaceuticals. Consequently, new therapeutic categories are gaining prominence, such as antibody-drug conjugates, bispecific antibodies, advanced therapies, among others. This rapid evolution requires constant vigilance to identify breakthroughs and guiding strategic decision-making in this dynamic field. The aim of this strategic foresight analysis is to discuss technological trends for the future of biopharmaceuticals.

5:10 PLENARY FIRESIDE CHAT




Moderator: Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

Kicking off with three focused 10-minute presentations, the Fireside Chat transitions into an engaging 30-minute fireside discussion. Panelists will delve into cutting-edge topics, including the role of AI/ML in biologics discovery, advancements in next-generation analytics and tools, entrepreneurial trends and investment landscapes, and emerging therapeutic modalities. In tribute to Dr. King's legacy, this session will also highlight the importance of fostering diversity, equity, and inclusion within the biotech innovation ecosystem.

Panelists:
Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences
Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil
Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

5:40 Networking Reception in the Exhibit Hall with Poster Viewing

YOUNG SCIENTIST MEET-UP

Meet the Moderator at the Plaza in the Exhibit Hall

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

6:40 Close of Day

WEDNESDAY, JANUARY 21

7:15 am Registration Open

BuzZ Sessions

7:30 BuzZ Session with Continental Breakfast

BuzZ Sessions are informal, moderated discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the BuzZ Sessions page on the conference website for a complete listing of topics and descriptions.

BuzZ Table 5: Trends in Analytical Data

Marcel Passon, PhD Researcher, Biopharmaceutical Technology, Ghent University / Technical University of Munich

BuzZ Table 6: Current Control Strategies for Characterization- What is Next?

Kevin Zen, PhD, Principal Consultant, Biologics CMC Consulting

MOLECULAR INTERACTION CHARACTERIZATION CONTINUED

8:15 Chairperson's Remarks

Wei Wang, PhD, Senior Principal Scientist, Therapeutic Discovery, Amgen, Inc.

8:20 Affinity Analysis of Novel Binders and Target Specificity

Eric Janezic, PhD, Principal Scientist, Genentech Inc.

Characterizing antibody-receptor interaction kinetics (kon, koff, KD) is crucial for drug discovery, but traditional biophysical methods are not always amenable for complex antibodies or targets. This talk presents alternative cell-based binding assays. We also introduce a novel label-free pre-equilibrium assay to simultaneously determine kon, koff, and KD for up to 30 therapeutic antibodies on live cells using the Gyrolab platform, offering a solution for screening challenging drug formats.

8:50 Application of SPR Chaser Assay to Study Biomolecular Interactions with Very Slow Off Rate

Wei Wang, PhD, Senior Principal Scientist, Therapeutic Discovery, Amgen, Inc.

Binding kinetics of therapeutics and its target protein are crucial for the efficacy and safety of the drug. Using surface plasmon resonance (SPR) technology, we performed a competitive SPR chaser assay, a method to study biomolecular interactions with very slow dissociation rate constants (kd < 1E-4 s-1). In this talk, the principle and the experimental setup of the chaser assay will be discussed.

9:20 Application of Molecular Interaction Characterization in Support of Bioanalysis of Therapeutics

Xiangdan Wang, PhD, Senior Principal Scientist, BioAnalytical Sciences, Genentech, Inc.

Bioanalytical assays are crucial for therapeutic development, enabling dose regimen determination, efficacy, and safety assessment. Integrating molecular interaction (MI) characterization into bioanalytical assay development provides deeper insights into underlying interaction mechanisms, thereby enhancing assay performance, expediting the development process, and ultimately improving therapeutic outcomes. This presentation will highlight case studies on applying various MI characterization tools in supporting the bioanalysis of biotherapeutics, showcasing their benefits in bioanalytical workflows.

9:50 High-Resolution Biotherapeutic Structural Characterization by Flash Oxidation (Fox®) Protein Footprinting

Emily Chea, Applied Research & Product Manager, GenNext Technologies Inc.

GenNext's innovative Fox® Protein Footprinting Platform provides rapid, high-resolution insights into biotherapeutic structures, offering throughput and reproducibility that exceed conventional structural biology approaches. Fox Technology enables highly sensitive detection of conformational changes and interaction sites across complex protein systems. Purpose-built for research on biotherapeutics and monoclonal antibodies, small molecule drugs, and AI model validation, the platform supports applications such as epitope and paratope mapping, aggregation analysis, biosimilarity assessment, and target engagement studies. This presentation highlights the workflow's key advantages, compares automated protein footprinting with traditional methods, and reviews an epitope mapping experiment that demonstrates both exceptional structural resolution and unprecedented analytical throughput.

10:20 Coffee Break in the Exhibit Hall with Poster Viewing

SPEED NETWORKING

Meet the Moderator at the Plaza in the Exhibit Hall

Kevin Brawley, Project Manager, Production Operations & Communications, Cambridge Innovation Institute

CHARACTERIZING SINGLE PARTICLE AND HOST CELL PROTEINS

11:00 Current Control Strategies for Host Cell Proteins in Biotherapeutic Products

Kevin Zen, PhD, Principal Consultant, Biologics CMC Consulting

Residual host cell proteins (HCPs) in biotherapeutic drug products are the process impurities that can compromise stability and safety and must be carefully monitored and evaluated. Current control strategies of HCPs in biotherapeutic drug products involve a combination of upstream process controls, downstream chromatography and filtration, as well as advanced analytical methods such as immunoassays (ELISA) and proteomic mass spectrometry for monitoring and risk mitigation.

11:30 Automated, Quantitative Capillary Western Blots to Analyze Host Cell Proteins in COVID-19 Vaccine Produced in Vero Cell Line

Richard R. Rustandi, PhD, Senior Research Scientist, Vaccine Analytical R&D, Merck & Co.

Host cell proteins are critical attribute for biologics and vaccines. Currently, there are only two methods to analyze this, namely, ELISA for official release method, and mass spectrometry for characterization. However, ELISA method is actually not compatible with anti-sera reagent validation method of 2D western blot. Here we developed quantitative and automated alternative method for HCP, capillary western blot, which is compatible with reagents validation.

12:00 pm Single Particle Analysis Technology for Applications in Both Vaccines and Therapeutics

Sabrina Leslie, PhD, Associate Professor, Department of Physics, The University of British Columbia

CLiC (Convex Lens-Induced Confinement) is a platform for quantitative single-particle and single-cell imaging, combining label-free interferometric scattering (iSCAT) with multi-channel fluorescence. This enables simultaneous measurement of nanoparticle size, mRNA payload, mass, and dynamics in cell-like conditions (Kamanzi et al., ACS Nano 2024, 2021; Boateng et al., Nano Lett. 2025). CLiC supports high-throughput, precision characterization for mechanistic studies and quality control of mRNA-LNP vaccines and therapeutics across manufacturing and biological settings.

12:30 Transition to Lunch

12:40 Enjoy Lunch on Your Own

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

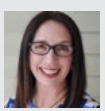
1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:




Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

2:15 Close of Conference

WEDNESDAY, JANUARY 21

1:00 pm Registration Open

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:

Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

NOVEL MODALITIES AND HIGH-CONCENTRATION BIOLOGICS

2:15 Chairperson's Remarks

Pin-Kuang Lai, PhD, Assistant Professor, Chemical Engineering and Materials Science, Stevens Institute of Technology

2:20 High-Throughput Small-Angle X-Ray Scattering for Rapid Screening of High-Viscosity mAbs

Pin-Kuang Lai, PhD, Assistant Professor, Chemical Engineering and Materials Science, Stevens Institute of Technology

High-throughput small-angle X-ray scattering (SAXS) enables early viscosity prediction of high-concentration monoclonal antibody (mAb) formulations by detecting self-association at dilute concentrations. Synchrotron SAXS was applied to 22 mAbs, revealing low-q upturns below 10 mg/mL for high-viscosity candidates. A classification based on structure factor transitions accurately distinguished high- and low-viscosity mAbs. This SAXS-based method offers a scalable, sample-efficient alternative to traditional, volume-intensive viscosity measurements.

2:50 Naturally Occuring Deep Eutectic Solvents (NADES): Identification, Characterization and Low Temperature Applications

Allison Hubel, PhD, Professor, Mechanical Engineering, University of Minnesota Twin Cities

NADES typically contain natural metabolites such as sugar, sugar alcohols and amino acids. We have developed methods of prescreening candidate NADES forming molecules and then using quantum chemical modeling (COSMO-RS) to predict the phase behavior of NADES forming combinations. In addition, characterization of the NADES at low temperatures will be discussed as well as applications for NADES across a variety of applications including protein stabilization, cryopreservation and de-icing/anti-icing applications.

3:20 NMR Insights into Solution Behavior and Formulation Challenges of Novel Biologics and High-Concentration MAbs

Mark McCoy, PhD, Senior Principal Scientist, Quantitative Biosciences, Merck

Advanced NMR techniques provide critical insights into the solution behavior of novel biologics, particularly under high-concentration conditions relevant to therapeutic formulations. We will highlight how NMR reveals aggregation, conformational stability, and molecular interactions that impact developability and shelf-life. These insights help address key formulation challenges, enabling the design of stable, effective biologic drugs.

3:50 HPβCD as a Stabilizing Excipient: Reducing Soluble and Insoluble Aggregates in Protein Formulations

Bowen Jiang, PhD, Principal Scientist, Bioformulation & Process Development, Gilead Sciences Inc

Protein drug products offer high specificity and potency but face a major challenge: aggregation, which can compromise safety and efficacy. This study evaluates Hydroxypropyl-β-cyclodextrin (HPβCD) as an excipient to reduce both soluble and insoluble aggregation by stabilizing protein conformation and mitigating interfacial stress. Using six protein formulations under various storage and stress conditions, we assessed HPβCD's impact on aggregation and explored its mechanisms through experimental and *in silico* modeling.

4:20 Refreshment Break in the Exhibit Hall with Poster Viewing

4:50 Optimizing Monoclonal Antibody Structure and Dynamics through Formulation Variables: Insights from Diffusing Wave Spectroscopy and Microfluidic Analysis

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

This presentation addresses the challenges of developing stable, high-concentration mAb formulations, where protein-protein interactions increase viscosity and affect stability and injectability. Using minimal-sample techniques (DLS,DWS, and NanovisQ), it examines how pH, salt type, and temperature influence aggregation behavior and rheological properties. The findings provide actionable insights into how formulation variables can be turned to control aggregation and improve product stability.

5:20 Cuvette-Based Spectroscopic Technology for the Formulation and Stabilization of Biologics

Sylvia Austin, Commercial Lead, Biologics Spectroscopy, Tulane University

Tulane University has developed a cuvette-based spectroscopic platform providing comprehensive formulation data on the stability and aggregation of biologics. By enabling real-time monitoring of protein, peptide, or other biologic aggregation under a continuous excipient concentration gradient, researchers can identify optimal formulation parameters to support formulation development and

optimization. This presents an overview of the technology's design and capabilities, and summarizes market research findings on its applications in biologic drug development.

5:50 Close of Day

THURSDAY, JANUARY 22

8:00 am Registration Open

PLENARY KEYNOTE SESSION: End-to-End *in silico*-Designed Biologics

8:25 Welcome Remarks

Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

8:30 Plenary Keynote Introduction

Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 PLENARY FIRESIDE CHAT: End-to-End *in silico*–Designed Biologics




Moderator: Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

- How is the path to drug development different with ML/AI?
- How far off is *de novo* design for biologics? For antibodies?
- How is ML/AI used for target selection?
- How do you accelerate DMTA cycles?
- Data standardization—how to incorporate historical data?
- Federated learning—how do you ensure you have enough data to build a model?
- Promoting change management

Panelists:
Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)
Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:30 Coffee Break in the Exhibit Hall with Poster Viewing

WOMEN IN SCIENCE MEET-UP

Meet the Moderators at the Plaza in the Exhibit Hall

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

CUTTING-EDGE APPROACHES TO PROTIEN STABILITY

10:20 Chairperson's Remarks

Christian Schoeneich, PhD, Takeru Higuchi Distinguished Professor & Chair, Pharmaceutical Chemistry, University of Kansas Lawrence

10:25 FEATURED PRESENTATION: Mechanisms of Near-UV and Visible-Light Degradation of Therapeutics Proteins

Christian Schoeneich, PhD, Takeru Higuchi Distinguished Professor & Chair, Pharmaceutical Chemistry, University of Kansas Lawrence

Evidence is mounting that formulations of therapeutic proteins are susceptible to photo degradation by near-UV and visible light, but little to no information is available on the underlying chemical reactions. Here, we present evidence that monoclonal-antibody photo degradation is promoted by common excipients such as histidine and impurities, such as Fe(III), leading to site-specific fragmentation and radical conversion mechanisms of amino acid residues located within one or more metal-binding domains.

10:55 Spectroscopic Monitoring of Biologic Stability under Continuously-Changing Formulation Conditions

Wayne F. Reed, PhD, Professor, Physics, Tulane University

A new device and methodology spectroscopically monitor how biologics behave as formulation conditions change continuously using dialysis. This allows rapid, real-time determination of regions of biologic stability as the concentrations of electrolytes, surfactants, and other excipients vary. Using complete dialysis cycles the reversibility of aggregates and other associations can also be assessed

11:25 Freeze/Thaw of Biologicals: Degradation Mechanisms and Stabilization Strategies

Evgenyi Y. Shalaev, PhD, FAAPS, Distinguished Research Fellow, Pharmaceutical Sciences, Abbvie, Inc.

Although many biotech products are successfully stored in the frozen state, there are cases of degradation of biologicals during freeze storage. The degradation (e.g., aggregation) has been often linked to crystallization of a cryoprotector or pH changes while other factors include protein crowding and unfolding (either due to cold denaturation, interaction of protein molecules with ice crystals, or air bubbles formed on the ice crystallization front) and mechanical stresses.

11:55 Industry Highlight: Protein Stability

Danny Chou, PhD, President and Founder, Compassion BioSolution, LLC

12:25 pm Transition to Lunch

12:30 Enjoy Lunch on Your Own

1:00 Ice Cream & Cookie Break in the Exhibit Hall with Last Chance for Poster Viewing

FORMULATION STRATEGIES FOR PEPTIDES

1:40 Chairperson's Remarks

Huyen Tran, PhD, Director, Formulation Research, Eli Lilly & Company

1:45 Controlling Gastric Delivery of a GIP/GLP1 Peptide in Monkeys by Mucoadhesive SNAC Tablets

Huyen Tran, PhD, Director, Formulation Research, Eli Lilly & Company

In this presentation, we will discuss strategies to enhance oral peptide bioavailability. This includes understanding the impact of peptide properties on oral absorption in the presence of permeation

enhancers, as well as the effect of delivery site. Combining peptide engineering for oral delivery and formulation optimization for site-specific delivery can improve oral bioavailability. Additionally, we will present the controlled gastric delivery of a GIP/GLP-1 peptide in monkeys using mucoadhesive SNAC tablets.

2:10 Immunogenicity of Generic Peptide Impurities: Current Orthogonal Approaches

Aimee Mattei, Director of Bioinformatics, EpiVax Inc.

Widespread use of peptide drugs like Ozempic raises concerns about the immunogenicity risks posed by generic versions. This presentation introduces orthogonal immunogenicity risk assessment methods for generic peptide drug impurities under the FDA's Abbreviated New Drug Application (ANDA) pathway, focusing on two case studies: salmon calcitonin and teriparatide, to illustrate that understanding the inherent immunogenicity of the active pharmaceutical ingredient (API) is critical to estimating the potential immunogenicity of impurities.

2:35 Next-Generation Delivery of Peptides: Enhancing Stability and Barrier Penetration

Nitin Joshi, PhD, Assistant Professor, Harvard Medical School, Associate Bioengineer, Department of Anesthesiology, Peripoperative and Pain Medicine, Brigham and Women's Hospital

Our work focuses on biointelligent biomaterial platforms that overcome the intrinsic barriers limiting peptide therapeutics.I will discuss how enzyme-responsive nanoparticles and hydrogels sense and respond to diseased microenvironments—stabilizing fragile peptides, navigating mucus and epithelial barriers, and localizing therapy with precision. These adaptive systems enable sustained delivery in the lung, mucosa, and osteoarthritic joints, opening new possibilities for clinically transformative peptide medicines.

3:00 MA-[D-Leu-4]-OB3: A Safe, Effective, and User-Friendly Synthetic Peptide Leptin Mimetic for the Treatment of Metabolic and Neurologic Dysfunctions

Patricia Grasso, PhD, Professor, Medicine, Neurosciences & Experimental Therapeutics, Albany Medical College

MA-[D-Leu-4]-OB3 is a synthetic peptide leptin mimetic encompassing the functional epitope of the leptin molecule and engineered for optimal pharmacokinetics, efficacy, and oral or nasal administration. In mouse models of obesity, diabetes, and cognitive impairment, MA-[D-Leu-4]-OB3 has been shown to be safe and to have therapeutic and prophylactic efficacy. MA-[D-Leu-4]-OB3 reduces body weight gain, enhances insulin sensitivity, normalizes blood glucose, reverses diabetic dyslipidemia, promotes bone turnover, and enhances memory/cognition.

3:25 PANEL DISCUSSION: Formulating the Future—Innovations in Peptide Therapeutics

Moderator: JiMin Lee, PhD, Professor, KAIST

- Innovations in design to overcome stability, solubility, and delivery challenges of peptides
- Advances in delivery technologies (oral, transdermal, long-acting injectables, nanoparticles) shaping the future of peptide drugs
- Manufacturing innovations and scale-up considerations for clinical and commercial success
- Regulatory and clinical hurdles in bringing novel peptide formulations to patients
- Future outlook: where peptides can best compete or complement small molecules and biologics

Panelists:

Patricia Grasso, PhD, Professor, Medicine, Neurosciences & Experimental Therapeutics, Albany Medical College

Nitin Joshi, PhD, Assistant Professor, Harvard Medical School, Associate Bioengineer, Department of Anesthesiology, Peripoperative and Pain Medicine, Brigham and Women's Hospital

Aimee Mattei, Director of Bioinformatics, EpiVax Inc.

4:15 Close of Conference

PepTalk

The Protein Science and Production Week

PEPTIDE EXPRESSION & DEVELOPMENT - NEW

The peptide field is evolving, with high-throughput platforms and biologically relevant systems driving the next generation of leads with powerful discovery platforms including AI/ML, high-throughput screening, and advanced display technologies. While chemical synthesis remains a foundational tool, the integration of recombinant expression is expanding what's possible, offering scalable, sustainable, and cost-effective routes to complex peptides.

JANUARY 19
SYMPOSIUM

Peptide Drug Hunting 101: The Life of a Peptide

AGENDA

JANUARY 20-21

Peptide Targets: Discovery, Expression, and Validation

AGENDA

JANUARY 21-22

Peptide Therapeutics: Accelerating Discovery and Development

AGENDA

MONDAY, JANUARY 19

8:00 am Registration and Morning Coffee

SCREENING TOOLS AND DESIGN RULES FOR PEPTIDE DRUG HUNTING

9:00 Organizer's Welcome Remarks

Mary Ann Brown, Executive Director, Conferences; Team Lead, PepTalk, Cambridge Healthtech Institute

9:05 Chairperson's Welcome Remarks

Charles Johannes, PhD, Founder, President, and Chief Scientist, EPOC Scientific LLC; Vice President, Peptide Drug Hunting Consortium

9:10 Multidisciplinary Peptide Science and Breakthrough Peptide Medicines

Charles Johannes, PhD, Founder, President, and Chief Scientist, EPOC Scientific LLC; Vice President, Peptide Drug Hunting Consortium

The amazing story of peptide science and breakthrough peptide medicines is still being written. Great advancements in peptide chemistry, biology, structural biology, computational chemistry, pharmacokinetics, and drug delivery have been achieved. Leveraging such knowledge, a new generation of multidisciplinary peptide-drug hunters is now contributing to diverse peptide modalities, lead optimization, screening tools, design rules, and translation into the clinic campaigns. This talk will highlight this inspiring, yet unfinished story.

9:40 Novel Ways for Generating Cyclic Peptides

Parisa Hosseinzadeh, PhD, Assistant Professor, Department of Bioengineering, University of Oregon

Proteins have long been central to biological design, but peptides offer unique advantages, such as membrane interaction and ease of synthesis. Yet, key questions remain: Can deep learning be applied to them? How do they cross membranes? In this talk, I will share recent successes in peptide research and discuss the challenges and opportunities that lie ahead.

10:10 Harnessing AI and Molecular Modeling for Next-Generation Helical Peptide Design

Kellon A. A. Belfon, PhD, Senior Computational Chemist, Parabilis Medicines

This talk reviews computational approaches to peptide design and introduces our integrated computational-experimental platform for Helicons. Helicons are helically constrained peptides that enable modulation of intracellular targets often inaccessible to small molecules. Early traditional structure-based methods showed promise but faced transferability limits across peptide modalities. Emerging frameworks that combine predictive and/or generative machine learning with physics-based modeling offer new opportunities to achieve greater predictive accuracy and efficiency.

10:40 Selected Poster Presentation Functional Screening of AI-Designed Peptide Libraries Identifies Novel Opioid GPCR Agonists

Simon R. Bushell, PhD, External Innovation & Business Development, Orbit Discovery

AI tools can generate vast therapeutic libraries, but biological evaluation remains a major bottleneck. Orbit Discovery's Functional Screening platform combines microfluidics with DNA-encoded peptide libraries to rapidly assess millions of peptides. In collaboration with ProteinQure, we screened an AI-designed library to identify novel Delta and Mu Opioid Receptor agonists. We present our screening workflow and validation data, demonstrating efficient translation of AI designs into therapeutic hits.

11:00 Networking Coffee Break

11:15 High-Throughput Screening Platforms for *de novo* Peptide Discovery

Olena S Tokareva, PhD, Director, Hit Discovery Platform, Parabilis Medicines

Advances in high-throughput screening methods have been critical for enabling peptide-based drug discovery. In this talk, we present an overview of the screening approaches commonly used today, including ribosomal-based methods such as phage display and mRNA display, and synthetic methods such as DNA-encoded libraries and one-bead-one-compound screening. We will share examples where parallelized phage screening was used to discover novel helical peptides (Helicons) and molecular glues to challenging intracellular targets.

11:45 Discovery of Oral Macrocyclic Peptide Leads from High-throughput Screening

Emel Adaligil, PhD, Executive Director, Chemical Biology and Peptide Macrocycles, Eli Lilly and Company

Although there are several examples of macrocyclic peptides showing that they are promising drug candidates to inhibit protein-protein interactions, developing orally available macrocyclic peptides is still a challenge. Developing oral macrocyclic peptides is a two-step process that is required to be optimized simultaneously due to its complex 3D solution conformations: optimization of affinity/activity and oral bioavailability. This talk reviews how to utilize mRNA display platforms to develop oral macrocyclic peptides.

12:15 pm Enjoy Lunch on Your Own

TARGET SPACE, DRUG DELIVERY AND PEPTIDE THERAPEUTIC CASE STUDIES

1:45 Chairperson's Welcome Back

Charles Johannes, PhD, Founder, President, and Chief Scientist, EPOC Scientific LLC; Vice President, Peptide Drug Hunting Consortium

1:50 Peptide Therapeutics Target Selection Strategies

Anastasia Velentza, PhD, Vice President, Biology, Vilya Therapeutics

Peptide-based therapeutics hold a unique and advantageous space in the pharmacological landscape of therapeutic modalities. They bridge the gap between conventional small molecules and biologics, allowing them to combine their best attributes while overcoming their limitations. Drug-target selection strategies are fundamental in providing therapeutic modality advantage while creating opportunities to address unmet medical needs. Target-selection strategies and experimental approaches for target identification will be discussed.

2:20 Challenges in Oral Peptide Delivery and Ways How to Overcome Them

Thomas Von Erlach, PhD, Co-Founder & CSO, Vivtex Corporation

Despite decades of research, peptide therapeutics are still largely limited to needle administration due to insufficient oral bioavailability. This presentation will go over current limitations in the field of peptide drug delivery and most recent advancements to overcome them. Specifically, the identification of suitable permeation enhancers and challenges associated converting these from liquid formulation concepts into clinically and commercially viable solid dosage formulations.

2:50 Networking Refreshment Break

3:15 Oral Peptide Antagonists Targeting the IL-23/IL-17 Axis

Mariana Manrique, PhD, Senior Director, Biology, Protagonist Therapeutics Inc

Oral peptide antagonists targeting IL-23/IL-17 are an emerging class for chronic immune-mediated diseases. Icotrokinra (JNJ-2113), the first oral IL-23 receptor antagonist, showed strong efficacy and safety, achieving durable skin clearance in Phase 3 psoriasis trials and clinical response and remission in Phase 2 ulcerative colitis, advancing to Phase 3 for UC and Crohn's. PN-881, a next-generation oral IL-17 antagonist, offers broad IL-17 inhibition, high stability, and compelling preclinical efficacy.

3:45 Discovery of FOG-001, a Clinical-Stage Helicon Inhibitor of the Beta-Catenin/TCF4 Interaction

Brian White, PhD, Senior Director, Parabilis Medicines

Wnt signaling pathway mutations leading to constitutive activation of ß-catenin occur in at least 15% of all human cancers. We have developed FOG-001, a hyperstabilized a-helical peptide (Helicon) that binds directly to ß-catenin, achieves cytosolic exposure, and inhibits Wnt pathway signaling. Multiple backbone cyclizations enforce peptide helicity, and unnatural amino acids on ß-catenin-facing residues yield picomolar binding affinity. FOG-001 demonstrates pharmacodynamic modulation and efficacy in Wnt pathway activated tumors.

4:15 PANEL DISCUSSION: Breaking Down Silos—Integrating Disciplines to Accelerate Peptide Drug Discovery

Moderator: Charles Johannes, PhD, Founder, President, and Chief Scientist, EPOC Scientific LLC; Vice President, Peptide Drug Hunting Consortium

As peptide therapeutics grow in complexity, cross-disciplinary collaboration has become critical for success. Panelists will discuss strategies to bridge functional silos, share lessons from real-world peptide programs, and highlight enabling tools that foster translational progress. We will also examine how external experts can amplify internal teams to accelerate peptide programs from design to translation. The session aims to inspire a unified approach to advancing the next generation of peptide medicines.

Panelists:

David J. Craik, PhD, Professor & UQ Laureate Fellow, The University of Queensland

Immanuel Lerner, PhD, CEO, Pepticom Ltd

Ewa Lis, PhD, Founder & CEO, Koliber Biosciences

Tomi K. Sawyer, PhD, Founder, Maestro Therapeutics & President, Peptide Drug Hunting Consortium (PDHC)

Anastasia Velentza, PhD, Vice President, Biology, Vilya Therapeutics

5:00 Close of Peptide Drug Hunting 101 Symposium

Peptide Targets: Discovery, Expression, and Validation

Recombinant Platforms, Display Technologies & Data Modeling for Functional Peptide Discovery

NEW **PEPTIDE EXPRESSION & DEVELOPMENT**

TUESDAY, JANUARY 20

7:30 am Registration and Morning Coffee

ADVANCING PEPTIDE TARGET DISCOVERY THROUGH DISPLAY INNOVATION

8:30 Organizer's Remarks

Lynn Brainard, Conference Producer, Cambridge Healthtech Institute

8:35 Chairperson's Remarks

Wenshe Ray Liu, PhD, Harry E. Bovay, Jr. Endowed Chair, Professor in Chemistry, Texas A&M University

8:40 Next-Generation Libraries of Peptide Macrocycles for mRNA Display

Albert A. Bowers, PhD, Professor, Division of Chemical Biology and Medicinal Chemistry, University of North Carolina Chapel Hill

mRNA display allows production and selection of vast macrocyclic peptide libraries. We present a strategy for making target class-selective mRNA display libraries by using N-terminal selective cyclization chemistry to allow post-translational chemical derivatization of internal cysteines. We thus install analogs of dimethyl lysine (KMe2) in selections against epigenetic targets UHRF1 and RBBP7. We further combine this methodology with late-stage barcoding strategy for rapid preparation of focused libraries for hit-to-lead optimization.

9:10 Beyond Binding Affinity: Optimizing Peptide Discovery for Targeted Therapeutics

Mette Soendergaard, PhD, Co-Founder & CSO, Cell Origins LLC

Phage display has become a cornerstone of peptide discovery, enabling the identification of high-affinity binders against a wide array of targets. However, binding affinity alone is not a reliable predictor of therapeutic success. Enhancing the translational potential of peptides requires addressing critical factors such as off-target effects, biodistribution, and pharmacokinetics in the discovery process. By employing selection strategies under physiologically relevant conditions, we can prioritize candidates with optimized therapeutic profiles.

9:40 Using Phage Display Methods for Rapid Identification of Covalent Cyclic Peptides Targeting Diverse Proteins

Matthew Bogyo, PhD, Professor, Department of Pathology, Stanford University School of Medicine

Hydrolases are enzymes that often play pathogenic roles in diseases such as cancer, asthma, arthritis, atherosclerosis, and infection by pathogens. Probes that allow dynamic monitoring of their activity can be used as diagnostic and imaging agents, as well as for identification of enzymes as drug leads. I will describe efforts using phage display, mRNA display, and high-throughput fragment screening to identify selective covalent-binding probes for diverse protein targets.

10:10 Accelerating Bioprocess Development with AI + Automation

GenScript

Justin Byers, President & CEO, Axio Biopharma

Bioprocess development faces increasing challenges from accelerated timelines, fragmented data, and process variability, leading to delayed patient access. This presentation explores how AI and high-quality data generation can address these challenges, introducing Axio's federated approach to secure, collaborative learning. A case study featuring the GenScript Quatro ProAb 1300 highlights how automated purification accelerates antibody discovery and development through AI-powered workflows.

10:40 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

11:20 Phage-Assisted Active Site-Directed Ligand Evolution of Peptide Ligands for Epigenetic Drug Targets

Wenshe Ray Liu, PhD, Harry E. Bovay, Jr. Endowed Chair, Professor in Chemistry, Texas A&M University

The conventional phage display technique, while a powerful tool for drug discovery, is limited by its reliance on the 20 genetically encoded amino acids. To increase the versatility of the technique, we have integrated both chemical cyclization and genetically incorporated noncanonical amino acids into phage display. Unique applications afforded by new technology platforms in drug discovery have been demonstrated on multiple epigenetic drug targets, including SIRT2, HDAC8, ENL, and BRD9.

11:50 Accurate Sequence-to-Affinity Models from High-Throughput Peptide Binding Assays

Harmen J. Bussemaker, PhD, Professor, Biological Sciences & Systems Biology, Columbia University

Affinity selection on random peptide libraries, coupled with next-generation sequencing, yields high-throughput yet sparse data, which we use to train biophysical models that predict SH2 domain binding free energy and c-Src kinase efficiency over the full theoretical sequence space. Our model predictions are validated against biophysical measurements of synthesized peptides. This unbiased approach enables scalable, accurate prediction of protein functional properties, supporting more effective identification and optimization of drug candidates.

12:20 pm Transition to Lunch

12:30 LUNCHEON PRESENTATION: Automate Your Protein Chromatography Workflows: Strategies For Increasing Throughput

cytiva

Akemi Kunibe, Field Application Scientist, Cytiva

1:00 Refreshment Break in the Exhibit Hall with Poster Viewing

LINKEDIN SKILLS WORKSHOP

Meet the Moderator at the Plaza in the Exhibit Hall

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

FROM ARRAYS TO ALGORITHMS: INTEGRATING DISCOVERY PLATFORMS

1:30 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

1:35 AI-Driven Peptide Discovery: Unlocking the Potential of Peptide Arrays for Therapeutic Development

Ewa Lis, PhD, Founder & CEO, Koliber Biosciences

Standard peptide discovery methods like phage and mRNA display, face issues like high false positives or costly licensing, limiting therapeutic advances. We introduce a high-throughput discovery platform merging machine learning (ML) and peptide arrays, demonstrating high hit rates and the ability to leverage ML to optimize weak binders toward nanomolar affinity. Additionally, we

present visualization techniques for binding-mode detection and offer insights into the future of ML-driven peptide optimization.

2:05 High-Throughput Mapping of the Presentable Peptidome to Guide T Cell Vaccine Design

Joseph G. Jardine, PhD, Assistant Professor, Immunology & Microbiology, Scripps Research Institute

Understanding the MHC presentable peptidome is critical for rational vaccine and immunotherapy design. We developed a scalable yeast-display platform to map peptides from pathogens and tumors that are stably presented by MHC. Using HIV as a test case, we defined the viral peptidome; identified conserved, stable epitopes; and characterized potential escape mutations. This strategy provides a generalizable framework for defining peptidomes and guiding the design of T cell vaccines.

2:35 *De novo* Design of Miniprotein Agonists and Antagonists Targeting G Protein-Coupled Receptors

Chris Norn, PhD, Co-Founder & CEO, Skape Bio

GPCRs are vital drug targets, yet remain difficult to target with biologics. We combine computational *de novo* design with a high-throughput, microscopy-based "receptor diversion"–pooled screen to create high-affinity, selective miniprotein agonists and antagonists. The platform produced MRGPRX1 agonists, as well as CXCR4, GLP1R, GIPR, GCGR, and CGRPR antagonists. Cryo-EM reveals atomic-level accuracy, demonstrating precise control of GPCR function and broad therapeutic potential.

3:05 Designing Peptides Inspired by Regenerative Biology for the Treatment of Inflammatory and Fibrotic Disease

Peter Licari, PhD, CEO & Co Founder, ANIMATE Biosciences

Fibrosis underlies progressive dysfunction across multiple organs and remains poorly addressed by current therapies. We describe an AI-enabled peptide discovery platform informed by regenerative biology that enables rapid identification of short, multi-mechanistic peptides with anti-fibrotic activity. Lead peptides demonstrated multi-organ suppression of fibrotic and inflammatory markers. These findings highlight the potential of regenerative, AI-designed peptides as a novel therapeutic approach for inflammatory and fibrotic diseases.

3:35 Refreshment Break in the Exhibit Hall with Poster Viewing

PLENARY KEYNOTE SESSION: TRENDS AND INNOVATION DRIVING THE FUTURE OF BIOTHERAPEUTICS

4:30 Welcome Remarks

Mimi Langley, Executive Director, Life Sciences, Cambridge Healthtech Institute

4:35 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 From Targets to Biologics: AI Powering the Next Leap in Discovery at Takeda

Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

Takeda's AI/ML strategy is redefining the path from targets to biologics, using advanced models to identify and validate novel targets, decode complex biology, and design the next generation of high-quality therapeutic molecules. By integrating agentic, generative, and large language model–driven approaches, AI is powering the next leap in discovery at Takeda.

4:50 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing

Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences

As biotherapeutics become more complex, automation of traditional testing labs falls short of delivering the insights needed for regulatory success. This talk introduces a GxP-native, full-stack AI platform designed to orchestrate and optimize mass spectrometry-based testing workflows across CMC, bioanalysis, and regulatory reporting. Rooted in regenerative system design, this infrastructure enables scalable, adaptive, and compliant operations, empowering biopharma teams to accelerate product development with confidence, clarity, and scientific precision.

5:00 Technological Trends Shaping the Landscape of Biopharmaceuticals

Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/ Fiocruz, Brazil

Currently, the biopharmaceutical industry is undergoing rapid technological advancements that are revolutionizing development and production of biopharmaceuticals. Consequently, new therapeutic categories are gaining prominence, such as antibody-drug conjugates, bispecific antibodies, advanced therapies, among others. This rapid evolution requires constant vigilance to identify breakthroughs and guiding strategic decision-making in this dynamic field. The aim of this strategic foresight analysis is to discuss technological trends for the future of biopharmaceuticals.

5:10 PLENARY FIRESIDE CHAT

Moderator: Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

Kicking off with three focused 10-minute presentations, the Fireside Chat transitions into an engaging 30-minute fireside discussion. Panelists will delve into cutting-edge topics, including the role of AI/ML in biologics discovery, advancements in next-generation analytics and tools, entrepreneurial trends and investment landscapes, and emerging therapeutic modalities. In tribute to Dr. King's legacy, this session will also highlight the importance of fostering diversity, equity, and inclusion within the biotech innovation ecosystem.

Panelists:
Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences
Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil
Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

5:40 Networking Reception in the Exhibit Hall with Poster Viewing

YOUNG SCIENTIST MEET-UP

Meet the Moderator at the Plaza in the Exhibit Hall

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

6:40 Close of Day

WEDNESDAY, JANUARY 21

7:15 am Registration Open

BuzZ Sessions

7:30 BuzZ Session with Continental Breakfast

BuzZ Sessions are informal, moderated discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the BuzZ Sessions page on the conference website for a complete listing of topics and descriptions.

BuzZ Table 7: Challenges in Advancing Peptides to the Clinic

Raymond S. Norton, PhD, Professor, Monash Institute of Pharmaceutical Sciences, Monash University

Topics for Discussion:

- Proteolytic stability
- Pharmacokinetics
- Oral bioavailability
- Cell surface vs intracellular targets
- Cost of goods: synthetic vs recombinant

BuzZ Table 10: Innovations in Peptide Discovery and Hit Validation: Overcoming Bottlenecks

Fei Cai, PhD, Scientist 4, Department of Biological Chemistry, Genentech Inc.

Sunhee Hwang, PhD, Scientist 4, Peptide Therapeutics, Genentech Inc.

Topics for Discussion:

- Strategies to improve the identification of high-affinity & selective peptide binders
- Focus on early screening of selected hits from discovery efforts (e.g leveraging M/L models)
- How can we prioritize candidates effectively, and what workflows can optimize this process?
- What are the most effective methods for synthesizing peptides quickly and accurately?
- Exploration of innovative approaches including bioproduction

RECOMBINANT EXPRESSION PLATFORMS: TRANSFORMING PEPTIDE PRODUCTION PIPELINES

8:15 Chairperson's Remarks

David J. Craik, PhD, Professor & UQ Laureate Fellow, The University of Queensland

8:20 PANEL DISCUSSION: Transforming Peptide Production with Scalable, Sustainable Expression

Moderator: David J. Craik, PhD, Professor & UQ Laureate Fellow, The University of Queensland

What's old is new again. The resurgence of therapeutic peptides has renewed interest in peptide target discovery, but with new tools, new workflows, and new urgency. With longer and more structurally complex peptides and mini-proteins, recombinant peptide expression in biological hosts offers a scalable, sustainable, and effective alternative, especially when paired with modern prediction and validation tools. This panel facilitates discussion on advancing the next generation of peptide therapeutics.

Panelists:

Edson Carcamo Noriega, PhD, Investigator & Head, Biochemistry, AI Proteins

Charles Johannes, PhD, Founder, President, and Chief Scientist, EPOC Scientific LLC; Vice President, Peptide Drug Hunting Consortium

Robert M. Hughes, PhD, Associate Professor, Chemistry, East Carolina University

Jay Sarkar, PhD, Co-Founder, reThink64 Bionetworks

8:50 Rapid Recombinant Production of Therapeutic Miniproteins: A Scalable Solution for Discovery Pipelines

Edson Carcamo Noriega, PhD, Investigator & Head, Biochemistry, AI Proteins

We developed a high-throughput platform for expression and purification of peptides, miniproteins, and small scaffolds, optimized for target discovery and validation. Using *E. coli* and automated workflows with a magnetic bead–based protease elution, we produce over 1000 purified proteins weekly at >95% purity and >200 µg yield. This 4-day DNA-to-protein pipeline enables rapid evaluation, supports peptide screening campaigns, and generates robust datasets for machine-learning in peptide and protein engineering.

9:20 Enhancing Bioproduction of Disulfide-Constrained Peptides

Sunhee Hwang, PhD, Scientist 4, Peptide Therapeutics, Genentech Inc.

A versatile and highly efficient bioproduction platform to generate various forms of disulfide-constrained peptides (DCPs) has been developed as an environmentally sustainable alternative to SPPS. This platform can be used to generate: (1) multivalent DCPs with different geometries, (2) DCPs with functional chemical groups such as biotin, (3) DCPs with unnatural amino acids through amber codon suppression, and (4) isotope-labeled DCPs.

9:50 Mechanistic Characterization of GLP-1 Receptor Agonists Using Digital SPR

nicoya

Beatrice Sacripanti, Director, Products, Marketing, Nicoya

Peptide characterization is often limited by high sample requirements and complex SPR workflows. In this session, we introduce Revo, a new Digital SPR platform that combines BLI-like ease of use with high-quality SPR data on an automated 4-channel system using just 2 µL of sample. Using GLP-1 agonists, we show how Revo delivers reliable peptide kinetics, differentiates chemical variability, and enables earlier, more confident decision-making in discovery and development.

10:05 Selected Poster Presentation: Semaglutide Production by Semi-Recombinant Method with *Escherichia coli*

Sung-Gun Kim, PhD, Associate Professor, Biomedical Science, U1 Univ

We developed a semi-recombinant process for Semaglutide production using *Escherichia coli*. The tandem repeated precursor peptide (P29x8) is expressed at >10.0 g/L as inclusion bodies, then

solubilized, refolded, and enzymatically cleaved to yield monomeric P29. Subsequent fatty-acid side-chain acylation and dipeptide ligation complete Semaglutide synthesis. The integration of high-titer fermentation with optimized enzymatic and chemical steps enables a final Semaglutide production yield exceeding 4.0 g/L.

10:20 Coffee Break in the Exhibit Hall with Poster Viewing

SPEED NETWORKING

Meet the Moderator at the Plaza in the Exhibit Hall

Kevin Brawley, Project Manager, Production Operations & Communications, Cambridge Innovation Institute

RECOMBINANT EXPRESSION PLATFORMS TRANSFORMING PEPTIDE PRODUCTION PIPELINES *(CONT.)*

11:00 Recombinant Expression and Characterization of Histatin-Derived Peptides

Robert M. Hughes, PhD, Associate Professor, Chemistry, East Carolina University

Histatins comprise a family of ~12 histidine-rich peptides naturally present in human saliva. Their antimicrobial properties have attracted significant interest as potential therapeutics for combating oral infections. Recombinant expression of histatin peptides with *E. coli* has traditionally used cyanogen bromide to cleave the desired peptide sequence from a fusion protein. This talk will present an immobilized enzyme approach for obtaining histatin peptides that obviates the need for cyanogen bromide.

11:30 Engineering Cell-Free Glycosylation Systems for Immune-Optimized Vaccines

Zachary Shaver, Research Scientist, Michael Jewett Laboratory, Northwestern University

We developed a cell-free workflow combining gene expression and AlphaLISA to rapidly engineer and characterize post-translational modifications, including glycosylation, for conjugate vaccine production. Using this method, we optimized oligosaccharyltransferases and identified protein sites enabling efficient glycosylation. This approach supports scalable *in vitro* vaccine production and accelerates the development of more immunogenic conjugate vaccines through improved enzyme and carrier protein design.

12:00 pm KEYNOTE PRESENTATION: Yeast-Based Expression and Enzymatic Cyclization of Disulfide-Rich Cyclic Peptide Scaffolds for Drug Development

David J. Craik, PhD, Professor & UQ Laureate Fellow, The University of Queensland

Macrocyclic, disulfide-rich peptides are valuable in drug development, but traditional solid-phase peptide synthesis is environmentally harmful. We present a sustainable platform using yeast to secrete peptide precursors, which are matured *in vitro* via asparaginyl endopeptidases. Three peptide classes were produced, including the first recombinant α-conotoxin in native form. Yields reached 85–97 mg/L in bioreactors—surpassing prior methods—offering an eco-friendly, scalable alternative for cyclic peptide production.

12:30 Transition to Lunch

12:40 LUNCHEON PRESENTATION: Accelerating Membrane Protein Purification: Innovations with Nuclera

nuclera

Wenguang Liang, Sr Scientist, Molecular & Cell Sciences, Bayer CropScience

Membrane proteins are crucial for various cellular processes and serve as key targets in drug discovery as well as trait development in crop science. However, their purification presents significant challenges due to their hydrophobic nature and complex structural requirements. This talk will delve into recent innovations we have adapted using Nuclera that are transforming the landscape of membrane protein purification. We will discuss high-throughput screening methods that expedite optimization processes, followed by advanced expression systems and novel extraction techniques that enhance both yield and stability. By integrating these innovative approaches, researchers can effectively overcome traditional barriers in membrane protein purification, thereby facilitating more effective studies and accelerating product development. Join us to discover how these advancements can lead to breakthroughs in both drug discovery and agricultural biotechnology.

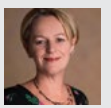
PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

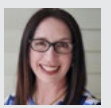
1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:




Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

2:15 Close of Conference

WEDNESDAY, JANUARY 21

1:00 pm Registration Open

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:

Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

PLATFORMS DRIVING LEAD IDENTIFICATION & SELECTION

2:15 Chairperson's Remarks

Sunhee Hwang, PhD, Scientist 4, Peptide Therapeutics, Genentech Inc.

2:20 ML-Guided Venom Library Design: Innovations and Applications

Fei Cai, PhD, Scientist 4, Department of Biological Chemistry, Genentech Inc.

The discovery of therapeutic peptides involves multiple rounds of screening, extensive peptide synthesis, and functional assays. To reduce the time- and cost-intensive aspects of this process, we employed an AI-assisted peptide library design strategy to ensure highly functional libraries with improved stability and folding properties. Subsequently, we used ML to guide the affinity maturation. This new workflow significantly reduced efforts in peptide synthesis, thereby accelerating the discovery of therapeutic peptides.

2:50 AI-Enabled Peptide Design for Diverse Functions

Gaurav Bhardwaj, PhD, Assistant Professor, Medicinal Chemistry, University of Washington

We recently developed deep learning (DL) methods, AFCycDesign and RFpeptides, for highly accurate structure prediction, sequence design, and *de novo* generation of macrocyclic peptides. These new DL tools outperform the traditional physics-based methods in their speed, accuracy, and overall success rates. In this talk, I will discuss the current status and next steps for improving these tools and applying them to diverse therapeutic targets.

3:20 Peptide-MHC Class II Nanomedicines to Treat Autoimmunity

Danielle Kroetz, PhD, Principal Scientist, Discovery Immunology, Parvus Therapeutics Inc

Autoimmunity results from the breakdown of mechanisms controlling immune tolerance. Parvus Therapeutics has developed iron-oxide nanoparticles coated with disease-relevant peptide MHC class II (pMHCII) molecules to induce antigen-specific regulatory TR1 cell conversion and expansion. This talk will focus on the identification of disease-relevant pMHCII complexes, pMHCII production and tetramer generation, reporter TCR cell line development, and *in vivo* TR1 conversion in PBMC-engrafted NSG mice with pMHCII nanoparticles.

3:50 Seeing What Other Methods Miss: Peptide Structure and Stability in Formulation by MMS REDSHIFTBio

Scott Gorman, Applications Scientist, R&D, RedShiftBio

Therapeutic peptides present analytical challenges due to low solubility, low sequence complexity, cyclization, and aggregation under formulation conditions. We demonstrate how Microfluidic Modulation Spectroscopy (MMS) on the Aurora TX enables quantitative measurement of peptide secondary structure, thermal stability, and early aggregation directly in formulation buffers and organic solvents. Case studies highlight detection of cyclization effects, formulation-dependent structural changes, and process-related degradation not resolved by conventional assays.

4:20 Refreshment Break in the Exhibit Hall with Poster Viewing

RECOMBINANT EXPRESSION: UNLOCKING THE NEW FRONTIERS IN PEPTIDE THERAPIES

4:50 Dermal Peptide Solutions: Unique Challenges for Actives and Delivery

Jay Sarkar, PhD, Co-Founder, reThink64 Bionetworks

Peptide actives are gaining traction, not just for internal medicine, also for topical usage. The challenges for dermal delivery, however, puts constraints on the types of peptide solutions that can be produced so far. Pushing the boundaries with longer sequences with more diversified targets necessitates the tandem evolution of large-molecule delivery solutions. This talk will review existing solutions as well as introduce novel modalities for dermal peptide products.

5:20 Applying Biologic CMC Principles to Peptide Production: From Discovery to Development

Steven Bowen, PhD, Principal Consultant, ELIQUENT Life Sciences

This talk explores how biologic CMC (Chemistry, Manufacturing, and Controls) principles can be effectively applied to peptide production across the discovery-to-development continuum. By leveraging established frameworks from biologics, we demonstrate strategies to enhance peptide quality and regulatory readiness. Key topics include process development, analytical characterization, and quality control, emphasizing a streamlined approach to accelerate peptide therapeutics toward clinical success.

5:50 Close of Day

THURSDAY, JANUARY 22

8:00 am Registration Open

PLENARY KEYNOTE SESSION: End-to-End *in silico*-Designed Biologics

8:25 Welcome Remarks

Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

8:30 Plenary Keynote Introduction

Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 PLENARY FIRESIDE CHAT: End-to-End *in silico*–Designed Biologics




Moderator: Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

- How is the path to drug development different with ML/AI?
- How far off is *de novo* design for biologics? For antibodies?
- How is ML/AI used for target selection?
- How do you accelerate DMTA cycles?
- Data standardization—how to incorporate historical data?
- Federated learning—how do you ensure you have enough data to build a model?
- Promoting change management

Panelists:
Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)
Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:30 Coffee Break in the Exhibit Hall with Poster Viewing

WOMEN IN SCIENCE MEET-UP

Meet the Moderators at the Plaza in the Exhibit Hall

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

VALIDATION & OPTIMIZATION STRATEGIES

10:20 Chairperson's Remarks

Sunhee Hwang, PhD, Scientist 4, Peptide Therapeutics, Genentech Inc.

10:25 Inhibitors of the Voltage-Gated Potassium Channels Kv1.3 for the Treatment of Autoimmune and Neuroinflammatory Diseases: An Unexpected Role for Peptide Dynamics

Raymond S. Norton, PhD, Professor, Monash Institute of Pharmaceutical Sciences, Monash University

The voltage-gated potassium channel Kv1.3 is upregulated in effector memory T cells, which are key drivers of autoimmune diseases, and in microglia in patients with Alzheimer's and Parkinson's diseases, making Kv1.3 a target for the treatment of autoimmune and neuroinflammatory diseases. The design and clinical development of venom-derived peptides as potent and selective inhibitors of Kv1.3 will be described. The importance of considering peptide dynamics will also be emphasized.

10:55 Overcoming Immune Checkpoint Inhibitor Resistance with Potent, Selective Integrin Inhibitors Based on Engineered Lasso Peptides

Mark J. Burk, PhD, CEO & Founder, Lassogen Inc.

Highly potent and selective dual integrin inhibitors were engineered from a natural lasso peptide scaffold by a combination of epitope scanning, computational design, and directed evolution. High titer production enabled the first detailed characterization of lassotide drug-like properties, including tunable *in vivo* PK and efficacy. Robust and durable regression of anti-mPD-1-resistant ovarian and triple-negative breast cancer tumors in mice was observed in combination with checkpoint inhibitors.

11:25 Membrane Translocation Domain Platform for Intracellular Delivery of Therapeutic Proteins

Prabhat Bhat, PhD, Research Senior Associate, Ohio State University

Antibodies and protein therapeutics largely target extracellular proteins, limiting their therapeutic potential. We engineered a family of membrane translocation domains (MTDs) by modifying loop sequences of a human fibronectin type III domain. One variant, MTD4, is highly cell-permeable, metabolically stable, and enables efficient cytosolic and nuclear delivery of diverse peptides and proteins *in vitro* and *in vivo* via recombinant fusion, serving as a general platform for intracellular protein delivery.

11:55 Enjoy Lunch on your Own

1:00 pm Ice Cream & Cookie Break in the Exhibit Hall with Last Chance for Poster Viewing

FORMULATION & DELIVERY APPROACHES

1:40 Chairperson's Remarks

Huyen Tran, PhD, Director, Formulation Research, Eli Lilly & Company

1:45 Controlling Gastric Delivery of a GIP/GLP1 Peptide in Monkeys by Mucoadhesive SNAC Tablets

Huyen Tran, PhD, Director, Formulation Research, Eli Lilly & Company

In this presentation, we will discuss strategies to enhance oral peptide bioavailability. This includes understanding the impact of peptide properties on oral absorption in the presence of permeation enhancers, as well as the effect of delivery site. Combining peptide engineering for oral delivery and formulation optimization for site-specific delivery can improve oral bioavailability. Additionally, we

will present the controlled gastric delivery of a GIP/GLP-1 peptide in monkeys using mucoadhesive SNAC tablets.

2:10 Immunogenicity of Generic Peptide Impurities: Current Orthogonal Approaches

Aimee Mattei, Director of Bioinformatics, EpiVax Inc.

Widespread use of peptide drugs like Ozempic raises concerns about the immunogenicity risks posed by generic versions. This presentation introduces orthogonal immunogenicity risk assessment methods for generic peptide drug impurities under the FDA's Abbreviated New Drug Application (ANDA) pathway, focusing on two case studies: salmon calcitonin and teriparatide, to illustrate that understanding the inherent immunogenicity of the active pharmaceutical ingredient (API) is critical to estimating the potential immunogenicity of impurities.

2:35 Next-Generation Delivery of Peptides: Enhancing Stability and Barrier Penetration

Nitin Joshi, PhD, Assistant Professor, Harvard Medical School, Associate Bioengineer, Department of Anesthesiology, Peripoperative and Pain Medicine, Brigham and Women's Hospital

Our work focuses on biointelligent biomaterial platforms that overcome the intrinsic barriers limiting peptide therapeutics.I will discuss how enzyme-responsive nanoparticles and hydrogels sense and respond to diseased microenvironments—stabilizing fragile peptides, navigating mucus and epithelial barriers, and localizing therapy with precision. These adaptive systems enable sustained delivery in the lung, mucosa, and osteoarthritic joints, opening new possibilities for clinically transformative peptide medicines.

3:00 MA-[D-Leu-4]-OB3: A Safe, Effective, and User-Friendly Synthetic Peptide Leptin Mimetic for the Treatment of Metabolic and Neurologic Dysfunctions

Patricia Grasso, PhD, Professor, Medicine, Neurosciences & Experimental Therapeutics, Albany Medical College

MA-[D-Leu-4]-OB3 is a synthetic peptide leptin mimetic encompassing the functional epitope of the leptin molecule and engineered for optimal pharmacokinetics, efficacy, and oral or nasal administration. In mouse models of obesity, diabetes, and cognitive impairment, MA-[D-Leu-4]-OB3 has been shown to be safe and to have therapeutic and prophylactic efficacy. MA-[D-Leu-4]-OB3 reduces body weight gain, enhances insulin sensitivity, normalizes blood glucose, reverses diabetic dyslipidemia, promotes bone turnover, and enhances memory/cognition.

3:25 PANEL DISCUSSION: Formulating the Future—Innovations in Peptide Therapeutics

Moderator: JiMin Lee, PhD, Professor, KAIST

- Innovations in design to overcome stability, solubility, and delivery challenges of peptides
- Advances in delivery technologies (oral, transdermal, long-acting injectables, nanoparticles) shaping the future of peptide drugs
- Manufacturing innovations and scale-up considerations for clinical and commercial success
- Regulatory and clinical hurdles in bringing novel peptide formulations to patients
- Future outlook: where peptides can best compete or complement small molecules and biologics

Panelists:

Patricia Grasso, PhD, Professor, Medicine, Neurosciences & Experimental Therapeutics, Albany Medical College

Nitin Joshi, PhD, Assistant Professor, Harvard Medical School, Associate Bioengineer, Department of Anesthesiology, Peripoperative and Pain Medicine, Brigham and Women's Hospital

Aimee Mattei, Director of Bioinformatics, EpiVax Inc.

4:15 Close of Conference

PepTalk

The Protein Science and Production Week

ANTIBODY ENGINEERING & THERAPEUTICS

Antibody therapies have been approved for the treatment of cancer, immune disorders, metabolic, cardiovascular, and infectious diseases. PepTalk's Antibody Engineering pipeline offers a forum for protein scientists who are working to discover and develop differentiated biotherapeutics for additional unmet medical needs quickly and efficiently. These programs explore targeting, delivery, conditional activation, masking, fragment-based approaches, alternative scaffolds, antibody drug conjugates, AI, computational design, t cell engagers, promising candidates, and the strong push toward multispecific formats. Join us to explore the important advances in this dynamic field.

JANUARY 19
SYMPOSIUM

Engineering Multispecifics: Oncology and Beyond AGENDA

JANUARY 20-21

Novel Formats and New Antibody Approaches AGENDA

JANUARY 21-22

Advancing Multispecific Engineering to the Clinic AGENDA

MONDAY, JANUARY 19

8:00 am Registration and Morning Coffee

TARGETING AND DELIVERY

8:50 Organizer's Opening Remarks

Nikki Cerniuk, Conference Producer, Cambridge Healthtech Institute

8:55 Chairperson's Opening Remarks

Fangzhu Zhao, PhD, Postdoctoral Fellow, Laboratory of Dr. Jim Wells, Pharmaceutical Chemistry, University of California San Francisco

9:00 Antibody Technology for Enhanced Solid-Tumor Targeting

Jon Sitrin, PhD, Director & Head, Translational Biology, EpiBiologics

EpiTACs are bispecific antibodies in which one arm binds a pathogenic target, and the other arm leverages tissue-enriched degrading receptors to selectively degrade a wide range of extracellular targets including membrane, soluble, and multi-span proteins. Our modular and industrial process for creating EpiTACs allows us to optimize antibody properties to maximize degradation. EpiTACs to multiple oncology and autoimmune targets demonstrate that target degradation can drive robust *in vivo* activity.

9:30 Exceptionally Broad HIV-1 Neutralization via Bispecific Antibody-Mediated Prepositioning

Soohyun Kim, PhD, Scientific Researcher, Biochemistry, Stanford

Antibodies targeting the transiently exposed N-heptad repeat (NHR) of the HIV-1 prehairpin intermediate (PHI) are typically weakly neutralizing. We enhanced their potency using bispecific antibodies (bsAbs) that preposition the NHR-targeting arm to the HIV-1 receptor or coreceptor. These bsAbs showed exceptionally broad neutralization and distinct resistance profiles despite sharing the same neutralizing arm. These findings validate the NHR as a therapeutic target for a new class of broadly neutralizing antibodies.

10:00 CNS Drug Delivery Using Bispecific Antibodies Targeting CD98hc and Transferrin Receptor

Peter M. Tessier, PhD, Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

The inability of diverse biomolecules to readily penetrate the blood-brain barrier is a key limitation to their use in research, diagnostic, and therapeutic applications. We are developing bispecific antibodies that engage either CD98hc or transferrin receptor, and efficiently transport biomolecules into the CNS. We will discuss the unique advantages of each shuttling pathway, our progress in developing next-generation shuttles, and their drug-delivery applications.

10:30 From Prediction to Validation: An Industry-Standard Approach to TCR-Mimic Antibody Development

Joerg Birkenfeld, PhD, CSO, Biocopy AG

BioCopy's ValidaTe platform is a pHLA-centric workflow for developing safer and more effective T-cell receptor mimic (TCRm) antibodies. It combines proprietary ultra-high-throughput pHLA kinetic screening with AI-based predictions, structural modeling, and deep *in vitro* validation to comprehensively assess target specificity and efficacy. The platform's strength is demonstrated by the discovery of novel, superior TCRms against the cancer-testis antigen MAGE-A4, showing an unprecedentedly minimized off-target profile.

11:00 Networking Coffee Break

11:15 Amplifying Antibody Penetration: Endovascular Osmotic Modulation for Overcoming Biological Barriers

Miroslaw Janowski, MD, Tenured Professor, Radiology, University of Maryland Baltimore

Antibodies have become mainstream therapeutics due to their high precision, potency, and limited adverse effects. For neurological disorders and cancer, especially with poor prognosis, they represent highly attractive therapeutic agents, yet organ penetration remains challenging. We demonstrated that endovascular increasing osmotic pressure beyond current clinical standards followed by intra-arterial antibody infusion dramatically improves antibody extravasation to the target organs, including brain, in a safe manner, offering a promising therapeutic strategy.

11:45 Hijacking Extracellular Targeted Protein Degrader–Drug Conjugates for Enhanced Drug Delivery

Fangzhu Zhao, PhD, Postdoctoral Fellow, Laboratory of Dr. Jim Wells, Pharmaceutical Chemistry, University of California San Francisco

Antibody–drug conjugates (ADCs) are constrained by their reliance on antigens that internalize efficiently. Similarly, extracellular targeted protein degradation (eTPD) depends on lysosomal trafficking. To address these limitations, we developed degrader–drug conjugates (DDCs), which exploit the natural endocytic and recycling activity of eTPD for enhanced lysosomal delivery of cytotoxic payloads. DDCs showed improved cytotoxicity compared to ADCs, highlighting their potential as a versatile platform for next-generation antibody therapeutics in cancer treatment.

12:15 pm Enjoy Lunch on Your Own

TOOLS AND COMPUTATIONAL STRATEGIES

1:30 Chairperson's Remarks

Peter M. Tessier, PhD, Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

1:35 Leveraging Single-Cell Sequencing to Identify Highly Precise T Cell Engager Targets

Colton Bracken, PhD, Senior Scientist, Antibody Engineering, Cartography Biosciences Inc

T cell engagers (TCEs) are a promising approach for solid tumors, however, progress is limited by a lack of tumor-selective targets that maximize efficacy while minimizing toxicity. We developed the ATLAS platform, a single-cell RNA-sequencing resource that leverages both healthy and tumor-derived datasets to identify highly precise TCE targets. Using ATLAS, we discovered LY6G6D as a tumor-specific colorectal-cancer (CRC) target, guiding the engineering of an LY6G6D TCE for CRC.

2:05 Understanding and Modulating Disease with Antibody Engineering and Physics-Aware Deep Learning

Dima Kozakov, PhD, Director, AI/Physics in Drug Discovery, UT Austin

Deep learning–based approaches have revolutionized protein structure prediction. Structural modeling and design of antibodies and novel protein interactions remain challenging. We present a physics-aware deep learning framework that addresses key limitations by incorporating biophysical principles into the learning and inference process. We demonstrate applications of this approach in combination with antibody engineering to design agonistic bispecific antibodies, as well as its integration with multi-omics data to uncover mechanisms of disease.

2:35 Next generation bispecific antibody manufacturing based on an innovative modular tool box

Stefan Schmidt, CEO, evitria AG

3:05 Networking Refreshment Break

3:30 Engineering T Cell Engagers for 'Complete on/off Killing' Selectivity by Combining Machine Learning and High-Throughput Experimentation

Winston Haynes, PhD, Vice President, Computational Sciences and Engineering, LabGenius Therapeutics

LabGenius Therapeutics' EVA platform leverages avidity-driven selectivity to overcome T cell engager (TCE) challenges, including on-target, off-tumor toxicity in solid tumors. In this talk, we describe how the closed-loop integration of high-throughput experimentation with machine learning has facilitated the discovery and optimization of multispecifics for function and developability. Specifically, we showcase how we have developed a pipeline of TCEs that exhibit 'on/off killing selectivity' for targets with minimal expression differences.

4:00 Computational Design of Multispecifics: Predicting Mutation Effects and Optimizing Binding Affinity

Maria Rodriguez Martinez, PhD, Associate Professor, Biomedical Informatics & Data Science, Yale University

The design of multispecific antibodies presents unique computational challenges due to the need to evaluate and optimize multiple binding interfaces simultaneously. In this talk, I will present a methodological framework that integrates structural models, protein language models, and affinity prediction data across diverse platforms and targets. By combining these representations with graph-based machine learning, our multi-layered approach supports mutation-effect prediction and affinity optimization, even with limited or noisy data.

4:30 FEATURED PRESENTATION: An AI-Guided Brain-Shuttle Platform for Bispecifics and Enhanced CNS Selectivity

John Avera, Scientist II, Protein Sciences, Manifold

This talk will introduce an AI-guided platform designed to create and optimize bispecifics for enhanced delivery to the central nervous system (CNS). By leveraging this technology, we can engineer these therapeutics with improved CNS selectivity and biodistribution, overcoming the blood-brain barrier. We will present case studies that demonstrate how this platform accelerates the development of novel bispecific treatments for neurological disorders.

TUESDAY, JANUARY 20

7:30 am Registration and Morning Coffee

ANTIBODY FRAGMENTS AND ALTERNATIVE APPROACHES

9:00 Organizer's Opening Remarks

Nikki Cerniuk, Conference Producer, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks

Anna M. Wu, PhD, Chair and Professor, Immunology & Theranostics, Center for Theranostic Studies, City of Hope

9:10 *De novo* Antibody Design for Biological Activity, Novel Formats, and Hard Targets Using Chai-2

Nathan Rollins, Founding Scientist, Chai Discovery

We introduce a new way to discover antibodies that enables epitope specification and unprecedented speed (24 hours to sequences, 2 weeks to KD determination) using our generative AI model, Chai-2. We discuss advanced, lab-validated case examples for antibody design leveraging Chai-2.

9:40 Engineering Affibody Binders to Death Receptor 5 and Tumor Necrosis Factor Receptor 1 with Improved Stability

Benjamin J. Hackel, PhD, Professor, Chemical Engineering & Materials Science, University of Minnesota

Aberrant signaling of the tumor necrosis factor receptor family has significant detrimental effects in multiple diseases. Ligand competition impacts multiple pathways, causing numerous side effects, and is challenged by native potency and high local concentrations. Synthetic scaffolds were engineered to bind receptors (separately TNFR1 and DR5) and inhibit signaling and downstream processes without competing for native ligand binding. We present on mechanism, engineered stability, and cross-reactivity.

10:10 Asymmetric Bispecific Antibody Purification Platforms Using Avidity Effects of Protein A and Protein L Affinity Ligands

cytiva

Mats Ander, Global Product Manager, Cytiva Life Sciences

Purification of asymmetric bispecific molecules is more complicated compared to standard monoclonal antibodies due to the need of correct pairing of the heavy and light chains. One way to purify these molecules is by using avidity effects on affinity protein A and protein L resins. In this work, we show a systematic approach to achieve high purity of the correctly paired antibody already in the capture step and how to design-in or design-out binding by varying the antibody sequence.

10:40 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

11:20 Design and Construction of a Multi-Paratopic Antibody-Drug Conjugate Incorporating Variable New Antigen Receptor (VNAR) Domains

Lauren Chisholm, PhD, Postdoctoral Fellow, Biomedical Engineering, John Hopkins University

Immune-checkpoint inhibitor antibodies have shown great success in a subset of patients; however, many treated patients (>70%) do not benefit. Towards providing a more effective therapy for these patients, the Spangler lab has developed a multispecific anti-PD-L1 antibody-drug conjugate. This molecule kills cancer cells through three mechanisms: disruption of the PD-1/PD-L1 immune checkpoint, internalization and downregulation of PD-L1, and direct killing of cancer cells via the drug payload.

11:35 Size Matters in Making Antibody Magic Bullets Penetrating Barriers to Precision Imaging and Therapy

Jan E. Schnitzer, MD, Institute Director, Proteogenomics Research Institute for Systems Medicine

Most fatal diseases occur in nonleaky solid tissues difficult to specifically target and treat even with our best precision therapies. Poor passive transvascular delivery limits specific uptake, target access and therapeutic efficacy. Active tranendothelial shuttling of size-optimized bispecific antibodies via the caveolae pumping system can boost precision targeting and drug potency by orders of magnitude.

12:20 pm Transition to Lunch

12:30 Enjoy Lunch on Your Own

1:00 Refreshment Break in the Exhibit Hall with Poster Viewing

LINKEDIN SKILLS WORKSHOP

Meet the Moderator at the Plaza in the Exhibit Hall

Julie Ming Liang, PhD, Co-Founder & CSO, Opera Bioscience

ANTIBODY-FRAGMENT AND ALTERNATIVE APPROACHES *(CONT.)*

1:30 Chairperson's Remarks

Roy Heng, Research Scientist, R&D, AbbVie

1:35 Determining Key Residues of Engineered scFv Antibody Variants with Improved MMP-9 Binding Using Deep Sequencing and Machine Learning

Maryam Raeeszadeh-Sarmazdeh, PhD, Assistant Professor, Chemical and Materials Engineering, University of Nevada

Matrix metalloproteinases (MMPs) and a disintegrin and metalloproteinase (ADAMs) are key regulators of tissue remodeling, and their dysregulation contributes to diseases such as cancer and neurodegeneration. We are developing two protein-based inhibitors—engineered TIMPs and synthetic scFvs—to selectively target metalloproteinases. Using yeast display, FACS screening, and next-generation sequencing, we identified high-affinity binders. Machine learning and computational modeling further guide our understanding of sequence-function relationships to optimize therapeutic design.

2:05 FEATURED PRESENTATION: Improving the Penetration of Antibodies into Solid Tumors by Reengineering with CreaTap

Zahra Jawad, PhD, CEO & Founder, Creasallis

Antibody therapies have been revolutionary in oncology, however, this is only benefiting 20-30% of patients. Part of the problem is the penetration of antibody macromolecules into solid tumors. Reengineering the hinge region of antibodies with CreaTap increases their penetration into solid tumors without impacting the stability or manufacturability of these molecules. CreaTap can be applied to any antibody-based therapy, making it a simple solution to enhance efficacy.

2:35 Optimizing Fragment-Based Radioimmunotherapy through Fc Engineering

Anna M. Wu, PhD, Chair and Professor, Immunology & Theranostics, Center for Theranostic Studies, City of Hope

The therapeutic index of radioimmunotherapy describes the balance between the accumulation and retention of cytotoxic radiation in the tumor, the blood half-life, and the clearance of the radioactive tracer.

While the long plasma half-life of IgGs can cause hematological toxicities, the rapid renal clearance of smaller fragments often leads to nephrotoxicity. Antibody fragments (scFv-Fc) with hepatobiliary clearance can spare the radiosensitive kidneys. Fc-engineering to modulate pharmacokinetics reduces bone-marrow toxicity.

3:05 Accelerating Discovery of Therapeutic Antibodies and Antibody Fragments Using Transgenic Mice

Jane Seagal, SVP of R&D, AlivaMab Biologics LLC

The discovery of therapeutic-quality antibody binding domains is critical for enabling novel biologic modalities and fragment-based therapeutics. To facilitate optimal lead selection, key parameters, including specificity, affinity, potency, and biophysical properties, must be addressed as early as practical. Here, we present data illustrating how AlivaMab Biologics utilizes novel AlivaMab® Mouse strains for the discovery of antibodies and antibody fragments, enabling efficient identification of molecules with therapeutic potential.

3:35 Refreshment Break in the Exhibit Hall with Poster Viewing

PLENARY KEYNOTE SESSION: TRENDS AND INNOVATION DRIVING THE FUTURE OF BIOTHERAPEUTICS

4:30 Welcome Remarks

Mimi Langley, Executive Director, Life Sciences, Cambridge Healthtech Institute

4:35 Chairperson's Remarks

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

4:40 From Targets to Biologics: AI Powering the Next Leap in Discovery at Takeda

Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

Takeda's AI/ML strategy is redefining the path from targets to biologics, using advanced models to identify and validate novel targets, decode complex biology, and design the next generation of high-quality therapeutic molecules. By integrating agentic, generative, and large language model–driven approaches, AI is powering the next leap in discovery at Takeda.

4:50 Agentic AI for Biologics: Scalable Infrastructure for GxP-Compliant, Insight-Driven Testing

Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences

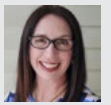
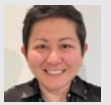
As biotherapeutics become more complex, automation of traditional testing labs falls short of delivering the insights needed for regulatory success. This talk introduces a GxP-native, full-stack AI platform designed to orchestrate and optimize mass spectrometry-based testing workflows across CMC, bioanalysis, and regulatory reporting. Rooted in regenerative system design, this infrastructure enables scalable, adaptive, and compliant operations, empowering biopharma teams to accelerate product development with confidence, clarity, and scientific precision.

5:00 Technological Trends Shaping the Landscape of Biopharmaceuticals

Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil

Currently, the biopharmaceutical industry is undergoing rapid technological advancements that are revolutionizing development and production of biopharmaceuticals. Consequently, new therapeutic categories are gaining prominence, such as antibody-drug conjugates, bispecific antibodies, advanced therapies, among others. This rapid evolution requires constant vigilance to identify breakthroughs and guiding strategic decision-making in this dynamic field. The aim of this strategic foresight analysis is to discuss technological trends for the future of biopharmaceuticals.

5:10 PLENARY FIRESIDE CHAT

Moderator: Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

Kicking off with three focused 10-minute presentations, the Fireside Chat transitions into an engaging 30-minute fireside discussion. Panelists will delve into cutting-edge topics, including the role of AI/ML in biologics discovery, advancements in next-generation analytics and tools, entrepreneurial trends and investment landscapes, and emerging therapeutic modalities. In tribute to Dr. King's legacy, this session will also highlight the importance of fostering diversity, equity, and inclusion within the biotech innovation ecosystem.

Panelists:
Lieza M. Danan, PhD, Co-Founder & CEO, LiVeritas Biosciences
Aline de Almeida Oliveira, PhD, Competitive Intelligence Office (AICOM), Bio-Manguinhos/Fiocruz, Brazil
Yves Fomekong Nanfack, PhD, Head of AI/ML Research, Takeda

5:40 Networking Reception in the Exhibit Hall with Poster Viewing

YOUNG SCIENTIST MEET-UP

Meet the Moderator at the Plaza in the Exhibit Hall

Maria Calderon Vaca, PhD Student, Chemical Environmental & Materials Engineering, University of Miami

6:40 Close of Day

WEDNESDAY, JANUARY 21

7:15 am Registration Open

BuzZ Sessions

7:30 BuzZ Session with Continental Breakfast

BuzZ Sessions are informal, moderated discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the BuzZ Sessions page on the conference website for a complete listing of topics and descriptions.

BuzZ Table 8: Antibody-Based Technologies for CNS Drug Delivery

Peter M. Tessier, PhD, Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

- CD98hc vs transferrin receptor shuttling: pros/cons & applications
- Impact of bispecific antibody properties on CNS delivery efficiency, selectivity, and retention
- Tailoring antibody shuttles to specific CNS drug delivery applications: nucleic acids, proteins, enzymes, IgGs, and more
- Outstanding challenges in biologics delivery to the CNS and future directions

BuzZ Table 9: Engineering Multispecifics for the Clinic: Potency, Safety, and Manufacturability

Hamzeh Rahimi, PhD, Scientist, City of Hope National Medical Center

- Safety-by-design mechanisms
- Potency vs. selectivity engineering
- Manufacturability & developability funnel: what are some early predicters of a go/no go?

ANTIBODY DRUG CONJUGATE BREAKTHROUGHS

8:15 Chairperson's Remarks

Maryam Raeeszadeh-Sarmazdeh, PhD, Assistant Professor, Chemical and Materials Engineering, University of Nevada

8:20 XB371: A Novel Anti-Tissue Factor ADC?

Seema Kantak, PhD, Senior Vice President, Biotherapeutics, Exelixis

Tissue factor is aberrantly expressed in various cancers. XB371 is an anti-TF antibody-drug conjugate and is designed to deliver a cytotoxic payload to TF-expressing tumors while minimizing adverse events in normal tissues. XB371 is composed of a tandem-cleavage topoisomerase-inhibitor-based linker payload conjugated to a monoclonal antibody that binds to TF with high affinity and does not interfere with the clotting cascade. Preclinical characterization of XB371 will be presented.

8:50 Novel *in Vitro* Screening Assays for ADC Characterization and Matrix Stability Assessment

Roy Heng, Research Scientist, R&D, AbbVie

Antibody drug conjugates (ADC) are susceptible to various modifications and degradation pathways during circulation, which may impact their stability and efficacy. Moreover, the increasing complexity of the protein scaffold requires additional effort to understand and assess their stability liabilities. We explore a suite of various *in vitro* characterization assays, for identification of liabilities such as aggregation, cleavage, and non specific payload release.

9:20 JK06: A Novel Biparatopic ADC for 5T4-Expressing Solid Tumors

Jijun Dong, PhD, CSO, Salubris Biotherapeutics

JK06 is a biparatopic antibody-drug conjugate targeting two non-overlapping 5T4 epitopes with tetravalent binding capacity. This design enhances internalization and cytotoxic payload delivery in 5T4-expressing solid tumors, including lung, breast, ovarian, and colorectal cancers. Preclinical studies demonstrated superior internalization versus mono-specific antibodies and potent anti-tumor activity in xenograft models. JK06 showed favorable safety in GLP toxicology studies. A Phase 1/2 clinical trial is ongoing.

9:50 Decoding ADC spectra for DAR measurements at warp speed

UNCHAINED LABS

Kevin Lance, Dir Product Mgmt, Product Mgmt, Unchained Labs

UV/Vis is often cited as the fastest way to measure average DAR – unless your ADC breaks the rules. Traditional approaches require already knowing info about the drug-linker spectrum and need drug absorbance to be significantly different than antibody absorbance. For the first time, we'll show how Stunner can decode even highly overlapping spectra without prior drug-linker knowledge, delivering DAR results in a super-simple, lightning-fast, and sample-sparing assay.

10:20 Coffee Break in the Exhibit Hall with Poster Viewing

SPEED NETWORKING

Meet the Moderator at the Plaza in the Exhibit Hall

Kevin Brawley, Project Manager, Production Operations & Communications, Cambridge Innovation Institute

11:00 Turning Proximity into Therapies: MINT Platform Discovery of a Bispecific ADC targeting EGFR

Ertan Eryilmaz, PhD, Vice President Biologics, InduPro Boston

The MINT platform integrates photocatalytic proximity proteomics and machine learning to map tumor-specific surface protein interactions and reveal novel co-localized target pairs. Using MINT, we identified a proximity partner to EGFR that enabled rational design of a bispecific ADC. Our lead molecule, IDP-001, demonstrates potent and selective anti-tumor activity in preclinical models, highlighting the translational potential of proximity-guided discovery for first-in-class targeted therapeutics.

11:30 Leveraging AI to Optimize Antibody-Drug Conjugate Internalization

John Corbin, Chief Development Officer, BigHat Biosciences

This talk highlights how artificial intelligence can accelerate the design and optimization of antibody-drug conjugates (ADCs), with a focus on improving internalization efficiency. By integrating high-throughput screening data with AI-driven modeling, we demonstrate how predictive tools can guide the development of more effective ADCs, ultimately enhancing therapeutic performance. The approach offers a scalable framework for rational ADC engineering with broad applications across oncology and beyond.

12:00 pm Fine-Tuning Next-Generation Bispecific Antibody-Drug Conjugates for Improved Efficacy and Safety

Sarka Stehlikova, Director, Biologics Core Technologies, SOTIO Biotech

SOTIO is advancing a pipeline of ADCs through collaborations leveraging multiple leading site-specific conjugation and linker-payload technologies. Our preclinical pipeline of next-generation bispecific molecules aspires to minimize on-target toxicity and to overcome tumor heterogeneity. The talk will highlight our discoveries on how to optimize the bispecific format for optimal effect on tumor cells with varying antigen expression and discuss how to translate functional *in vitro* data into *in vivo* efficacy.

12:30 Transition to Lunch

12:40 LUNCHEON PRESENTATION: A Function-Based Screening Platform Accelerating T-Cell Engager Discovery

Musheng Bao, VP & Head, Biology, Nona Biosciences

T-cell engagers (TCEs) are a powerful modality in cancer immunotherapy. Nona's fully human heavy chain–only antibodies (HCAbs) from HCAb Harbour Mice® offer an ideal scaffold due to their small size, high stability, strong affinity, favorable manufacturability, and low immunogenicity. To address the limitations of binding-based screening, we developed a function-based platform that directly measures antigen-dependent T-cell activation and target cell killing, enabling rapid identification of potent and selective TCE candidates.

PEPTALK KEYNOTE PANEL: CELEBRATING 25 YEARS OF SCIENCE AND THE NEXT ERA OF PROTEIN RESEARCH

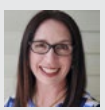
1:10 PANEL DISCUSSION: The PepTalk Legacy and What's Next

Dominic Esposito, PhD, Senior Director, Protein Sciences, Septerna

Join us for a special keynote panel as we celebrate 25 years of PepTalk. Hear from past and present leaders who have shaped the field and the event, reflect on the breakthroughs that defined PepTalk's legacy, and explore what the future holds for protein engineering, expression, and production. This milestone moment honors our shared journey and looks ahead to the discoveries yet to come.

Panelists:




Nicola Burgess-Brown, PhD, Professorial Research Fellow, UCL, London; COO, Protein Sciences, Structural Genomics Consortium
Henry C. Chiou, PhD, retired Senior Director General Manager, Biosciences, Thermo Fisher Scientific
Ian Hunt, PhD, Global Head of Scientific Engagement, Biomedical Research, Novartis
Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics
David W. Wood, PhD, Professor, Chemical & Biomolecular Engineering, Ohio State University

1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

2:15 Close of Conference

WEDNESDAY, JANUARY 21

1:00 pm Registration Open

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1:45 Celebrating 25 Years: Cake Cutting in the Exhibit Hall with Poster Viewing

NEXT-GEN CELL ENGAGERS

2:15 Chairperson's Opening Remarks

Nathan Robertson, PhD, Scientific Director, Biologics Discovery & Development, LifeArc

2:20 Structure and Engineering of an Anti-CD3 Heavy Chain-Only Antibody for T-Cell Engaging Immunotherapeutics

Robert Pejchal, PhD, Director, Antibody Engineering, Adimab LLC

We describe the 1.9Å resolution crystal structure of anti-CD3 single domain antibody ADI-98214, which is equipotent to UCHT1 when paired with IgG or TCR modalities but greatly simplifies bi- and multispecific assembly. The structure reveals a novel binding mode that overlaps with but is distinct from UCHT1 and informs further tuning to optimize affinity, with the aim of advancing the next generation of T-cell engagers.

2:50 Unlocking the Power of Bispecific Antibodies for Treating Solid Tumors

Tatjana Petojevic, PhD, Director, Protein Sciences, Rondo Therapeutics

CD3-targeting T cell engagers show significant clinical benefit in hematological malignancies, but limited efficacy in treating solid tumors partially due to the immunosuppressive TME. To overcome this challenge, we develop bispecific antibodies that activate the CD28 costimulatory receptor when bound to a tumor-associated antigen for the treatment of solid tumors. Here, we describe our lead molecule RNDO-564, a potency optimized CD28 x Nectin-4 bsAb for the treatment of metastatic bladder cancer.

3:20 Engineering Next-Generation T Cell Engagers: A Trispecific Platform for Cancer Immunotherapy

Desmond Lau, PhD, Senior Scientist, Protein Engineering, Zymeworks

We engineered a trispecific T cell engager platform with integrated CD28 co-stimulation that provides a differentiated activity and safety profile facilitated by conditional CD28 co-stimulation, requiring CD3 engagement and obligate cis T cell binding resulting in no target-independent T cell activation or T cell-T cell bridging. Here, we present transferability of the TriTCE Co-Stim platform to improve anti-tumor activity and specificity via avidity-driven multivalent, logic-gated, and TCR mimetic targeting approaches.

3:50 Rapid, Multi-Parameter Optimization and Developability Assessment of Multispecific Building Blocks Using Integrated *In Vitro* and *In Silico* Workflows

Alloy Therapeutics

Dalton Markrush, Sr Scientist, Global Bioanalytics, Alloy Therapeutics

Proper developability assessments are critical for clinical success, and workflows for monoclonal antibodies are well established in literature. We have developed similar workflows for multispecific building blocks to facilitate multispecific development. Here, we describe a rapid, multi-parameter optimization strategy for bispecific building blocks that integrates *in vitro* and *in silico* workflows to evaluate developability and affinity.

4:20 Refreshment Break in the Exhibit Hall with Poster Viewing

4:50 Precision by Design: Next-Generation Immune Engagers with Improved Therapeutic Index

Even Walseng, PhD, Director, Biologics Engineering, AstraZeneca

The presence of multispecific modalities is rapidly increasing in clinical trials. Among these complex modalities are T cell engagers (TCEs), a category of T cell-retargeting immunotherapy transforming clinical cancer care. The application of TCEs has in part been limited by challenges including on-target, off-tumor toxicity and poor therapeutic index (TI) linked to aberrant cytokine release. To overcome this challenge, we have designed the TriMab, a dual-targeting TCE with improved TI.

5:20 Leveraging Natural Killer (NK) Cell Tri-Specific Killer Engagers (TriKEs) to Treat AML: Clinical Updates and Future Directions

Martin Felices, Assistant Professor, Medicine, Hematology & Oncology, University of Minnesota, Twin Cities

Natural killer (NK) cells are limited in their control of acute myeloid leukemia (AML) by lack of antigen specificity. To address this issue we have developed the Tri-specific Killer Engager (TriKE) platform, which imbues NK cells with antigen specificity and drives their expansion through an IL-15 moiety. Here we will discuss clinical findings from two generations of CD33 targeting TriKEs and ongoing efforts to develop next-generation molecules.

5:50 Close of Day

THURSDAY, JANUARY 22

8:00 am Registration Open

PLENARY KEYNOTE SESSION: End-to-End *in silico*-Designed Biologics

8:25 Welcome Remarks

Christina Lingham, Executive Director, Conferences and Fellow, Cambridge Healthtech Institute

8:30 **Plenary Keynote Introduction**

Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

8:35 **New Frontier of Biotherapeutic Discovery: Where Machine Learning Meets Molecular Design**

Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:00 **PLENARY FIRESIDE CHAT: End-to-End *in silico*–Designed Biologics**

Moderator: Andrew Nixon, PhD, Senior Vice President, Global Head Biotherapeutics Discovery, Boehringer Ingelheim Pharmaceuticals Inc.

- How is the path to drug development different with ML/AI?
- How far off is *de novo* design for biologics? For antibodies?
- How is ML/AI used for target selection?
- How do you accelerate DMTA cycles?
- Data standardization—how to incorporate historical data?
- Federated learning—how do you ensure you have enough data to build a model?
- Promoting change management

Panelists:
Charlotte M. Deane, PhD, Professor, Structural Bioinformatics, Statistics, University of Oxford; Executive Chair, Engineering and Physical Sciences Research Council (EPSRC)
Garegin Papoian, PhD, Co-Founder & CSO, DeepOrigin
Stephanie Truhlar, PhD, Vice President, Biotechnology Discovery Research, Eli Lilly and Company

9:30 **Coffee Break in the Exhibit Hall with Poster Viewing**

WOMEN IN SCIENCE MEET-UP

Meet the Moderators at the Plaza in the Exhibit Hall

Michelle R. Gaylord, MS, Former Principal Scientist, Protein Expression & Advanced Automation, Velia Therapeutics

Deborah Moore-Lai, PhD, Vice President, Protein Sciences, ProFound Therapeutics

CONDITIONAL ACTIVATION AND MASKING APPROACHES

10:20 **Chairperson's Remarks**

Tatjana Petojevic, PhD, Director, Protein Sciences, Rondo Therapeutics

10:25 **A Novel Anti-CTLA-4 Switch Antibody with Asymmetric Fc for Tumor-Selective Anti-Tumor Immune Activation**

Momoko Okuda-Miura, PhD, Researcher, Analytical Development, Chugai Pharmaceutical Co.

ROSE12 is a novel anti-CTLA4 antibody that activates in response to high concentrations of extracellular ATP in the tumor microenvironment. In addition, affinity of ROSE12 against FcγRs is increased by asymmetric Fc. Therefore, ROSE12 shows very strong ADCC activity. ROSE12 also selectively depleted intratumoral Tregs, demonstrating anti-tumor effects without inducing systemic immune activation in mouse models. Currently, ROSE12 is undergoing a Phase I clinical study.

10:55 **FEATURED PRESENTATION: Structure-Aided Design and Engineering of an FGFR1c x KLB Multispecific Altibody Agonist for MASH**

Yang Shen, PhD, Executive Director of Antibody Engineering, Bispecifics, Regeneron

Multispecific antibody targeting multiple epitopes or targets has emerged with advantages over bispecifics on better potency, broader target space and higher specificity. FGF21 is a master coordinator for lipid homeostasis. Via structure-aided design, a multispecific FGF21-mimicking Altibody was developed to achieve KLB-dependent FGFR1c activation. Our study illuminates combinatorial factors can contribute to the improved agonism. The multispecific antibody-based FGF21 mimetics also demonstrates potential dosing and developability advantages over ligand-based mimetics.

11:25 **Next-Gen T-MATE T Cell Engagers: Transforming Cancer Therapies**

Aude Segaliny, PhD, Vice President, Research & Development, Amberstone Biosciences

The therapeutic potential of T Cell Engagers (TCE) has been limited by a narrow safety window, with excess cytokine release and on-target toxicity limiting their clinical usefulness. Our Tumor-Microenvironment Activated Therapeutics (T-MATE) technology overcomes these challenges by utilizing a pH-dependent conformational switch. This innovative mechanism attenuates TCE activity at physiological pH while preserving full potency within the tumor microenvironment, enabling a new class of safe and effective T cell engagers.

11:55 **Enjoy Lunch on Your Own**

1:00 pm **Ice Cream & Cookie Break in the Exhibit Hall with Last Chance for Poster Viewing**

PROMISING CANDIDATES AND LESSONS FROM THE CLINIC

1:40 **Chairperson's Remarks**

Even Walseng, PhD, Director, Biologics Engineering, AstraZeneca

1:45 EVOLVE104: T Cell Engager with Integrated CD2 Costimulation for Treating ULBP2/5/6-Expressing Solid Tumors

Oksana Sergeeva, PhD, Principal Scientist, EvolveImmune Therapeutics

EvolveImmune has developed the EVOLVE platform by integrating CD2 costimulation with precisely tuned CD3 affinity to sustain T cell effector function and decrease target-independent cytokine release. EVOLVE104 targets not only CD3 and CD2 on the T cell but also ULBP2/5/6 on tumor cells of which there is enriched expression in squamous-cell tumors and urothelial cancer. EVOLVE104 is now in the clinic for the treatment of these solid-tumor indications.

2:15 Rational Design and Engineering POV for Humanizing Therapeutic Antibodies

Nathan Robertson, PhD, Scientific Director, Biologics Discovery & Development, LifeArc

Antibody humanization remains pivotal in the development of therapeutic antibodies, reducing immunogenicity while retaining antigen specificity and affinity. We present LifeArc case studies of the humanization of mAbs leading to licensed candidates. Antibody engineering approaches, including CDR grafting, framework region modification, and *de novo* design. By integrating these strategies, we enhance the safety profiles of therapeutic antibodies, maintain functional characteristics while enhancing human content, reducing immunogenicity, and enhancing developability.

2:45 Multifunctional Cell Engagers with Conditional Effector Functions for Precision Immunotherapies

Nikolai Kley, PhD, Founder & President & CEO, Orionis Biosciences

We are developing various types of multifunctional cell-engager modalities that harness molecular cooperativity and induced-proximity mechanisms to modulate immune-cell connections and functions with a high level of precision. These include in-*cis* and in-*trans* acting molecules that encode engineered cytokines with on-target localized effector functions. Several such modalities and their potential as novel immunotherapies will be discussed.

3:15 Triple Threat: Targeting c-Met, EGFR, and VEGF with the Trispecific Antibody TAVO412 for Comprehensive Tumor Control

Mark L. Chiu, PhD, CSO, Tavotek Biotherapeutics

TAVO412 is a humanized trispecific EGFR x cMET x VEGF antibody with the potential to control abnormal EGFR signaling, dysfunctional cMET activation, and VEGF-induced angiogenesis which are responsible for the growth and metastasis in difficult-to-treat solid tumors. We highlight the clinical Phase 1 execution to determine the safety and tolerability in patients with advanced solid tumors. We present where TAVO412 has clinical responses in esophageal, colorectal, and lung cancers.

3:45 Bridging Bench and Bedside: Translating Multispecific Protein Therapies into Real-World Cancer Care, What Protein Scientists Need to Know about the Patient Experience—Through the Eyes of an Integrative Physician

David James, ND, Licensed Naturopathic Physician, PLLC

As multispecific immune-engagers move from hematologic cancers into the solid tumor space, clinicians need practical frameworks to explain, monitor, and support these therapies in real-world patients. This talk explores off-the-shelf alternatives to CAR T therapy from the bedside perspective, integrating tumor microenvironment insights, patient safety, and shared decision-making. Attendees will learn how integrative oncology can help translate complex science into meaningful, accessible care.

4:15 Close of Conference

PRESENT A POSTER AND SAVE $50!

Cambridge Healthtech Institute encourages attendees to gain further exposure by presenting their work in the poster sessions. To secure an onsite poster board and/or ensure your poster is included in the conference materials, your full submission must be received, and your registration paid in full by November 21, 2025.

Register and indicate that you would like to present a poster. Once your registration has been fully processed, we will send an email with a unique link and instructions for submitting your materials. Please see below for more information.

Reasons you should present your research poster at this conference:

- Your research will be seen by our international delegation, representing leaders from top pharmaceutical, biotech, academic and government institutions
- Discuss your research and collaborate with other attendees
- Your poster will be published in our conference materials
- Receive $50 off your registration

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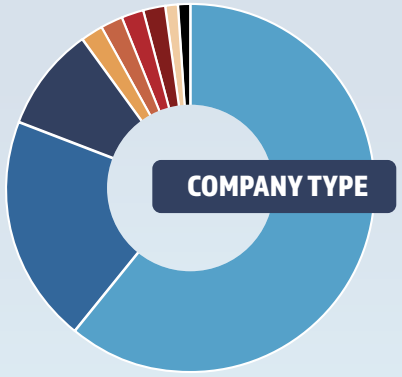
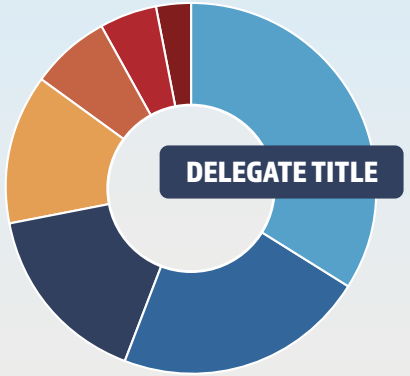


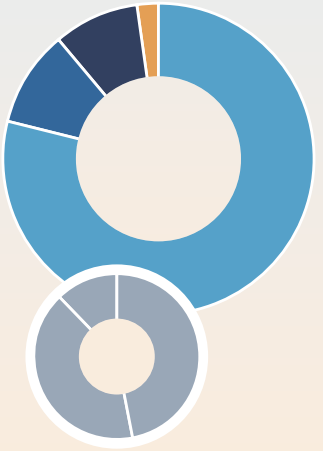
- 61% Biotech
- 20% Pharma
- 9% Academic
- 2% Government
- 2% Healthcare
- 2% Services
- 2% Other
- 1% CRO
- 1% Societies



- 34% Scientist/ Technologist
- 22% Sales & Marketing
- 16% Director
- 13% Executive
- 7% Manager
- 5% Professor
- 3% Assistant

GEOGRAPHIC LOCATION

- 79% United States
- 10% Asia
- 9% Europe
- 2% Rest of World



US BREAKDOWN

- 47% West Coast
- 41% East Coast
- 12% Midwest

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PODIUM PRESENTATIONS

— Available within Main Agenda!

Showcase your solutions to a guaranteed, targeted audience through a 15- or 30-minute presentation during a specific program, breakfast, lunch, or a pre-conference workshop. Package includes exhibit space, on-site branding, and access to cooperative marketing efforts by CHI. Lunches are delivered to attendees who are already seated in the main session room. Presentations will sell out quickly! Sign on early to secure your talk.

ONE-TO-ONE MEETINGS

CHI will set up 6-8 in-person meetings during the conference, based on your selections from the advance registration list. Our staff will handle invites, confirmations and reminders, and walk the guest over to the meeting area. This package also includes a meeting space at the venue, complimentary main-conference registrations, branding, an 8'x10' exhibit space, and more.

EXHIBIT

Exhibitors will enjoy facilitated networking opportunities with qualified delegates, making it the perfect platform to launch a new product, collect feedback, and generate new leads. Exhibit space sells out quickly, so reserve yours today!

Additional branding and promotional opportunities are available, including:

- Conference Tote Bags
- Literature Distribution (Tote Bag Insert or Chair Drop)
- Registration Area Sponsor
- Badge Lanyards
- Conference Materials Advertisement
- Padfolios and More...

FOR ADDITIONAL INFORMATION, PLEASE CONTACT:

COMPANIES A-K

Jason Gerardi
Sr. Manager, Business Development
781-972-5452 | jgerardi@healthtech.com

COMPANIES L-Z:

Ashley Parsons
Manager, Business Development
781-972-1340 | ashleyparsons@healthtech.com

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HOTEL & TRAVEL

Conference Venue and Hotel:
Hilton San Diego Bayfront
1 Park Boulevard
San Diego, CA 92101

Discounted Room Rate: $309 s/d
includes complimentary Wi-Fi

Discounted Room Rate Cut-off Date: December 21, 2025

VISIT THE TRAVEL PAGE CHI-PepTalk.com/travel
to make your hotel reservations and for additional information

SAVE $100 off the Conference Registration by reserving your Hotel Room with the Hilton San Diego Bayfront!

Your reservation must be made under the Peptalk/BioLogic Room block for a minimum of 4 nights. Must be reserved by December 21, 2025. Only one discount applicable per hotel room.

Can't Make it to San Diego?

Connect from anywhere. Join via our robust virtual platform and access these dynamic features.

- INTUITIVE INTERFACE
- COMPANY BRANDING (LOGO)
- DOWNLOADS
- LIVE CHAT
- LIVE SESSIONS
- RECORDED SESSIONS
- POSTER SESSIONS
- PANEL DISCUSSIONS

Celebrating 25 Years

PepTalk

January 19-22, 2026
San Diego, CA
The Protein Science and Production Week

2026 PRICING PACKAGES

PepTalk All Access Package

Includes access to (4 days) all conferences, symposia, networking events, and on-demand access. You are allowed to move between Conferences to attend presentations taking place at the same time.

	COMMERCIAL	ACADEMIC, GOVERNMENT, HOSPITAL-AFFILIATED
Advance Registration Rates until November 21, 2025	$3199	$1599
Standard Pricing After November 21, 2025	$3399	$1699

PepTalk Basic Package

Includes access to ONE conference (1.5 days), networking events, and on-demand access. You are allowed to move between Conferences to attend presentations taking place at the same time.

Advance Registration Rates until November 21, 2025	$2199	$1199
Standard Pricing After November 21, 2025	$2499	$1299

Symposium Only Pricing

Includes access to 1 symposium on Monday, January 19

1 Symposium	$999	$599

Does not include Training Seminars happening at the BioLogic Summit on Monday, January 19.
If you are attending the BioLogic Summit, separate registration is required for the PepTalk Symposia on Monday, January 19.

For Additional Registration Options, Visit Our Event Website:

CHI-PepTalk.com

reg@healthtech.com | P: 781.972.5400 or Toll-free in the U.S. 888.999.6288

Please use keycode **PTK EF** when registering!

Group Discounts are Available!

Have your colleagues or entire team attend PepTalk. Purchase a full-price registration here, and participants from the same organization will receive a 20% discount when registering through the Group Registration page.

For more information on group discounts contact **Uma Patel,** at 781-972-5447.

(Group registration package must be equal to or less than the value of the full price package.)

Alumni Discount - SAVE 20%

CHI appreciates your participation at its events. As a result of the great loyalty you have shown us, we are pleased to extend to you the exclusive opportunity to save an additional 20% off the registration rate.

** Alumni, X, LinkedIn, Facebook, or any other promotional discounts cannot be combined.*

Poster Discount

Present a Poster and Save $50 - Poster materials are due by November 21, 2025. Once your registration has been fully processed, we will send an email containing a unique link and instructions for submitting your abstract and other materials. If you do not receive your link within 5 business days, please contact **jring@healthtech.com.**

CHI reserves the right to publish your poster content in various marketing materials and products.