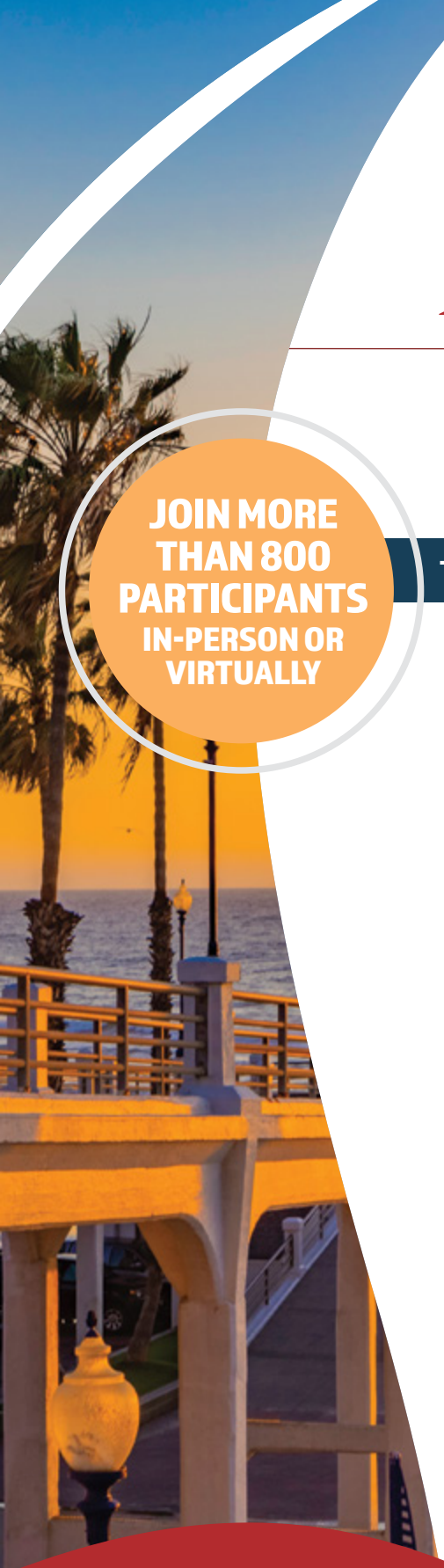
21st Annual

PepTalk

January 17-19, 2022 | San Diego, CA

Pacific Standard Time (UTC-8:00)

HILTON SAN DIEGO BAYFRONT AND VIRTUAL



JOIN MORE THAN 800 PARTICIPANTS IN-PERSON OR VIRTUALLY

THE PROTEIN SCIENCE AND PRODUCTION WEEK

KEYNOTE PRESENTERS INCLUDE

Zhimei Du, PhD,
Director, Biologics & Cell Therapeutics Process Development, Merck and Co., Inc.

John K. Kawooya, PhD,
Director, Biologics Optimization and Therapeutic Discovery, Amgen Inc.

Hanns-Christian Mahler, PhD,
Board Member, Bionter AG

Mano Manoharan, PhD,
Distinguished Scientist & Senior Vice President, Innovation Chemistry, Alnylam Pharmaceuticals

Paul Parren, PhD,
Executive Vice President & Head, Lava Therapeutics

Peter M. Tessier, PhD,
Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

2022 PROGRAMS

click stream titles to view full agenda

- ANTIBODY DISCOVERY & ENGINEERING
- PROTEIN & ANTIBODY THERAPEUTICS
- CHARACTERIZATION & AGGREGATION IN BIOPHARMACEUTICALS
- CELL & GENE THERAPY
- BIOTHERAPEUTIC EXPRESSION & PRODUCTION
- PROTEIN PRODUCTION & HTP
- TS TRAINING SEMINARS

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21st Annual

PEPTALK 2022

THE PROTEIN SCIENCE AND PRODUCTION WEEK

January 17-19, 2022 | San Diego, CA

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Conference Programs

(click title to view program)

ABOUT THE EVENT

Continuing 20 Years of Advanced Protein Science and Innovation

For twenty years, PepTalk has served as a gathering place for industry experts from around the world to connect, share knowledge, form collaborations, and accelerate biotherapeutics development.

We look forward to reuniting the PepTalk community in-person in San Diego on January 17-19, with a live virtual stream for those that cannot attend.

Customize an agenda that best fits your research and networking objectives with cutting-edge presentations, case studies, interactive discussions, networking activities, and so much more.

12 CONFERENCES AND 2 TRAINING SEMINARS covering protein and antibody engineering and therapeutics, characterization of biotherapeutics, cell and gene therapies, protein expression, production, and more.

170+ PRESENTATIONS from top pharma, biotech, academic, and government institutions.

CUSTOMIZED AGENDA created by you using our integrated scheduling tool and flexible track hopping.

GLOBAL PARTICIPANTS sharing biotherapeutic protein drug development opportunities.

INTERACTIVE DISCUSSIONS, BUZZ SESSION BREAKOUT groups, speed networking, Q&A sessions, panel discussions, and more.

EXHIBIT HALL featuring 50+ companies showcasing novel technologies and solutions.

RESEARCH POSTERS featuring the latest in biotherapeutics discovery.

SPONSORED TALKS by leading technology and service providers showcasing new offerings.

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

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PepTalk 2022

EVENT AT-A-GLANCE

click stream or track titles to view full agenda

	Monday, January 17- Tuesday, January 18 AM	Tuesday, January 18 PM- Wednesday, January 19
ANTIBODY DISCOVERY & ENGINEERING	Intelligent Antibody Discovery	Creative Protein Engineering
PROTEIN & ANTIBODY THERAPEUTICS	Developability of Bispecific Antibodies	Targeting Immune Cells for Emerging Immunotherapies
CHARACTERIZATION & AGGREGATION IN BIOPHARMACEUTICALS	Characterization of Biotherapeutics	Characterizing Protein Aggregates and Impurities
CELL & GENE THERAPY	Cell Therapy Analytics & Manufacturing	Gene Therapy Analytics & Manufacturing
BIOTHERAPEUTIC EXPRESSION & PRODUCTION	Cell Line Engineering and Development	Recombinant Protein Expression and Production
PROTEIN PRODUCTION & HTP	Higher-Throughput Protein Production	Optimizing Bioproduction & Processing
TRAINING SEMINARS	Introduction to Antibody Engineering	Analysis and Interpretation of Antibody Deep Sequencing and Single Cell Analysis Data

CHI's Mandatory COVID-19 Vaccination Policy

Your Safety is Our Top Priority

To ensure maximum safety, CHI has instituted a **mandatory COVID-19 vaccination policy** for all in-person participants of our events. Attendees will be asked to furnish proof of vaccination. Additional details on the vaccine policy will be provided upon registration.

Attendees that cannot participate because of this policy, or due to travel restrictions, are encouraged to participate using our virtual event platform. CHI virtual events provide you with an in-person experience at your convenience, anywhere, anytime. **See our website for details.**

Our Code of Conduct

All in-person attendees must agree to **CHI's Code of Conduct**

CHI-PepTalk.com **#PTK22**

PEPTALK

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Bon Opus Biosciences
Boston Analytical
Chemglass Life Sciences
Chemical Computing Group
CovalX
Cyrus Biotechnology
DRS Daylight Solutions
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Precision Antibody
Protein BioSolutions
Purolite Life Sciences
Refeyn
RheoSense, Inc.
Selexis SA
Spectradyne
Wyatt Technology

Training SEMINARS

By Cambridge Healthtech Institute

PEPTALK 2022

MONDAY, JANUARY 17 9:00 AM-7:30 PM,
TUESDAY, JANUARY 18 9:00 AM-12:00 PM

TS7A: Introduction to Antibody Engineering - VIRTUAL ONLY

Instructors: *Andrew R.M. Bradbury, PhD, CSO, Specifica, Inc.*

James D. Marks, MD, PhD, Professor and Vice-Chairman, Department of Anesthesia and Perioperative Care at the University of California, San Francisco (UCSF) and Chief of Performance Excellence, Zuckerberg San Francisco General Hospital and Trauma Center (ZSFG)

In this training seminar, students will learn about antibody basics, including structure, genetics and the generation of diversity, as well as the generation of potential therapeutic antibodies. This latter part will include antibody humanization, affinity and specificity maturation, display technologies, creation of naïve libraries and antibody characterization. The seminar will be fully interactive with students provided ample opportunities to discuss technology with instructors.

TUESDAY, JANUARY 18 2:00-6:00 PM,
WEDNESDAY, JANUARY 19 9:00 AM-4:50 PM

TS7B: Analysis and Interpretation of Antibody Deep Sequencing and Single Cell Analysis Data - IN PERSON ONLY - Session Room: Sapphire 411

Instructors: *Brandon DeKosky, PhD, Phillip and Susan Ragon Career Development Professor of Chemical Engineering, MIT Core Member, The Ragon Institute of MGH, MIT, and Harvard*

Matias Gutierrez-Gonzalez, PhD, Research Fellow, The Ragon Institute of MGH, MIT, and Harvard

In this training seminar, participants will learn about recently developed methods for Next-Generation Sequencing (NGS) and single-cell analysis of antibody repertoires. Part 1 will provide an introduction to antibody repertoires, including genetic background, generation of diversity, and sequencing technologies. Part 2 will incorporate an introduction and hands-on session on computational tools for analyzing antibody repertoire NGS data. We will focus on pre-processing, analysis, and visualization of data, along with presentation of existing bioinformatics pipelines available. Part 3 will focus on an overview of the development of newer methods in single-cell analysis of antibody immune responses. The course will be interactive with case studies, participants will be able to download data and examples. Please bring your computer.

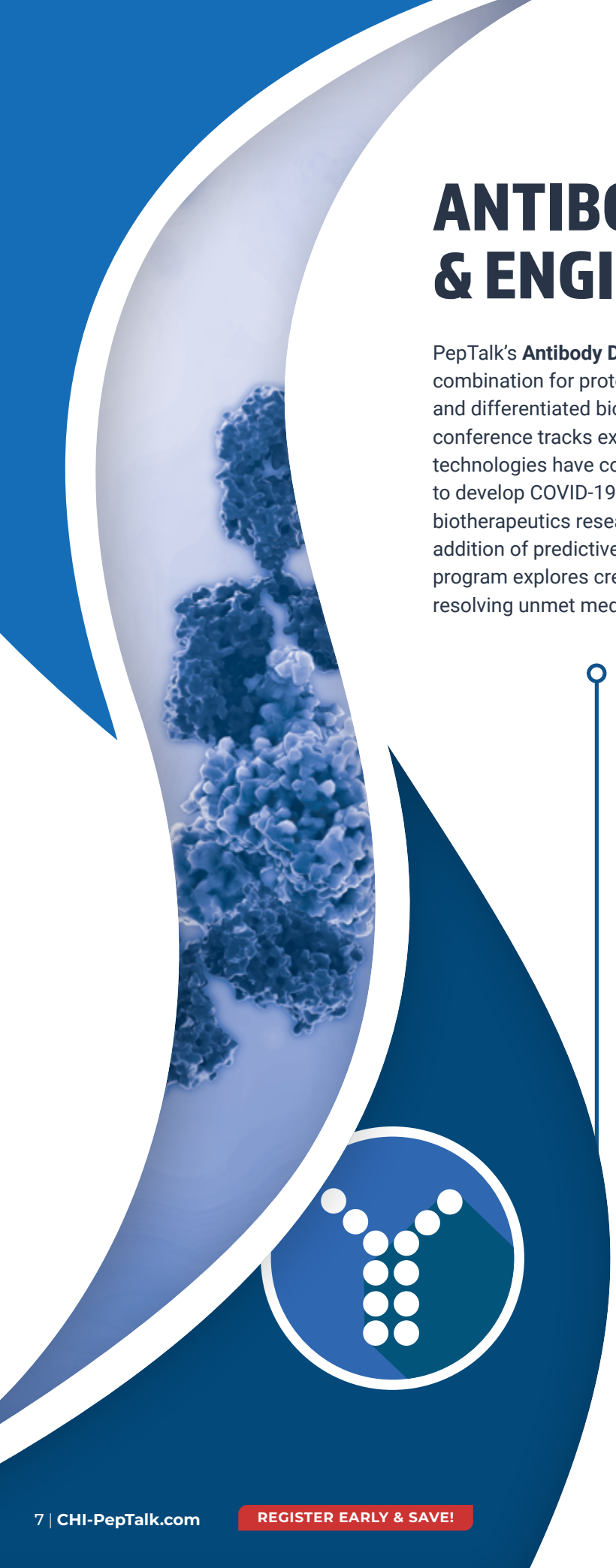
CHI Training Seminars Offer:

- **1.5-day instruction**
- **Morning and afternoon refreshments (as applicable; specific times included in the onsite agendas)**
- **Registered Attendees Receive:**
- **A hard copy handbook for the specific seminar of registration (limited additional handbooks are available for non-registered attendees)**

CHI requests that Training Seminars not be interrupted once they have begun. We ask that attendees commit to attending the entire program to not disturb the hands-on style instruction being offered to other participants.

ANTIBODY DISCOVERY & ENGINEERING

PepTalk's **Antibody Discovery & Engineering** pipeline offers a useful meeting combination for protein scientists working to discover and develop unique and differentiated biotherapeutics quickly and efficiently. For 2022, these conference tracks explore how cutting-edge discovery and engineering technologies have combined with lessons learned from the expansive efforts to develop COVID-19 vaccines and therapeutics to drive a new paradigm in biotherapeutics research. At the early stage, emphasis is on the use of the addition of predictive methods to screening platforms, while the engineering program explores creative new ways of reaching cells of interest and resolving unmet medical needs.



JANUARY 17-18

Intelligent Antibody Discovery

AGENDA

JANUARY 18-19

Creative Protein Engineering

AGENDA

REGISTER EARLY & SAVE!

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INTELLIGENT ANTIBODY DISCOVERY

SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

HIGH-THROUGHPUT FUNCTIONAL SCREENING

Session Room: Sapphire P

9:00 Organizer's Welcome Remarks

Kent Simmons, Senior Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Remarks

Gregory C. Ippolito, PhD, Research Associate Professor, Molecular Biosciences, University of Texas at Austin

9:10 Precision Functional Screening for Intelligent Antibody Discovery Against Public Health Targets

Brandon DeKosky, PhD, Phillip and Susan Ragon Career Development Professor of Chemical Engineering, MIT Core Member, The Ragon Institute of MGH, MIT, and Harvard

Recent work has revealed critical vulnerable antibody targets that interrupt malaria and HIV-1 transmission. We performed efficient antibody engineering by screening all possible single amino acid substitutions throughout the antibody variable region, enabling exquisite anti-malarial protective potency. Using the same strategy, we engineered the most broadly-neutralizing antibody reported against the HIV-1 fusion peptide. This presentation will share these unpublished molecular studies and outline effective strategies for precision drug discovery.

9:40 High-Throughput Mapping of B Cell Receptor Sequences to Antigen Specificity

Ivelin Georgiev, PhD, Associate Professor, Pathology, Microbiology, and Immunology, Vanderbilt University Vaccine Center

LIBRA-seq (LInking B-cell Receptor to Antigen specificity through sequencing) enables high-throughput antibody discovery through simultaneous screening of B cells against a theoretically unlimited number of antigens at a time. Using LIBRA-seq, we have identified antibodies with unique phenotypic properties against a number of pathogens, including HIV-1, hepatitis C, and coronavirus. Overall, the LIBRA-seq technology offers unmatched capabilities for high-throughput discovery of novel antibody therapeutics and for assessment of vaccine efficacy.

10:10 *In Vitro* Screening Tools for the Selection of Membrane-Permeable Peptides

Iriny Ekladious, PhD, Associate Principal Scientist, Sterile & Specialty Products, Merck

Peptides are a highly promising class of therapeutics; however, their potential has not yet been realized due to their poor cell permeability and limited oral bioavailability. mRNA-display is a powerful high-throughput screening technology in which peptide drug candidates are screened against a target of interest. The work described herein demonstrates the utility of ***in vitro*** approaches that interrogate peptide permeability, with the goal of integrating these tools into mRNA display.

10:40 Networking Coffee Break (Sapphire West Foyer)

NEXT-GENERATION REPERTOIRE MINING

11:00 Accelerating Antibody Discovery with *in silico* Repertoire Screening and Rational Design

Bryan Wu, PhD, NGS Lead, GlaxoSmithKline Biopharm Discovery, United Kingdom

Antibody repertoire sequencing has enabled us to access unprecedented amounts of antibody sequences. Here we will demonstrate our approach to comprehensive screening of antibody repertoires and ***in silico*** development of potent antibody leads.

11:30 Plasma IgG Proteomics for the Discovery of Pan-Coronavirus Antibodies Induced by SARS-CoV-2 Infection or Vaccination

Gregory C. Ippolito, PhD, Research Associate Professor, Molecular Biosciences, University of Texas at Austin

The most clinically advanced COVID-19 vaccines use the full SARS-CoV-2 spike (S1 + S2) as immunogen. Molecular proteomics of plasma IgG (Ig-Seq) indicates that S2-targeting antibodies typically comprise the most abundant antibody lineages in circulation and that S2-targeting antibodies arise predominantly from pre-existing cross-ß-coronavirus lineages. These Ig-Seq observations, and others, are being harnessed in the development of a new pan-ß-coronavirus vaccine based on S2-only antigens.

12:00 pm An Antibody Discovery Operating System for Hard-to-Hit Multipass Membrane Proteins

AbCellera

Roza Bidshahri, PhD, Senior Research Scientist and BD Liaison, AbCellera

GPCRs and ion channels are highly sought-after drug targets, but only two antibody drugs targeting them have been approved. AbCellera tackles the biggest challenges limiting antibody discovery for transmembrane proteins: producing antigens, driving antibody responses, and finding hits. Optimized immunization strategies, single-cell screening, and hyper-scale data science leads to hundreds of hits, and by integrating Tetrahymena — a natural membrane protein factory — we're driving powerful solutions to unlock these targets.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Antiviral mAb Discovery Using Antigen Barcoding

10x GENOMICS

Jonathan Hurtado, PhD, Post-doctoral fellow, The Scripps Research Institute

1:10 Session Break

PREDICTION OF BIOTHERAPEUTIC PROPERTIES

1:50 Deep Learning Approaches for Neoantigen Prediction

Kai Liu, PhD, Principal AI Scientist, Head, Medical Language Processing, Early Clinical Development, Genentech, Inc.

This neoantigen recognition mechanism is one of the pillars of the immunological surveillance of tumor cells for cancer therapies. By leveraging the enriched immunopeptidomics dataset, we developed deep learning based models to characterize the peptide-MHC interaction and predict the antigen presentation and immunogenicity. The ranking of the neoantigens from patients could pave the way for the development of personalized cancer immunology therapies.

2:20 Epitope-Specific Antibody Design via Deep Learning-Based Structural Modeling

Possu Huang, PhD, Assistant Professor, Bioengineering, Stanford University

Epitope-specific binders can potentially be created by computational protein design strategies. By leveraging the unique properties of neural networks, we developed a generative model for immunoglobulin structures, with which diverse structures can be modeled with unprecedented speed. A design pipeline incorporating this neural network model can achieve flexible backbone

protein-protein interface design. We will discuss this novel protein docking/design strategy and its potential application in creating epitope-specific novel immunoglobulin binders.

2:50 Find Your Table and Meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 1: *In Silico* Antibody Design

Possu Huang, PhD, Assistant Professor, Bioengineering, Stanford University

BuzZ Table 2: Antigens, Antibody Engineering and Specificity

John Williams, PhD, Professor of Molecular Medicine and Co-Director, Drug Discovery and Structural Biology Core, Beckman Research Institute at City of Hope

DISCOVERY STRATEGIES FOR CHALLENGING TARGETS

4:00 Blood-Brain Barrier Delivery in Non-Human Primates by Single Domain VNAR Antibodies to TfR1

Pawel Stocki, PhD, Director, Research, Ossianix, Inc., United Kingdom

Poor brain delivery is a major hurdle in the development of biological therapeutics for neurologic diseases because of poor Blood-Brain Barrier penetration. Numerous BBB shuttles based on single-domain VNAR antibodies were developed by Ossianix. These include TXP1 which was demonstrated to penetrate the brain with high efficiency when inject at low therapeutic dose in non-human primates with an over 30-fold increase in comparison to the control.

4:30 Merging Antibody and Small Molecule Drug Discovery: CLAMPs to Study and Drug Dynamic Proteins

James T. Koerber, PhD, Principal Scientist, Antibody Engineering, Genentech, Inc.

We will describe Conformation Locking Antibodies for Molecular Probe discovery (CLAMPs) to distinguish and induce rare protein conformational states. We discover novel KRAS CLAMPs that recognize and induce a rare KRAS conformation. These CLAMPs enable new biology insights through visualization of inhibitor-bound KRAS in cells and tumors, a high-throughput screen to discover small molecule ligands, and structure-based characterization to provide a new framework for drug discovery against dynamic proteins.

5:00 KEYNOTE PRESENTATION: Merging MOA, Structural Information & Single Cell Screening to Identify Potent mABs as Potential Therapeutic Candidates

John Williams, PhD, Professor of Molecular Medicine and Co-Director, Drug Discovery and Structural Biology Core, Beckman Research Institute at City of Hope

Beyond their unique specificity and high affinity, mAbs are imbued with additional functionality including ADCC/ADCP/CDC where the position of the epitope within the antigen has emerged as a critical determinant driving these activities. Herein, we provide examples where we leverage such information to create unique reagents and combine these reagents with single cell screening efforts to identify multiple hits that differentiate healthy and disease cells and elicit potent immune activity.

5:30 A Naive Antibody Library Platform Directly Yielding Developable Drug-Like Antibodies as Potent as Immune Sources

Andrew Bradbury, PhD, CSO, Specifica

The Specifica Generation 3 Library Platform is based on highly developable clinical scaffolds, into which natural CDRs purged of sequence liabilities have been embedded. The platform uses phage+yeast display to directly yield highly diverse (100-1000 clusters differing by Levenshtein distance 30-40), high affinity (20% subnanomolar), extremely developable (>80% lack biophysical liabilities), drug-like antibodies, which in a recent Covid campaign were as potent as antibodies from immune sources.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

RAPID COVID DISCOVERY & DEVELOPMENT PROJECTS

Session Room: Sapphire P

9:00 Chairperson's Remarks

Vu L. Truong, PhD, CEO & CSO, Aridis Pharmaceuticals, Inc.

9:05 Rapid Discovery of Infectious Disease Targets

Vu L. Truong, PhD, CEO & CSO, Aridis Pharmaceuticals, Inc.

The COVID-19 pandemic has provided an unprecedented incentive for researchers to devise strategies for rapid target discovery and development of therapeutics and vaccines. This presentation will provide an overview of discovery and product development platform approaches that could set the tone for the future development of infectious disease therapies. Case studies will be presented on viral and bacterial targets.

9:35 Discovery and Development of SARS-CoV-2 Neutralizing Antibody LY-CoV555

Bryan E. Jones, PhD, Research Fellow, BioTechnology Discovery Research, Eli Lilly & Co.

Near the start of the 2020 SARS-CoV-2 pandemic, AbCellera and Eli Lilly & Co. partnered to discover and develop neutralizing antibodies. From this partnership, Ly-CoV555 (bamlanivimab), was rapidly identified from a blood sample of a convalescent patient. Bamlanivimab became the first SARS-CoV-2 targeted antibody to enter US clinical trials, just three months after discovery. The rapid discovery and progression of bamlanivimab into clinical evaluation will be described.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:00 Rapid Generation of Potent SARS-CoV-2 Nanobodies by Autonomous Hypermutation in Yeast

Alon Wellner, PhD, Postdoctoral Researcher, Biomedical Engineering, University of California, Irvine

Autonomous Hypermutation yEast surfAce Display (AHEAD) is a synthetic antibody generation technology that imitates somatic hypermutation inside engineered yeast. By encoding antibody fragments on an error-prone orthogonal DNA replication system, surface-displayed antibodies continuously mutate through simple cycles of yeast culturing and enrichment for antigen binding to produce high-affinity clones in as little as 2 weeks. AHEAD was applied to generate diverse sets of potent nanobodies targeting the SARS-CoV-2 S glycoprotein.

INTELLIGENT ANTIBODY DISCOVERY CONTINUED

11:30 From Grass to Greener Grass – The Construction of a Biomanufacturing Facility on Budget and in Record Time

Maria J. Aubrey, Vice President, Biologics Manufacturing Center Project, National Research Council Canada

The NRC was mandated by the Government of Canada to establish the new Biologics Manufacturing Centre in Montréal to help support Canada's biomanufacturing vaccine production capacity and pandemic readiness in response to the COVID-19 pandemic and in the future. A team of industry professionals and subject matter experts was assembled to design and build a facility within one year that would normally take 2 to 3 years in normal circumstances.

12:00 pm Discovery of Antibodies with Challenging TPPs: AbCheck's Microfluidics Platform for Tailored, High-Throughput Sorting

Volker Lang, Managing Director, AbCheck s.r.o.

Specific requirements have to be met for the discovery of antibodies with challenging Target Product Profiles (TPPs). AbCheck has developed a technology to efficiently meet these requirements; e.g., functional antibodies or antibodies against targets with high homology. Our novel, tailored microfluidics technology is based on high throughput functional sorting of immune plasma cell repertoires at single cell level.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Discovery and Prioritization of Novel Antibodies with Advanced Repertoire Analysis and Exposed Liability Predictions

Piotr van Rijssel, Application Scientist, ENPICOM

The integration of high-throughput sequencing data in antibody screening accelerates and improves the discovery of novel therapeutic antibodies. However, getting from millions of sequences to a diverse set of developable antibodies with the right therapeutic properties can be incredibly challenging, time-consuming, and requires significant software and computational resources. In this session, we will discuss how you can predict exposed liability for thousands of antibodies to accelerate and de-risk your candidate selection.

1:10 Close of Intelligent Antibody Discovery

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

CREATIVE ENGINEERING STRATEGIES

Session Room: Sapphire P

2:00 Organizer's Welcome Remarks

Kent Simmons, Senior Conference Director, Cambridge Healthtech Institute

2:05 Chairperson's Remarks

G. Jonah Rainey, PhD, Vice President, Antibody Engineering, AlivaMab Discovery Services

2:10 Progress and Challenges for the *in silico* Instantaneous Generation of Fit-for-Purpose Monoclonal Antibodies

Rahmad Akbar, PhD, Researcher, Computational Systems Immunology, University of Oslo, Norway

We leveraged a lattice-based antibody-antigen binding simulation framework, which incorporates a wide range of physiological antibody binding parameters to test arbitrarily large numbers of antibody sequences for their most critical design parameters: paratope, epitope, affinity, and developability. We found that a deep generative model, trained exclusively on antibody sequence (1D) data can be used to design native-like conformational (3D) epitope-specific antibodies.

2:40 Development of Antibody-Based PROTACs

Thomas Pillow, PhD, Senior Scientist, Genentech, Inc.

The ability to degrade proteins with heterobifunctional *small* molecules has the potential to dramatically alter therapy in many human diseases. We have demonstrated the first example of a targeted degrader (aka PROTAC) conjugate. This talk will focus on our discovery of degrader-antibody conjugates, their efficacy and safety, and how this general approach can expand the utility of directed protein degradation as both a biological tool and a therapeutic possibility.

3:10 Precision Execution of Bispecifics at Scale from Design to Delivery Lonza

Devarshi Kapadia, MSc, MBA, Product Manager Marketing, Licensing Business Unit, Lonza

Heavy-light chain mispairing is one of the major concerns for producing bispecific antibodies. bYlok™ technology is a design engineering approach that solves this whist retaining molecule's closer-to-nature structure and simplified downstream purification. The presentation will also include how GS System® is set to support development of bispecific molecules by streamlining vector construction process and improved titers using GS piggyBac® transposon system.

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

ENGINEERING MULTI-SPECIFIC & MULTIMERIC ANTIBODIES

4:30 Rapid Discovery and Development of Common Light Chain Bispecific Antibodies with Unique Mechanisms of Action

Pawel K. Dominik, PhD, Principal Scientist, BioMedicine Design, Pfizer Inc.

Next-generation therapies for cancer require complex modalities to increase specificity and limit off-target toxicities. Efficient discovery, optimization and manufacturing of multispecific modalities require improvements to current technologies. We established efficient workflows to generate multispecific antibodies from single cell lines under short timelines. Based on example of bispecific antibody for immuno-oncology we share our experience on discovery and development of human bispecific antibodies with a common light chain.

5:00 From Data to Predictions: Computational Optimization of Multi-Specific Protein Therapeutics

Norbert Furtmann, PhD, Head, Computational & High-Throughput Protein Engineering, Large Molecule Research, Sanofi, Germany

Our novel, automated high-throughput engineering platform enables the fast generation of large panels of multi-specific variants (up to 10.000) giving rise to large data sets (more than 100.000 data points). By combining data science and structure-based design workflows we leverage the potential of our unique data sets to guide the computational engineering of our next-generation antibody therapeutics.

5:30 Making Multivalent Antibodies Using Novel Quadrucept Technology to Create Unique Formats with Enhanced Functionalities

Hanif Ali, PhD, Co-Founder and Director, Quadrucept Bio Limited, Cambridge, United Kingdom

We have developed and established a unique class of multivalent and multispecific antibody formats using our proprietary Quad technology to produce the next-generation of antibody-based therapeutics. We use simple protein engineering, in a plug-and-play fashion, to generate a plethora of novel antibody formats with varying size, shape, flexibility and binding domain valences. The technology has wide ranging potential for generating novel therapeutics with enhanced binding, functionality and efficacy.

6:00 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 1: The Making of Bispecific Antibodies

G. Jonah Rainey, PhD, Vice President, Antibody Engineering, AlivaMab Discovery Services

DISCOVERY & DEVELOPMENT OF CORONAVIRUS THERAPEUTICS & VACCINES

Session Room: Sapphire P

9:00 Chairperson's Remarks

G. Jonah Rainey, PhD, Vice President, Antibody Engineering, AlivaMab Discovery Services

9:05 KEYNOTE PRESENTATION: CDR Swapping and Multivalency Protein Engineering Approaches for Generating Broadly Neutralizing Nanobodies against SARS-CoV-2

Peter M. Tessier, PhD, Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

We have developed a surprisingly simple directed evolution method for generating nanobodies with high affinities and neutralization activities against SARS-CoV-2. We demonstrate that CDR swapping between low-affinity lead nanobodies results in matured nanobodies with unusually large increases in affinities and neutralization activities. We have also developed a multivalent engineering approach to achieve large synergistic improvements in the neutralizing activity of SARS-CoV-2 nanobodies against key variants of concern.

9:35 Anti-SARS-CoV-2 B Cell Responses Induced by Homologous and Heterologous Prime-Boost Vaccination

Laura M. Walker, PhD, CSO, Adagio Therapeutics

The continued spillover of coronaviruses from zoonotic reservoirs and the emergence of resistance SARS-CoV-2 variants in the human population highlights the need for broadly active counter measures. Here I will describe the identification of broadly neutralizing monoclonal antibodies (bnAbs) that potently neutralize SARS-CoV-2 variants of concern as well as pre-emergent bat SARS-like viruses. The results support the development of bnAbs for the treatment of COVID-19 and future emerging sarbecovirus threats.

10:05 International Leading Innovative Antibody Drug Integrated R&D Platform

Run Yan, PhD, Director, BD, SanyouBio

Sanyou Biopharmaceuticals is a leading international high-tech biotechnology company focusing on R&D and integrated solutions of innovative antibody drugs. Sanyou is dedicated to provide new technologies, products, services and solutions of " the best quality, fastest speed and most cost-efficiency". The presentation is going to introduce Sanyou's distinct technologies for antibody drug discovery, validation and development, as well as the capability of the integrated platforms and an example project.

10:20 Polysarcosine as a Nonimmunogenic Alternative to PEG

Vicent J. Nebot, PhD, CTO, Polypeptide Therapeutic Solutions

Polysarcosine (poly-N-methylglycine) is a non-toxic, biodegradable, aminoacid-based polymer with low immunogenicity that could serve as a replacement for polyethyleneglycol (PEG). Our company Polypeptide Therapeutic Solutions (PTS) provides a custom-made synthesis and GMP-grade manufacturing of the drug substance.

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 Where Are We Now? One Year of SARS-CoV-2 Antibody Structures

Christopher Barnes, PhD, Assistant Professor, Biology, Stanford University

In less than a year, researchers have uncovered structure-function details for many of the proteins encoded by SARS-CoV-2. We report structures that reveal how the SARS-CoV-2 spike glycoprotein binds to ***de novo*** designed angiotensin-converting enzyme 2 (ACE2) receptor decoys, the specificities of polyclonal antibody responses in COVID-19-convalescent individuals, and how monoclonal neutralizing antibodies bind spike to prevent infection. Collectively, these structures provide the foundation for the development of potential therapeutics.

SPECIAL PRESENTATIONS

11:45 The Application of Ribosome Display to Optimize 'Hard to Mature' Antibodies

Maria Groves, PhD, Director and Head of the Antibody Alliance Laboratory, AstraZeneca, United Kingdom

This talk describes the use of ribosome display to optimize 'hard to mature' clones, using the affinity optimization of an inhibitory antibody to human Arginase 2 as a case study. This work exemplifies the application of novel Shuffle and Shuffle/StEP libraries as well as pool maturation and error prone libraries to deliver significant improvements in potency, affinity, and mode of binding, that would not be achievable through more conventional methods.

12:15 pm Engineered Cytokines for Cancer and Autoimmune Diseases

Katrina Bykova, PhD, Group Leader, Cell Biology, Xencor, Inc.

Cytokines are potent regulators of the immune system, and their therapeutic potential has been established in animal disease models and clinical trials. Clinical application of native cytokines is limited by their short half-life and narrow therapeutic window. Xencor has pioneered the creation of potency-reduced cytokine-Fc fusions to promote increased ***in vivo*** persistence and superior tolerability. Examples to be discussed include potency-reduced IL15/Ra-Fc (Phase 1), IL2-Fc (Phase 1), and IL12-Fc (preclinical).

12:45 Session Break

12:55 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

ENGINEERING CONJUGATES

2:20 Drug Conjugates from Engineered Affibody Molecules

Torbjörn Gräslund, PhD, Professor, Protein Science, KTH - Royal Institute of Technology, Sweden

Affibody molecules are small engineered alternative scaffold affinity proteins that can be site-specifically loaded with cytotoxic drugs creating homogenous conjugates with a desired drug-to-carrier ratio. The presentation will explore the impact of affibody-carrier architecture, drug load, and peptide-linker composition on biodistribution and ***in vitro*** and ***in vivo*** cytotoxic efficacy.

2:50 Systematic Evaluation of Conjugates on the Yeast Surface

James A. Van Deventer, PhD, Assistant Professor, Chemical and Biological Engineering, Tufts University

The limited chemical diversity of proteins constrains molecular recognition. Noncanonical amino acids and efficient conjugation reactions offer powerful alternatives for expanding capabilities. Here, we describe the preparation and characterization of diverse conjugates on yeast. Starting from recently described fibronectin-maleimide-sulfonamide conjugates, we identified examples of drastic amino acid and small molecule substitutions retaining isoform-specific carbonic anhydrase binding. These findings highlight promising opportunities for performing protein-based drug discovery on yeast.

3:20 Fc Engineering for Site-Specific Antibody Conjugation through Engineered Double Cysteine Residues

Qun Zhou, PhD, Project Head, Large Molecules Research, Innovation U.S., Sanofi

We designed and introduced free cysteine residues into antibody Fc regions for antibody conjugation with drug-to-antibody ratio greater than two using THIOMAB. The top single cysteine mutants were selected and combined as double cysteine mutants. Most double cysteine mutants display good expression and low aggregation. PEGylation screening identified many top double cysteine mutants with high conjugatability and selectivity. These mutants can potentially be applied to site-specific antibody conjugation.

EMERGING MODALITIES

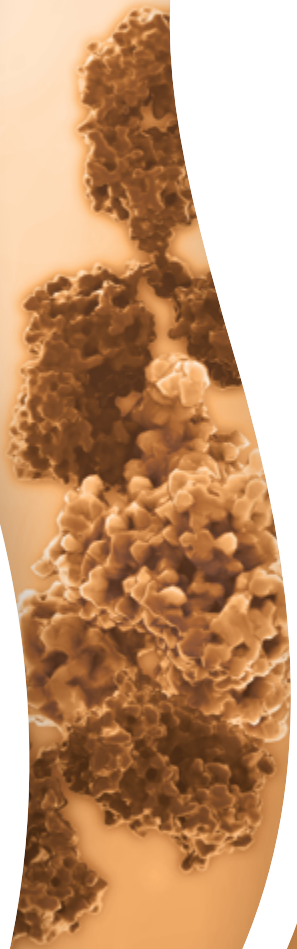
3:50 Screening for Tumor-Reactive B Cell Utilizing Antibody Repertoire Analysis

Yariv Wine, PhD, Assistant Professor, The Shmunis School of Biomedicine and Cancer Research, Tel Aviv University, Israel

The role of B-cells in the tumor microenvironment has largely been under-investigated. B cell receptor high-throughput sequencing enabled profiling antibody repertoire signature of tumor-infiltrating lymphocyte B-cells (TIL-Bs) in comparison to B cells from three compartments in a mouse model of triple-negative breast cancer. TIL-Bs exhibit a distinct antibody repertoire, suggesting an antigen-driven B-cell response. The distribution of TIL-B across compartments indicated that they migrate to and from the TME.

4:20 Close of Conference

PROTEIN ANTIBODY & THERAPEUTICS



The **Protein & Antibody Therapeutics** pipeline highlights innovative strategies and technologies being created to develop the next generation of bispecific antibodies and immunotherapies that promise to deliver unprecedented progress in medicine with resulting benefits to human health. The rate of drug approvals for these therapies is increasing and this pipeline will look at options for combining and leveraging them together to advance the state-of-the-art for antibody therapies further.

JANUARY 17-18

Developability of Bispecific Antibodies

AGENDA

JANUARY 18-19

Targeting Immune Cells for Emerging Immunotherapies

AGENDA

REGISTER EARLY & SAVE!

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SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

HOW TO CHOOSE THE RIGHT BISPECIFIC FORMAT AND TARGET COMBINATIONS

Session Room: Sapphire L

9:00 Organizer's Welcome Remarks

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

9:10 KEYNOTE PRESENTATION: Developability of Bispecific Antibodies

Paul Parren, PhD, Executive Vice President, Lava Therapeutics; Professor, Leiden University Medical Center

Dual-targeting concepts enabled by bispecific antibodies (bsAbs) hold great therapeutic promise, but translation of these concepts into treatments has proved challenging. Solutions for technical difficulties in both discovery and developability of bsAbs, which hampered the field for many years, have been sought. This presentation provides an overview of the research that led to the development of the DuoBody technology which stood at the basis for the recently approved bsAb amivantamab.

9:40 Developability of Complex Multispecifics

Sagar V. Kathuria, PhD, Senior Principal Scientist, Large Molecule Research, Sanofi

Evolving analytics for developability assessment of highly engineered antibodies. With the advent of highly engineered antibodies in the therapeutic landscape, analytical methods for developability assessment have had to keep pace. The unique properties of multispecific antibodies and the challenges associated with their assessment will be discussed.

10:10 Design Meets Biology – Engineering a PD-1/CTLA-4 Monovalent Bispecific Antibody to Improve Both Safety and Efficacy

Yariv Mazor, PhD, Senior Director, Biologics Engineering, AstraZeneca

MEDI5752 is a monovalent bispecific IgG1 antibody (DuetMab), targeting the two clinically validated receptors; PD-1 and CTLA-4. The bispecific antibody introduces novel MOAs that may provide an improved therapeutic index when compared to the two monotherapies and mAb combinations. MEDI5752 is currently being clinically evaluated for safety and efficacy.

10:40 Networking Coffee Break (Sapphire West Foyer)

11:00 KEYNOTE PRESENTATION: Trispecific Antibodies – Taking the Concept of Multi-Targeting One Step Further

Ercole Rao, PhD, Group Leader Biologics Research, Engineered Protein Therapeutics, Sanofi Germany GmbH

In the past decade, the dream of designing bispecific antibodies capable of simultaneously engaging two targets has become reality and this modality is considered by many as "the new magic bullet." Antibody engineers are working on innovative ways to add even more functionality and specificity to the ever-growing antibody toolbox. We have developed novel tri-specific antibodies, that are currently being evaluated in clinical studies.

11:30 PrecisionGATE: Developing the Next Generation of T Cell Redirecting Technology

Allison Colthart, PhD, Scientist, Revitope Oncology

12:00 pm Navigating the Diverse Antibody Pipeline with Chromatography Ligand Innovations

Josefin Bolik, MS, Global Product Manager - Antibody Platforms, Marketing, Cytiva

The pipeline for antibodies, the largest class of biotherapeutics today, is growing in diversity with variants such as bispecifics, conjugates, or fragments. Platform approaches for purification work well for many monoclonal antibodies (mAbs) on the market but selecting purification schemes can be challenging for antibody variants due to molecular diversity. We'll discuss how to select affinity resins to achieve selectivity and purification outcomes using established and new ligand innovations.

12:30 Enjoy Lunch on Your Own

1:10 Session Break

MACHINE LEARNING, DATA MINING AND COMPUTATIONAL DESIGN FOR CANDIDATE SELECTION

1:45 Chairperson's Remarks

Nimish Gera, PhD, Head, Biologics, Mythic Therapeutics

1:50 Developability Algorithms

Peter M. Tessier, PhD, Albert M. Mattocks Professor, Pharmaceutical Sciences & Chemical Engineering, University of Michigan

We have developed machine learning models for identifying antibodies with optimal combinations of high affinity and drug-like biophysical properties. Our approach combines novel descriptors of antibody molecular features with neural networks to identify Pareto optimal antibody variants with different levels of affinity improvement while minimizing natural trade-offs involving other key properties (e.g., specificity). These methods greatly reduce the required experimentation needed during antibody engineering efforts for co-optimizing multiple antibody properties.

2:20 Predicting Antibody Developability Profiles through Early Stage Discovery Screening

Laurence Fayadat-Dilman, PhD, Senior Director, Protein Sciences, Merck Research Laboratories

We developed a practical high-throughput developability workflow (100's-1,000's of molecules) implemented during the early phase of antibody generation and screening to guide the selection process of the best lead candidates. Mining of our high-quality datasets identified novel patterns and correlations between biophysical assays. These patterns and correlations represent the basis for training deep neural networks and establishing machine learning algorithms for *in silico* interrogation and prediction of developability profiles.

2:50 Find your table and meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 8: *In Silico* Downstream Process Development

Thiemo Huuk, PhD, Sales Leader, GoSilico, Cytiva

- Drivers for developing processes ***in silico***
- Smart model selection: statistical, mechanistic, or both?
- Good modeling practices: workflow and best practices
- Modeling opportunities beyond antibody applications

BISPECIFICS FOR DISEASE AREAS BEYOND ONCOLOGY

3:55 Chairperson's Remarks

Nimish Gera, PhD, Head, Biologics, Mythic Therapeutics

4:00 Brain Delivery of Therapeutic Proteins Using a Novel Fc Fragment Blood-Brain Barrier Transport Vehicle

Mihalis Kariolis, PhD, Senior Scientist, Antibody & Protein Engineering, Denali Therapeutics, Inc.

Effective delivery of protein therapeutics to the central nervous system (CNS) has been greatly restricted by the blood-brain barrier (BBB). We describe the engineering and characterization of a BBB transport vehicle (TV) comprising an engineered Fc fragment that exploits receptor-mediated transcytosis for CNS delivery of biotherapeutics. The TV platform readily accommodates numerous configurations, including bispecific antibodies and protein fusions, yielding a highly modular CNS delivery platform.

4:30 Identification and Evaluation of Antibodies Targeting the Brain Vasculature

Eric V. Shusta, PhD, Howard Curler Distinguished Professor, Chemical & Biological Engineering, University of Wisconsin, Madison

The blood-brain barrier presents a major obstacle to brain drug delivery. We have developed several different enabling platforms for the identification of antibodies against blood-brain barrier resident receptors that could ultimately be used to ferry drug cargo into the brain. Here we will describe our recent efforts using new screening paradigms to identify blood-brain barrier targeting antibodies capable of delivering therapeutic payloads to the central nervous system.

5:00 Discovery and Development of Faricimab, a CrossMab Antibody Targeting Both Vascular Endothelial Growth Factor (VEGF-A) and Angiopoietin (Ang)-2, for the Treatment of Retinal Diseases

Christoph Ullmer, PhD, Senior Principal Scientist, pRED Discovery Ophthalmology, F. Hoffmann-La Roche AG

Multiple pathways (e.g., VEGF-A, Ang-2) drive retinal disease by promoting vascular instability; however, current treatments only target VEGF-A. In preclinical studies, faricimab, a bispecific antibody targeting VEGF-A + Ang-2 developed using CrossMab technology, promoted vascular stability. In Phase 3 clinical trials, faricimab resulted in noninferior vision gains, improved anatomic outcomes, and demonstrated potential for extended dosing and comparable safety compared with aflibercept, a VEGF inhibitor, in patients with retinal diseases.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

PROCESS DEVELOPMENT FOR BISPECIFICS

Session Room: Sapphire L

9:00 Chairperson's Remarks

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

9:05 From Design to Delivery: How Concepts Impact Manufacturing of Multispecific Antibodies

Stefan R. Schmidt, MBA, PhD, COO & Head, Operations, BioAtrium AG

Multifunctional antibodies represent a major trend in therapeutic modalities. More than 50 different concepts have been established and many of them reached advanced clinical studies. This presentation compares the leading approaches, discusses pros and cons, gives recommendations on design and manufacturing supported by examples from case studies, and reviews the current multispecific antibody pipeline in the context of biological function and molecular design.

9:35 Bispecific mAb2 Format Harnesses Platform IgG Processes for Rapid and Cost-Effective Drug Development

Mateusz Wydro, PhD, Senior Director, CMC, F-star Therapeutics, Inc.

Typical development and manufacturing of monoclonal antibodies (mAbs) use established platform methods and processes which enable desired combination of high yielding cell lines and rapid development timelines. Due to similarity to mAbs, in structure and physicochemical properties, F-star's mAb2 bispecific format harnesses the well-established mAbs platform approaches for drug development. This talk will explore the application of the platform technologies in manufacturing process development for mAb2 bispecific format.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

12:00 pm Enjoy Lunch on Your Own

1:10 Close of Developability of Bispecific Antibodies

TARGETING IMMUNE CELLS FOR EMERGING IMMUNOTHERAPIES

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

PSMA TARGETING BY DIFFERENT APPROACHES

Session Room: Sapphire L

2:00 Organizer's Welcome Remarks

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

2:05 Chairperson's Remarks

Paul Parren, PhD, Executive Vice President, Lava Therapeutics; Professor, Leiden University Medical Center

2:10 Novel Chimeric Antigen Receptor T Cell Therapies for Advanced Prostate Cancer: Recent Clinical Trials (and Tribulations)

Vivek Narayan, MD, Assistant Professor, Hematology Oncology, University of Pennsylvania

Advanced prostate cancer represents a compelling model for CAR T therapy. We will review current mechanisms and rationale for re-directed T cell therapies for advanced prostate cancer; describe an early experience with CAR T therapy for advanced prostate cancer; and discuss challenges and future approaches for prostate cancer CAR T therapy.

2:40 PSMA-Directed CAR T Cell Platforms – Can We Maximize Efficacy to Improve PSMA Targeting?

Susan F. Slovin, PhD, Medical Oncologist, Genitourinary Oncology Service, Memorial Sloan Kettering Cancer Center

PSMA-directed CARs have been studied in the Phase I setting in metastatic castration resistant prostate cancer (mCRPC) using various platforms. Despite success in preclinical models, ongoing trials suggest that clinical toxicity may be limiting. The structural diversities of PSMA-directed CAR T cell platforms for mCRPC will be discussed including the role for companion imaging as immune monitoring alone may not provide sufficient input regarding correlations between immune response and biologic impact.

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

4:30 Human Costimulatory Bispecific Antibodies in Cancer Immunotherapy: Focus in Prostate Cancer

Dimitris Skokos, PhD, Senior Director, Cancer Immunology, Regeneron Pharmaceuticals

Combining a novel class of co-stimulatory bispecific antibodies with PD-1 mAb or the emerging class of TAAxCD3 bispecifics may provide well-tolerated, "off-the-shelf" antibody therapies with potentially enhanced anti-tumor efficacy.

5:00 Bispecific Gamma-Delta T Cell Engagers Targeting PSMA for the Treatment of Prostate Cancer

Paul Parren, PhD, Executive Vice President, Lava Therapeutics; Professor, Leiden University Medical Center

The development of next-generation bispecific gamma-delta T cell engagers (bsTCE) with a widened therapeutic window characterized by high potency and high tumor selectivity has strong potential. Lava Therapeutics' platform is based on the selective recruitment of Vγ9Vδ2 T cells for eradicating tumor cells. This presentation will discuss our bsTCEs designed to engage Vγ9Vδ2 T cells against tumor cells expressing PSMA for the development of novel therapeutics in prostate cancer.

5:30 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

TARGETING NON-TRADITIONAL CELLS

Session Room: Sapphire L

9:00 Chairperson's Remarks

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

9:05 Developing EBV-Specific Allogeneic T Cell Immunotherapies for a New Tomorrow

Jakob Dupont, MD, Global Head, R&D, Atara Biotherapeutics

Autologous T cell therapies have been life-changing for many patients; but virus-specific, allogeneic platforms hold the promise of effective, off-the-shelf treatments manufactured at scale, and delivered to patients within days. In this talk, the flexibility and advantages of EBV T cells and how allogeneic treatments may change the treatment paradigm for cancer and autoimmune diseases will be discussed.

9:35 Efficient NK Cell Redirection by Triggering NKp30

Stefan Zielonka, PhD, Associate Director, Protein Engineering & Antibody Technologies, Merck KGaA

Activating NK cell receptors represent promising target structures to elicit potent anti-tumor immune responses. We have generated efficient NK cell engagers that bridge Natural Cytotoxicity Receptor NKp30 on NK cells with EGFR on tumor cells in several multifunctional IgG-like bispecific formats. In this talk I will discuss different strategies for targeting NKp30.

10:05 Engineering Transmembrane Proteins for Cancer Immunotherapy

Nicholas Abuid, PhD, Application Scientist, ACROBiosystems

Transmembrane proteins (TPs) are embedded in the cell membrane and span the intracellular and extracellular environments. The transmembrane region directly interacts with the phospholipid bilayer and is an important channel bridging these environments enabling transport of various ions and molecules and relaying activation and response reactions to extracellular stimuli. These reactions propagate intracellularly through downstream signaling pathways and regulate cell metabolism, cellular activity, and cellular fate. TPs have broad applications in cancer immunotherapy and autoimmune diseases. Our team has engineered methods to formulate TPs to support research in understanding the role of various diseases.

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 CAR-M: Engineered Macrophages for Cancer Immunotherapy

Sascha Abramson, PhD, Vice President, Scientific Operations, Carisma Therapeutics

Adoptive cell therapies have demonstrated remarkable outcomes in hematologic malignancies, but efficacy in solid tumors is still lacking. We have established a novel, proprietary monocyte and macrophage based cell therapy platform based on chimeric antigen receptor macrophages (CAR-M). In this talk we will review the CAR-M platform, present novel preclinical data, and discuss the ongoing Phase I, first-in-human CAR-M trial for HER2+ metastatic solid tumors.

11:45 Innovative Translational CAR NK Cell Engineering

Tamara J. Laskowski, PhD, Senior Director, Head, Clinical Development, Personalized Medicine, Lonza Global

Advancements in cellular engineering have led to the development of novel strategies aimed at overcoming current challenges. In this presentation, we will discuss the advantages of allogeneic NK cells as a resource for cell therapy. We will focus on strategies to leverage the intrinsic anti-tumor properties of NK cells, and will discuss our work to develop novel approaches to enhance NK function and persistence though genetic engineering.

12:15 pm Enjoy Lunch on Your Own

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

NEXT-GENERATION CARS: WHAT DO THE NEW FORMATS LOOK LIKE?

2:15 Chairperson's Remarks

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

2:20 KEYNOTE PRESENTATION: Chimeric Antigen Receptor-Modified Immune Effector Cell Therapies: Learning from the Present; Charting a Path to the Future

Renier J. Brentjens, MD, PhD, Deputy Director and Chair, Department of Medicine, Roswell Park Comprehensive Cancer Center

CAR T cells have demonstrated marked clinical outcomes in several hematologic malignancies and yet, many patients either fail to respond or relapse after an initial response. We have developed a novel platform, armored CAR T cells, wherein T cells are further engineered to enhance CAR T cell anti-tumor efficacy as well as persistence.

2:50 Hypoxia-Sensing CAR T Cells Avoid Systemic Toxicity to Focus the Fight on Solid Malignancies

James N. Arnold, Lecturer, Cancer Cell Biology & Imaging, Kings College London

We have engineered a stringent oxygen-sensing system 'HypoxiCAR' which restricts CAR expression to hypoxic microenvironments, such as is found in solid tumors. In preclinical models, HypoxiCAR T cells provide robust anti-tumor efficacy while avoiding systemic toxicities associated with on-target off-tumor activation.

RECENT RESULTS IN THE CLINIC

3:20 Developing Allogeneic Vd1 (γδ) T Cell Therapies

Oliver Nussbaumer, PhD, Founder & Vice President, Immunology, GammaDelta Therapeutics, Ltd.

GammaDelta Therapeutics is developing allogeneic cell therapy platforms based on Vd1 (γδ) T cells. We are exploiting the biology and characteristics of these unconventional T cells to progress differentiated products for adoptive cell therapy of hematologic malignancies and solid tumors.

3:50 CD8ab CAR T Cell Development from TiPSC

Sjoukje van der Stegen, PhD, Research Fellow, Memorial Sloan Kettering Cancer Center

T cell-derived induced pluripotent stem cells (TiPSCs) provide a powerful platform for unlimited production of specific T cells. Initial differentiation platforms facilitated development of innate-like T lymphocytes. Through careful adjustment of the Notch and ITAM signaling, we can facilitate alpha-beta T lineage commitment, while utilizing the CAR to drive the cells through T cell development and maturation.

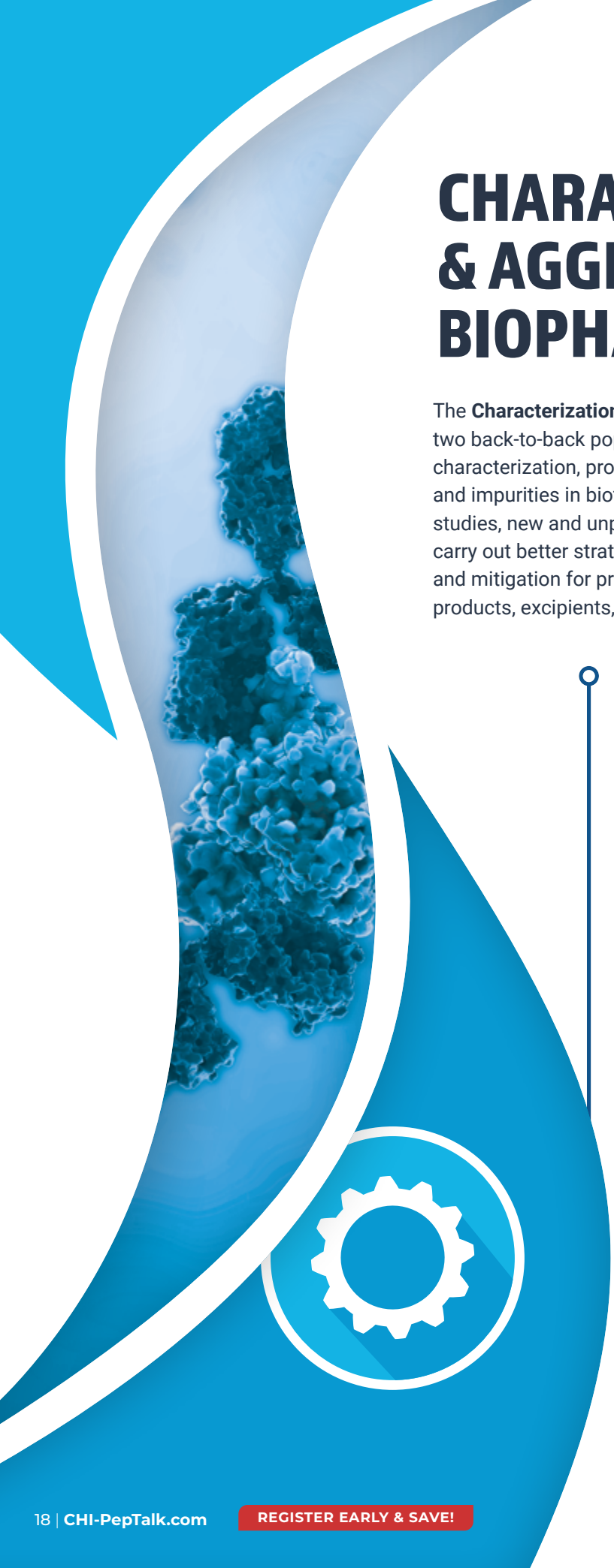
4:20 Off-the-Shelf, CD30, CAR-Modified EBV-Specific T Cells for the Treatment of CD30-Positive Lymphoma

Cliona M. Rooney, PhD, Professor, Center for Cell and Gene Therapy, Department of Pediatrics, Baylor College of Medicine

We are using banked EBV-specific T-cells (EBVSTs) modified to express a CD30. CAR for the treatment of allogeneic patients with CD30-positive lymphoma with impressive clinical responses.

4:50 Close of Conference

CHARACTERIZATION & AGGREGATION IN BIOPHARMACEUTICALS



The **Characterization & Aggregation in Biopharmaceuticals** pipeline features two back-to-back popular conferences focusing on critical topics such as characterization, protein aggregation, detection, and control of contaminants and impurities in biotherapeutics. These conferences will feature case studies, new and unpublished data, and interactive discussions on how to carry out better strategies and tools for characterization, risk assessment, and mitigation for protein aggregates, particles, and impurities arising from products, excipients, processes, and packaging in novel biologics.

JANUARY 17-18

Characterization of Biotherapeutics

AGENDA

JANUARY 18-19

Characterizing Protein Aggregates and Impurities

AGENDA

REGISTER EARLY & SAVE!

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SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

CHARACTERIZATION OF NOVEL BIOTHERAPEUTICS

Session Room: Sapphire H

9:00 Organizer's Welcome Remarks

Nandini Kashyap, MPharm, Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks

Kalie A. Mix, PhD, Senior Scientist, Large Molecule Research, Sanofi

9:10 Molecular Interaction Characterization Strategies for the Development of New Antibody Modalities to Enable IND Filing

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

Molecular interaction characterization (MIC) of therapeutic antibodies binding to their targets is critical at each stage of antibody therapeutic development. The introduction of new antibody modalities poses challenges to the MIC assay development due to their complex structural and molecular properties, and requires fit-for-purpose MIC assay strategies. This presentation will focus on case studies that demonstrate how fit-for-purpose MIC strategies are applied to overcome these challenges to enable IND filings.

9:40 Tumor-Targeted Cytokine/Antibody Fusion Proteins for Cancer Immunotherapy

Jamie B. Spangler, PhD, Assistant Professor, Biomedical Engineering and Chemical & Biomolecular Engineering, Johns Hopkins University

Recently developed cytokine/antibody fusion proteins (immunocytokines) that link IL-2 to biasing anti-IL-2 antibodies help to overcome challenges for IL-2 therapies. We build on this advance to target and retain immunocytokines within the tumor microenvironment. We characterize different fusion topologies and test multiple animal models using various routes of injection to identify the optimal formulation for our engineered immunocytokine.

10:10 Encapsulation State of Messenger RNA Inside Lipid Nanoparticles

Lin Jin, Senior Scientist, Analytical Development, Moderna

Understanding the structure of mRNA lipid nanoparticles, and specifically the microenvironment of the mRNA molecules within these entities, is fundamental to advancing their biomedical potential. Elucidating this detail via direct experimental methods has been a major objective in the field of RNA delivery. Here, we show that a combination of dye-binding and cryo-electron microscopy pinpoints the mRNA location, providing new insights into its encapsulation state and chemical microenvironment.

10:40 Networking Coffee Break (Sapphire West Foyer)

MASS ANALYIS AND CASE STUDIES

11:00 Multispecific Therapeutic Antibodies: Using Intact Mass Characterization to Guide Strategic Decisions in Early-Stage Research

Kalie A. Mix, PhD, Senior Scientist, Large Molecule Research, Sanofi

Multispecific antibody formats which employ multiple distinct chains and asymmetric pairing are especially challenging analytically due to the potential for chain mispairing. Characterization of these molecules by liquid chromatography-mass spectrometry (LC-MS) and analytical hydrophobic interaction chromatography (aHIC) enables identification and quantification of the molecules, respectively. This presentation highlights the insights revealed using a combination of these techniques, and how the data is used to guide early-stage research decisions.

11:30 iMAM – An Intact Mass Analysis Based Multi-Attribute Method

Sara Carillo, PhD, Team Lead, Application Development, National Institute for Bioprocessing Research & Training (NIBRT)

Peptide mapping based Multi-Attribute Method (MAM) is attracting many industry users as it allows deep characterization of biopharmaceuticals in a QC environment. We established an intact Multi-Attribute Method (iMAM) for a streamlined and automated processing of MS data acquired at intact monoclonal antibody level. Using three case studies, method robustness, accuracy and reproducibility were evaluated for correct protein ID confirmation, proteoforms quantitation and identification of new entities.

12:00 pm Climbing Everest: Making the First Immortalized Goat pAbs

Anthony Stajduhar, Director, Global Business Development, Rapid Novor

Polyclonal antibodies are popular reagents for their high sensitivity and robust cross-platform performance, but suffer reproducibility challenges and limited supply. Breakthrough polyclonal sequencing technology can overcome these limitations by capturing the most abundant IgG sequences and enabling indefinite recombinant antibody production. Here we report the first successful conversion of a [nepalese] goat polyclonal antibody into recombinant mAb cocktail using only the pAb protein sample.

12:15 Comprehensive Assessment of PTMs in Therapeutic Protein Candidates Using a Novel Fragmentation Technique

Loren Olson, Advanced Workflow Specialist, SCIEX

As the number of biotherapeutic candidates is increasing, the requirements of analytical tools to understand these molecules are rising. To understand product quality attributes (PQAs) fully, identification, localization, and relative quantification are key. Here, a novel mass spectrometry (MS) fragmentation technique was evaluated for peptide mapping: electron activated dissociation (EAD), that creates MS/MS fragment ions of the peptide backbone while maintaining intact PTMs on the fragments.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Rapid Characterization of Antibodies on the LabChip GXII Touch System

James Geiger, PhD, Senior Sales Specialist, American Region Sales, PerkinElmer

Utilizing capillary gel electrophoresis (CGE) and capillary zone electrophoresis (CZE), PerkinElmer's LabChip GXII Touch Protein Characterization System provides characterization of proteins and nucleic acids in as little as 42 seconds per sample, delivering data comparable to other methods of quantitation with as much as 70x increase in throughput. The system can quickly measure yield, purity, titer, charge variation, and glycosylation of proteins.

1:10 Session Break

DEVELOPABILITY, RISK ASSESSMENT, AND HTS SCREENING

1:45 Chairperson's Remarks

Benjamin J. Hackel, PhD, Associate Professor, Chemical Engineering & Materials Science, University of Minnesota

CHARACTERIZATION OF BIOTHERAPEUTICS CONTINUED

1:50 FEATURED PRESENTATION: A Systematic Approach to Evaluating Closed System Transfer Devices (CSTDs) During Drug Product Process Development

Sanket Patke, PhD, Associate Director, Sanofi

In this presentation, we will discuss an approach to perform drug product process development studies to de-risk DP manufacture at the commercial manufacturing site. We also discuss a QbD approach for technology transfer.

2:20 Testing and Improving Antibody Developability during Candidate Discovery and Optimization

Mark C. Julian, PhD, Scientist II, Biologics Drug Discovery, Biogen

The ability to rapidly identify and reduce off-target binding early during candidate selection can help improve the odds of selecting lead antibodies with drug-like properties. I will discuss trends in antibody developability from our analysis of clinical and pipeline datasets across antibody modalities, and apply these learnings with a recent case study that utilizes predictive library design and high-throughput developability screening to improve specificity during optimization.

2:50 Find Your Table and Meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 3: Characterization and Control Strategies for Novel Modalities

Kevin Zen, PhD, Executive Director, Chemistry, Manufacturing and Controls, AnaptysBio Inc

- MAM as release and stability
- Tools for elucidating structures of LNP and API
- Criteria of biotherapeutic developability

BuzZ Table 4: Application of Artificial Intelligence and Machine Learning

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

- Chemical stability of protein therapeutics
- Physical stability of protein pharmaceutics
- Chemical and physical stability of surfactants

DEVELOPABILITY, RISK ASSESSMENT, AND HTS SCREENING, CONT.

4:00 Engineering Protein Developability via Library-Scale Assays and Modeling

Benjamin J. Hackel, PhD, Associate Professor, Chemical Engineering & Materials Science, University of Minnesota

Protein developability challenges hinder the discovery and engineering pipeline. We present three high-throughput genotype-phenotype-linked assays that measure developability proxies for 105 variants (with efficient scalability to 107). A random forest model trained on the assay data predicted recombinant expression of scaffold variants with 5x greater efficiency and 35% increased accuracy than a sequence-derived model. These assays enable developable protein discovery, inform protein design, and allow more precise landscape visualization.

4:30 Structural Mass Spectrometry as Investigational Tool in Early Biotherapeutics Development

Harsha Gunawardena, PhD, Senior Scientist, Mass Spectrometry, Janssen Pharmaceutical Companies of Johnson & Johnson

In this, we demonstrate how product characterization can benefit from structural mass spectrometry approaches. Native SEC-MS and Native-MS coupled with ion mobility can be used to rapidly screen molecules for potential aggregation risks while HD exchange, crosslinking, and footprinting methods allow more in-depth structural information, i.e., binding interface, epitope, and paratope mapping. Emerging structural MS technologies will be presented in the context of discovery and early drug development of biotherapeutics.

5:00 Understanding the Structural Basis to Design Lipid Nanoparticle (LNP) Formulations

Yongchao Su, PhD, Principal Scientist, Analytical Research and Development, Merck & Co.

Molecular assembly of this lipid-based drug delivery system significantly impact the stability and drug release properties of the nanoparticles. However, the structural basis of LNP assembly and encapsulation for drug product development is largely unexplored. Our study aims to understand the interplay of formulation processing and composition parameters and their impact on LNPs formation and RNA encapsulation by elucidating high-resolution structural details.

5:30 High-Resolution Ion Mobility for Simplifying Complex Large Molecule Characterization

Erin Panczyk, Field Applications Manager, Applications, MOBILion Systems, Inc

Large molecule characterization assays can be cumbersome and difficult, largely due to inefficiencies in liquid-phase separation required for resolution of critical peptide modifications. High resolution ion mobility (HRIM) provides gas-phase separation of ions that rivals the most efficient liquid phase separations on a millisecond timescale. This seminar will focus on HRIM applications to current-generation LCMS assays and the analytical gains the system provides in identifying and monitoring critical quality attributes.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

SURFACTANTS IN BIOLOGICS

Session Room: Sapphire H

9:00 Chairperson's Remarks

Dhanashri Bagal, Senior Scientist, Discovery Attribute Sciences, Amgen, Inc.

9:05 KEYNOTE PRESENTATION: Novel Degradation Mechanisms in Pharmaceutical Formulations Induced by Near UV and Visible Light

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

Pharmaceutical formulations can be sensitive to near UV and visible light. This presentation focusses on mechanisms of photo-degradation under exposure to near UV or visible light, promoted by pharmaceutical excipients and transition metals. Metal complexes of excipients can undergo ligand-to-metal charge transfer reactions, which lead to excipient oxidation and activation of oxygen, where radical intermediates have been characterized by spin trapping combined with ESR spectroscopy and mass spectrometry.

ASSAYS AND PROTEIN CHARACTERIZATION

9:35 Key Concepts and Challenges in Freezing PROTEINS: Ice-Water Interface & Cold Denaturation

Haripada Maity, PhD, Chief Development Officer & Head of Biosimilars, Cipla

This presentation will discuss key concepts and challenges in freezing PROTEINS: ice-water interface & cold denaturation.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:00 Characterization of Challenging Proteins and Protein Complexes Using Native and Denaturing Mass Spectrometry

Dhanashri Bagal, Senior Scientist, Discovery Attribute Sciences, Amgen, Inc.

Thorough characterization of both reagent and therapeutic protein candidates through use of various analytical methods is critical to the success of a therapeutic drug discovery program. Here we highlight the utility, challenges and limitations of both native and denaturing mass spectrometry to characterize a variety of difficult proteins such as the heavily glycosylated SARS COVID-19 spike protein, various peptide-MHC complexes and a heavily clipped monovalent bispecific fusion antibody.

11:30 Single-Cell Analysis to Characterize CHO Cells

Colin Clarke, PhD, SFI Principal Investigator, National Institute for Bioprocessing Research and Training (NIBRT)

In this presentation, we will discuss single-cell analysis to characterize the CHO cells.

12:00 pm Protein Quantitation and Higher-Order Structure Analysis with Quantum Cascade Laser Mid-IR (QCL-IR) liquid analyzer

Santosh Hodawadekar, PhD, Director, Biopharma Application, Life Sciences, DRS Daylight Solutions

There is a growing need in biologics manufacturing for process analytical technologies (PAT) with the ability to accurately test protein product ID quantitation and higher-order structure assessment. We present Culpeo® a non-destructive QCL-IR liquid analyzer that provides protein ID testing, simultaneous protein quantitation, and secondary structure analysis in either in-line or at-line workflows. We show the specific workflow for using Culpeo® as an orthogonal tool in protein ID testing and quantitation.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Applications of Multi-Angle Light Scattering to the Characterization of Biotherapeutics

Jeffrey Ahlgren, Senior Applications Scientist, Wyatt Technology

Understanding the interactions of viral proteins with receptors and other binding partners is key to successful development. This presentation will cover the theory of light scattering and how size-exclusion chromatography coupled with multi-angle light scattering (SEC-MALS) and composition-gradient light scattering (CG-MALS) are used for biophysical characterization and determination of binding affinities highlighting case studies of various proteins and oligonucleotides.

1:10 Close of Characterization of Biotherapeutics

CHARACTERIZING PROTEIN AGGREGATES AND IMPURITIES

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

STANDARDS AND REGULATIONS

Session Room: Sapphire H

2:00 Organizer's Welcome Remarks

Nandini Kashyap, MPharm, Conference Director, Cambridge Healthtech Institute

2:05 Chairperson's Opening Remarks

Tobias Werk, PhD, CEO, Bionter AG, Switzerland

2:10 KEYNOTE PRESENTATION: Requirements for Particulates in the European Pharmacopeia

Hanns-Christian Mahler, PhD, CEO, ten23 health

This talk aims to discuss current requirements in the European Pharmacopeia (Ph.Eur.) related to particulates in parenteral preparations, specifically for biopharmaceuticals. Specific focus will be given on recent changes in the monographs and requirements.

ANALYSIS OF PROTEIN AGGREGATION

2:40 Qualitative Analysis of Protein Aggregates in Biotherapeutics by Backgrounded Membrane Imaging (BMI)

Markela Murphy, Dosage Form Design & Development, Biopharmaceuticals Development, R&D, AstraZeneca, Gaithersburg, US

Protein degradation via aggregation route is a common source of SVPs. Well-established methods for SVP analysis, such as light obscuration and microflow imaging, are not high-throughput and require significant amounts of sample volume. The focus of this work was to evaluate the backgrounded membrane imaging (BMI) for SVP analysis and identify critical experimental parameters. In conclusion, BMI can be used as a high-throughput method for qualitative particle analysis.

3:10 Sponsored Presentation *(Opportunity Available)*

3:10 Characterization of Protein Secondary Structure and Aggregation Utilizing Microfluidic Modulation Spectroscopy

REDSHIFTBio
See change

David Sloan, PhD, Director, Applications, RedShiftBio

The AQS3pro system, built upon microfluidic modulation spectroscopy, is an automated infrared platform optimized to determine a biomolecule's secondary structure in a complex buffer and at formulation concentrations. The AQS3pro combines a 24 or 96-well plate, a quantum cascade laser, and a microfluidic flow cell to produce highly precise, higher order structure measurements for the determination of stability, aggregation, lot-to-lot similarity, and formulation optimization of biomolecules.

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

ANALYSIS OF PROTEIN AGGREGATION CONTD.

4:30 Reliable Counting of Protein Aggregate Particles

Richard Cavicchi, PhD, Research Physicist, Biomolecular Measurement Division, Material Measurement Laboratory, National Institute of Standards and Technology

A case study of how the new NIST ETFE standard reference material can be used to help calibrate measurements. We will also show how aggregates made from fluorescently labeled NISTmAb can be used in simultaneous fluorescence/brightfield imaging and flow cytometry measurements data to estimate how many particles are being in the brightfield imaging or light scattering measurements. The effects become increasingly important when the particle diameter is < 2 mm.

5:00 How to Bring Sub-Visible Particle Analysis by Light Obscuration to the Next Level

Tobias Werk, PhD, CEO, Bionter AG, Switzerland

Particles remain a number one issue and reason for product recalls because they are critical for patient safety. Thus, sub-visible particle testing is mandatory for any bio-pharmaceutical preparation. Until today the commonly used technology comprises many manual steps and destroys the sample during testing. We show how little modifications can tailor the technology to the biotech needs, allowing scientists only requiring small sample volumes while staying compliant to the regulations.

5:30 Opportunities and Challenges in Real-Time Monitoring of Protein Aggregation during Biopharmaceutical Development and Manufacturing

Danny K. Chou, PharmD, PhD, President, Biopharmaceutical Characterization and Formulation Development, Compassion BioSolution, LLC

Real-time analytical techniques provide an opportunity for more effective monitoring and control of protein aggregation in bioprocessing as well as a better understanding of the mechanisms of protein aggregation. The objective of this presentation is to share these opportunities as well as challenges in the implementation of novel technologies that can aid in the detection of protein aggregates in real-time.

6:00 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 2: Aggregation in Protein Formulations

Richard Cavicchi, PhD, Research Physicist, Biomolecular Measurement Division, Material Measurement Laboratory, National Institute of Standards and Technology

BuzZ Table 3: Novel Excipients for Sterile Drug Product Formulation

Ankit Kanthe, PhD, Analytical Scientist, Sterile Drug Product Development, Bristol Myers Squibb

- Scope for new excipients in line with FDA's new initiative
- Understanding excipients ability to prevent protein-protein aggregation
- New experimental tools or computational methods to help screen novel excipients

DETECTION AND CHARACTERIZATION OF PARTICLES AND IMPURITIES

Session Room: Sapphire H

9:00 Chairperson's Remarks

Kevin Zen, PhD, Executive Director, Chemistry, Manufacturing and Controls, AnaptysBio Inc

CHARACTERIZING PROTEIN AGGREGATES AND IMPURITIES CONTINUED

9:05 High Molecular Weight Species in Therapeutic Monoclonal Antibody Products: Physicochemical Characterization and Analysis of Impact on Drug Safety and Efficacy

Nathan Joh, PhD, Senior Scientist, Amgen, Inc.

High molecular weight (HMW) species is a size-variant attribute of therapeutic monoclonal antibodies, and is of potential concern due to its possible impact on immune safety and efficacy. We demonstrate no measurable impact posed by HMW species enriched from drug substance from a typical monoclonal antibody, suggested by physicochemical analyses showing secondary and tertiary structures for HMW comparable to monomers, and a collection of biology-based evidence.

9:35 Detect, Characterize and Control the Impurities of Therapeutic Proteins

Kevin Zen, PhD, Executive Director, Chemistry, Manufacturing and Controls, AnaptysBio Inc

The presentation will overview impurity analytical technologies and highlight analytical control strategy in the context of regulatory filing.

10:05 High-Throughput, Automated Analysis of Process Related Impurities Accelerates Downstream Process Development

Maria Germana Sanna, PhD, Field Application Scientist, Gyros Protein Technologies

Monitoring impurities levels throughout bioprocess workflows is critical to quality. In this talk we will present data from different case studies in which biotherapeutic bioprocess samples and viral vector samples were assessed for process related impurities using the automated Gyrolab immunoassay system. Results demonstrate dynamic range, precision, dilutional linearity, and spike data that fulfills key regulatory bioanalytic method requirements with increased productivity in downstream process development.

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 Extended Characterization and Impact of Visible Fatty Acid Particles – A Case Study with a mAb Product

Anthony Tomlinson, Technical Development Scientist, Late Stage Pharmaceutical Dev, Genentech Inc

Inherent particle formation and detection has become a topic of increased scrutiny in biopharmaceutical formulations. These particles, derived from degradation products of the API and/or the excipients, can be difficult to identify and characterize due to their fragility. In this talk, a case study will be presented on the characterization of these particles under a variety of different conditions with multiple analytical techniques.

11:45 Quantitation of Particle Profiles in Biologics and Cell Therapies

Christine Probst, Quantitation of Particle Profiles in Biologics and Cell Therapie, Characterizing Protein Aggregates and Impurities, KBI Biopharma

Characterization of particles for injectable therapeutics is increasingly expected to establish product stability and minimize patient risk. We combined machine learning with imaging methods to develop 'particle profiles' customized to individual therapeutics, thereby allowing variations to be monitored. Case studies using closed-system transfer devices (CSTD) and cell-based therapeutics will be presented.

12:45 pm Session Break

12:55 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

AGGREGATION AND ITS ROLE IN DEVELOPABILITY AND FORMULATION DEVELOPMENT

2:15 Chairperson's Remarks

Wyatt N. Vreeland, Research Chemical Engineer, Chemical Engineering, NIST

2:20 Ultra-Dilute Solution Measurements of Antibody Self-Association

Charles G. Starr, PhD, Scientist, Developability & Preformulation Sciences, Sanofi Group

Identification of mAbs with low levels of self-association has traditionally required relatively concentrated protein solutions, confounding identification of such molecules during early antibody discovery and engineering. We introduce charge-stabilized self-interaction nanoparticle spectroscopy (CS-SINS), a colormetric assay that measures colloidal self-interaction of antibodies in ultra-dilute solutions (0.01 mg/mL). CS-SINS is predictive of high concentration properties such as viscosity and opalescence, which only emerge at orders of magnitude higher concentrations (100+ mg/mL).

2:50 Application of Unfolding Reversibility Studies to Candidate Selection and Formulation Development

Hristo Svilenov, PhD, Associate Professor, Ghent University, Belgium

In this presentation, I will discuss how the reversibility of protein unfolding is related to protein aggregation. Furthermore, I will introduce you to straightforward analytical approaches for studying unfolding reversibility to select aggregation-resistant antibodies and formulations that impede protein aggregation during storage. The presented concepts and techniques can be used for developability assessment and early-stage formulation development of various proteins.

3:20 Synthesis and Characterization of Nanometer-Scale Protein Aggregates Facilitated by Azide

Wyatt N. Vreeland, Research Chemical Engineer, Chemical Engineering, NIST

NIST reference proteins were thermomechanically stressed in sodium azide solutions. Characterization of aggregates by field flow fractionation with light scattering and UV spectrometry showed time-dependent increase in aggregate amount and molar mass. Reducing gel electrophoresis revealed reversible aggregation paths. Kinetic modeling of data implied aggregation mechanism (with azide present) starts by nucleated growth then aggregate-aggregate condensation. Thus, azide preservatives used in ***ex vivo*** experiments have demonstrable effects on protein aggregation.

3:50 Understanding the Dynamics and Phase Behavior of Mixed Antibody-Excipient Adsorption at the Air/Water Interface

Ankit Kanthe, PhD, Analytical Scientist, Sterile Drug Product Development, Bristol Myers Squibb

The interaction mAbs with air/water interfaces plays a crucial role for the manufacture, formulation and storage of these high molecular weight molecules. This talk will focus on the molecular-scale behavior of mAbs as they approach and adsorb to the interface using experimental tools and homology modeling. Additionally, competitive adsorption process between mAbs and surfactants will be discussed to determine the concentration of surfactant necessary to prevent significant mAb adsorption.

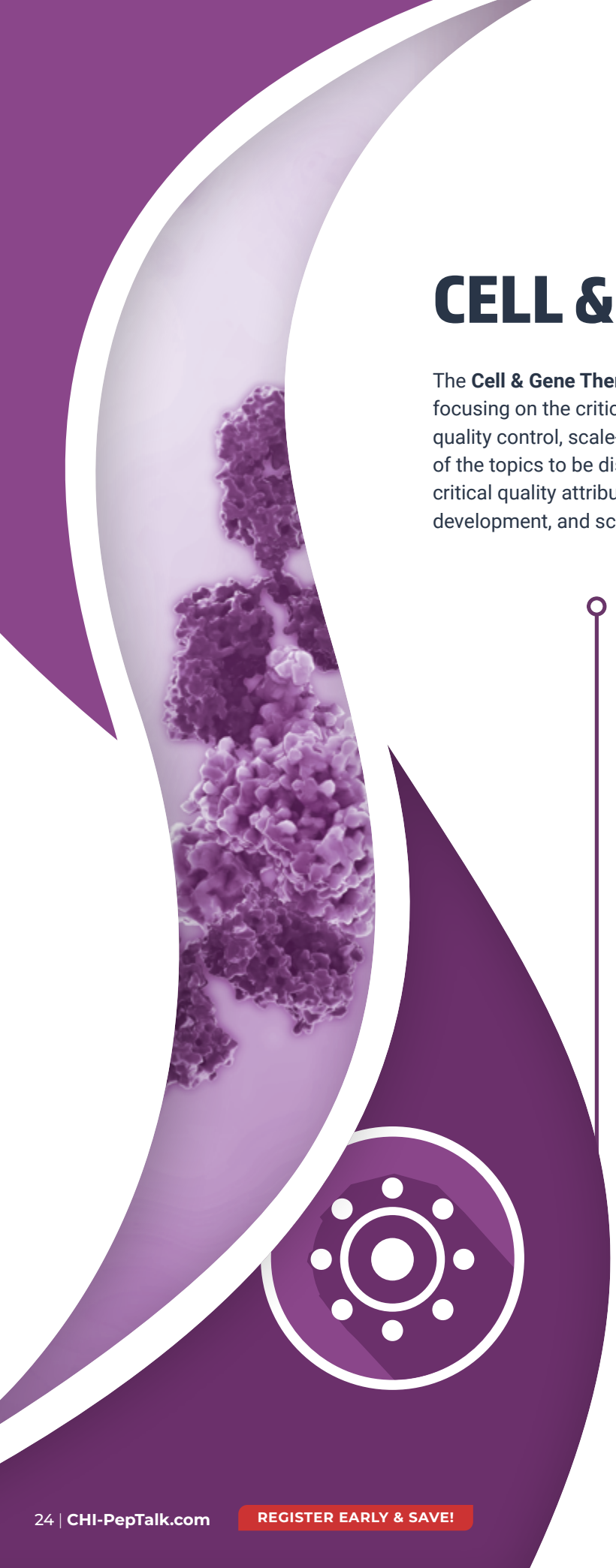
PREDICTIVE STUDIES AND APPLICATION OF AI/ML

4:20 Apply Machine Learning to Predict High Concentration Antibody Aggregation Rate

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

Predictive models that evaluate aggregation behaviors during early-stage design can facilitate drug development. Machine learning is a widely used tool to train models that predict data with different attributes. However, most machine learning techniques require more data than is typically available in antibody development. In this work, we describe a rational feature selection framework to develop accurate models with a small number of features.

4:50 Close of Conference



CELL & GENE THERAPY

The **Cell & Gene Therapy** pipeline features two back-to-back conferences focusing on the critical challenges facing the analysis, characterization, quality control, scale-up, and manufacture of cell and gene therapies. Some of the topics to be discussed include product and process characterization, critical quality attributes, analytical toolbox, product development, process development, and scale-up, the role of CDMOs.

JANUARY 17-18

Cell Therapy Analytics & Manufacturing

AGENDA

JANUARY 18-19

Gene Therapy Analytics & Manufacturing

AGENDA

REGISTER EARLY & SAVE!

TABLE OF CONTENTS

SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

ASSAYS AND METHODS

Session Room: Sapphire D

9:00 Organizer's Welcome Remarks

Nandini Kashyap, MPharm, Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Remarks

Bernardo Cordovez, PhD, Chief Science Officer and Founder, Halo Labs

9:10 KEYNOTE PRESENTATION: Non-Radioactive Assays for Cell Therapies

Preet M. Chaudhary, MD, PhD, Professor & Chief Hematology & Director, Blood & Marrow Transplant, University of Southern California

Despite the success of CAR-T in blood cancers, there are several limitations of this approach, including toxicities, disease relapse in blood cancers, and lack of efficacy in solid tumors. Dr. Chaudhary's talk will focus on the challenges facing the cell therapy field and describe a variety of luciferase-based assays that his laboratory has developed to engineer the next generation of cell therapies.

10:10 Characterization of CARs from the Cell Surface Combining Immunoprecipitation and Mass Spectrometry to Look at Post-Translational Modifications

Jenifer Kaplan, PhD, Principal Scientist I, Novartis Institutes for Biomedical Research

T cells expressing a chimeric antigen receptor (CAR) on their surface allow the T cell to engage an antigen on tumor cells, activate signaling, and cause tumor destruction. CAR surface expression is critical for therapeutic efficacy, but often differences in efficacy occur between constructs that show similar expression. We developed a workflow using immunoprecipitation of the CAR to characterize post-translational modifications by mass spectrometry to gain insights on efficacy differences.

10:40 Networking Coffee Break (Sapphire West Foyer)

CMC CHALLENGES AND CHARACTERIZATION FOR CELL-BASED THERAPIES

11:00 GMP Release Tests and Non-GMP Characterization for Multiple Phase I/II and III Clinical Trial

Riccardo Biavasco, PhD, Scientist, Analytical Development, Bluebird Bio

Cell-based gene therapy drug products require comprehensive analytical assays to characterize their safety and efficacy. This seminar will focus on the GMP release tests implemented across multiple phase I/II and III clinical trials and the additional non-GMP characterization assays performed to address heterogeneity of drug products. Correlative analyses between the results of different analytical assays will be discussed.

11:30 Starting Material Characterization Impact to Process Development and Manufacturing

Dominic Clarke, PhD, ISCT Process & Product Committee Co-Chair & CTO, Cell and Gene Therapy, Discovery Life Sciences

Cell and gene therapy processes and products are fundamentally complex. Cell-based therapies continue to be translated and advance through clinical trials. Long-term success may hinge on our ability to gain greater process and product understanding through enhanced analytics. For cell-based therapies, the starting source material is a vital component to ensuring therapeutic success. Given the inherent variability, well qualified and characterized starting materials are integral to developing robust, consistent therapies.

12:00 pm High throughput characterization of antibody, AAV and cell therapy aggregates using the Aura

Bernardo Cordovez, PhD, Chief Science Officer and Founder, Halo Labs

In all biological products, distinguishing aggregated API from other particle types matters for understanding the root cause of instability. Until now, subvisible particle characterization methods have been unreliable, slow, and difficult to use across many workflows. Introducing the Aura, a 96-well, low-volume, high throughput aggregate and particle imaging system can rapidly size, count, and characterize biological particles and identify them as proteins, non-proteins, cellular aggregates, or other types of molecules.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Application of ISO Cell Counting Standards to Improve the Quality of Cell Counting

James McDonald, PhD, Field Application Scientist, Nexcelom Bioscience

The increased utilization of cells in biomanufacturing and as therapeutic products over the last decade has prompted the development and publication of two ISO Cell Counting Standards, ISO 20391 – 1:2018 and ISO 20391 – 2:2019. This talk will discuss 6 success factors for obtaining high-quality cell counting results based on ISO standards, with specific recommendations for the cell therapy manufacturing environment.

1:10 Session Break

CMC CHALLENGES AND CHARACTERIZATION CONTD.

2:50 Find Your Table and Meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 5: Cell Therapy Drug Product Development

Bharathi Vellalore, PhD, Scientist, Biotherapeutics Drug Product Development, Janssen

- Process considerations for manufacturing autologous and allogeneic cell therapy products
- Drug product considerations for hematological malignancies and solid tumor indications
- Clinical vs commercial supply chain needs: Integrated drug product design

BuzZ Table 6: Topic to be Announced
Matthew B. Seefeldt, PhD, Executive Director & Research Instructor, Cell Therapy & Manufacturing, University of Colorado

FORMULATION DEVELOPMENT AND DELIVERY OF CELL THERAPIES

4:00 Challenges and Opportunities in Cell Therapy Formulation and Delivery
Bharathi Vellalore, PhD, Scientist, Biotherapeutics Drug Product Development, Janssen

CAR T drug products generally use commercial formulation media with complex, undisclosed stoichiometry of ingredients. The proprietary nature of the commercial formulation limits complete understanding of the impact of formulation excipients on product quality, safety and efficacy. In this talk, we present our formulation efforts to develop defined formulations for T and NK cells and also discuss the ability of formulation excipients to increase the product quality and recovery administration.

4:30 Forced Degradation of Cell-Based Medicinal Products Guided by Flow Imaging Microscopy with Machine Learning: Explorative Studies with Jurkat Cells
Tim Menzen, PhD, CTO & Pharmacist, Coriolis Pharma Research GmbH

Analytical characterization and stability assessment of cell-based medicinal products (CBMPs) is challenging because of their intrinsic complexity. We submitted differently formulated Jurkat cell suspensions to thawing and shaking stress mimicking conditions to which CBMPs might be exposed from cell procurement to administration to the patient. Cell viability and concentrations of cells and debris particles were determined by flow-imaging microscopy and machine learning.

5:00 Reprogramming Natural Killer Cells for Immunotherapy of Solid Tumors
Sandro Matosevic, PhD, Assistant Professor, Department of Industrial and Physical Pharmacy, Purdue University

Natural killer (NK) cell infiltration into and anti-tumor immunity against solid tumors is often low. Functional and metabolic impairment of NK cells is induced by the suppressive microenvironment of solid tumors due to, among others, hypoxia, metabolites, such as adenosine, and the expression of inhibitory NK checkpoints. Here, we discuss our work in redirecting NK cells to overcome immunosuppressive solid tumor by genetically rewiring their functional and immunometabolic responses.

5:30 Advanced Lentivirus Platform That Helps Achieve Higher Transduction Efficacy and Assists Projects in Cell Therapy
Jiangbo Zou, Manager of Cell Engineering Product Department, Cell Engineering Product Department, GenScript Biotech

Lentivirus is a very common tool in cell biology, especially in immunology and cell therapy, acting as an effective strategy for cell editing. However, for some challenging cells (ex: T & B), there are still some struggles to achieve high transduction efficiency and insert the targets into genome stably. At GenScript, our proprietary lentivirus system provides intact and functional viruses customized according to research needs and accelerate drug discovery process.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

PROCESS OPTIMIZATION, MANUFACTURING AND CASE STUDIES

Session Room: Sapphire D

9:00 Chairperson's Remarks
Vincenzo Di Cerbo, PhD, Lead Scientist, Cell & Gene Therapy Catapult

9:05 Considerations for Plasmid DNA Used in Cell Therapy Manufacturing
Basak Clements, PhD, Associate Director, Material Science, Janssen Pharmaceuticals, Inc.

Plasmids are starting materials consisting of double-stranded, circular DNA and used to produce viral vectors in cell and gene therapy modalities. While the regulatory classification of plasmids for cell therapy has evolved in the recent years, necessary controls for plasmids remain to be an area of continued debate and definition. This talk will cover the key considerations and elements of control strategy for plasmids used in cell therapy manufacturing.

9:35 Novel Analytical Assays for Characterisation of Lentiviral Vector Therapies
Vincenzo Di Cerbo, PhD, Lead Scientist, Cell & Gene Therapy Catapult

Manufacturing of lentiviral vectors and derived lentiviral-based cell therapies is complex and requires rapid and reliable analytical assays to measure product's critical quality attributes and demonstrate consistent manufacturing, safety, and efficacy. Cell and Gene Therapy Catapult has developed a portfolio of assays for LV product characterisation. This presentation will showcase some examples of novel analytical solutions for the characterisation of LV-based products, which aim to reduce variability and turnaround time.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:00 Gates Biomanufacturing Facility: The Experience of Building a Multi-Product Cell Therapy/Biologics Phase I cGMP Facility
Matthew B. Seefeldt, PhD, Executive Director & Research Instructor, Cell Therapy & Manufacturing, University of Colorado

The purpose of this talk will be to walk through the design and build-out of a multi-product GMP manufacturing facility in an academic setting. The talk would review both the technical design considerations as well as business components to ensure staffing and Phase I compliance.

11:30 AI and Laser Processing for Scalable Generation of Autologous iPSC-Based Cell Therapies
Marinna Madrid, PhD, Co-Founder, Cellino Biotech

Cellino's platform combines label-free imaging and high-speed laser editing with machine learning to automate cell reprogramming, expansion, and differentiation in a closed cassette format, enabling thousands of patient samples to be processed in parallel in a single facility.

12:00 pm Sponsored Presentation *(Opportunity Available)*

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Scalable Production of Adeno-Associated Virus (AAV) in the Gibco™ AAV-MAX Helper-Free AAV Production System
Chao Yan Liu, Senior Manager, Cell Biology, Thermo Fisher Scientific

Adeno-associated virus (AAV) has emerged as the leading platform for gene therapy; however, challenges exist in scaling up production to treat larger patient populations. The AAV-MAX System addresses key challenges by enabling scalable, high titer, and cost-effective production of AAV. Here, we will discuss data on the use of AAV-MAX for production of AAV across multiple scales in shake flasks and bioreactors, as well as downstream purification strategies and analytics.

1:10 Close of Cell Therapy Analytics & Manufacturing

Session Room: Sapphire D

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

2:00 Organizer's Welcome Remarks

Nandini Kashyap, MPharm, Conference Director, Cambridge Healthtech Institute

2:05 Chairperson's Opening Remarks

Dominic Clarke, PhD, ISCT Process & Product Committee Co-Chair & CTO, Cell and Gene Therapy, Discovery Life Sciences

2:10 KEYNOTE PRESENTATION: Nucleic Acids as Household Medicine: Living in the World of RNA Therapeutics

Mano Manoharan, PhD, Distinguished Scientist & Senior Vice President, Innovation Chemistry, Alnylam Pharmaceuticals

siRNAs are potent inhibitors of gene expression. To deliver therapeutic siRNAs into liver hepatocytes, we have further developed a three-pronged approach with the goals of enabling delivery to hepatocytes after both iv and sc admin. Methods include chemical modification of siRNAs, lipid nanoparticle (LNP) formulation of siRNAs, and multivalent N-acetylgalactosamine (GalNAc) conjugation of siRNAs and how GalNAc platform is used for the delivery of siRNAs for several approved drugs.

3:10 Improving Platform Methods for AAV Characterization, Supporting Process and Product Analysis

SCIEX The Power of Precision

Jane Luo, PhD, Senior Scientist, BioPharma Application Development, SCIEX

Recombinant adeno-associated viral vectors are an important technology for novel ***in vivo*** gene therapeutics. This presentation will highlight a high throughput, QC-ready, platform approach to AAV characterization.

- Discover analytical workflows for product and process related impurities including viral capsid purity, genome integrity and empty/full vector ratio assessment.
- Understand how these methods can be adopted in both high throughput and quality control settings

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

CMC STRATEGIES FOR GENE THERAPIES

4:30 Characterization of Primary and Higher-Order Structures for AAV Vectors

Susumu Uchiyama, PhD, Professor, Biotechnology, Osaka University

Detailed and comprehensive analysis of virus vectors are required to ensure their efficacy and safety. Recently, novel biophysical characterization methods of AAV have been emerged. Here we introduce primary structure analysis by the combination of information from CE-SDS and LC-MS, which also provides accurate ratio of VPs. Then, multiwavelength SV-AUC will be introduced that enable to identify comprehensive size distribution profile of particles with information on constituents in AAV samples.

5:00 Development of an IEC-UV HPLC Method for Determination of AAV Empty Capsids

Dana Tribby, Associate Scientist III, Analytical Development & Gene Therapy Chemistry, Biogen

Different analytical tools are used for in-process testing, product characterization, lot release, and stability testing during manufacturing and purification of AAV gene therapy products. An assay suitable for routine GMP QC testing that can accurately measure %Empty capsids, a product-related impurity, in both in-process samples and DS/DP is needed. This presentation describes a method of quantifying empty capsids, to enable its end-to-end analytical control strategy.

6:00 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 4: Stability Differences of AAV Serotypes

Jared S. Bee, PhD, Director, Formulation & Drug Product Development, REGENXBIO, Inc.

- Do they have different aggregation propensities?
- Is a single formulation suitable for different serotypes?
- Do serotypes have different freeze/thaw stability?

BuzZ Table 5: Cryopreservation Challenges of Biologics, Gene Therapy, and Cell Therapy Modalities

Sanket Patke, PhD, Associate Director, Sanofi

ASSAYS AND ANALYTICAL STRATEGIES

Session Room: Sapphire D

9:00 Chairperson's Remarks

Santoshkumar L. Khatwani, PhD, Director, Analytical Development, Sangamo Therapeutics

9:05 Characterization of Product and Process-Related AAV Impurities Using LC-MS

Jonathan Bones, PhD, Principal Investigator, Characterisation and Comparability Laboratory, National Institute for Bioprocessing Research and Training (NIBRT), Ireland

Regulatory guidelines require the determination of product and process-related impurities for gene therapy products. Here, we present methods for the characterization of AAV capsids on various levels using liquid chromatography-mass spectrometry. Application of native mass spectrometry for rapid assessment of empty and full capsids will also be presented. We will also outline methods for the analysis of residual host cell proteins at various stages of AAV downstream purification.

9:35 Multi-Attribute Assessment of AAV Samples by Size Exclusion Chromatography

Dennis Delgado, Principal Research Associate, Analytical Development, Sanofi-Genzyme

In this presentation, we will discuss the development of a high-throughput, QC-friendly, multi-attribute assessment of AAV samples and process-intermediates by size exclusion chromatography.

10:05 Squeeze Boatloads of Quantification and Stability Info from Just Microliters of AAV

Kevin Lance, PhD, Director of Analytics Marketing, Unchained Labs

Gathering the info you need about your AAVs chews up too much sample and time. From just microliters of AAV, Stunner gets you answers on titer, empty/full ratio and aggregation. Uncle gives a unique look at the stability of your capsids to solve capsid engineering and formulation problems. We'll look at how to gather so much info from so little sample, and how it can make your analytical strategy more robust.

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 FEATURED PRESENTATION: Analytics for AAV-Based Gene Therapy Products

Santoshkumar L. Khatwani, PhD, Director, Analytical Development, Sangamo Therapeutics

An overview of analytical development for AAV product characterization:

- AAV product characterization challenges
- Empty/Full capsids quantitation
- Viral protein ration quantitation

12:15 pm Mass-Photometry: The New Kid on the Block for Quantifying AAV Empty-Full Ratios

Gabriella Kiss, PhD, Director of Sales, North America, Sales, Refeyn

Mass photometry is a novel, easy-to-use bioanalytical technology that measures the empty-full AAV capsid ratio in minutes using minimal sample amounts and without the need of sample preparation. Circumventing the requirement of large capital expense and skilled operators, it can be employed throughout the manufacturing process. We present a novel mass photometry instrument dedicated to the challenges of AAV characterization.

12:45 Session Break

12:55 LUNCHEON PRESENTATION: Modernize Your Gene Therapy Analytics with Automated Tools from Bio-Techne

Tim Geiger, Senior Manager, Field Application Scientists, Western Business Unit, Bio-Techne

Innovative analytical tools from Bio-Techne can support gene therapy workflows from discovery to quality control and address certain critical quality attributes of your therapeutic. Today's presentation will explore the many ways viral vector analysis is streamlined with ProteinSimple instruments and how our products improve line-of-sight across the development process.

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

FORMULATION AND STABILITY CONSIDERATIONS

2:15 Chairperson's Remarks

Luca Biasco, PhD, Director, R&D, AVROBIO, Inc.

2:20 Stability of Adeno-Associated Virus Serotype 8 and 9 Gene Therapy Vector Formulations

Jared S. Bee, PhD, Director, Formulation & Drug Product Development, REGENXBIO, Inc.

There has been a rapid increase in the number of clinical studies of gene therapy using adeno-associated virus (AAV) vectors. There are several different AAV serotypes which have differences in their chemical and physical stability. In this presentation, we share data on the stability of AAV8 and AAV9 in different formulations under conditions relevant to manufacturing, labeling, long-term storage, and clinical use.

PROCESS DEVELOPMENT, OPTIMIZATION, AND ADVANCING GENE THERAPY MANUFACTURING

2:50 High-Resolution Single-Cell Profiling of Human Hematopoietic Stem Cell Drug Products

Luca Biasco, PhD, Director, R&D, AVROBIO, Inc.

Human CD34+ cells are the core components of ***ex vivo*** lentiviral gene therapy for the systemic treatment of monogenic diseases. Understanding the changes occurring in hematopoietic stem and progenitor cells (HSPC) upon genetic engineering is critical in determining the potency of GT drug products. We combined state-of-the-art multiparameter flow cytometry and next-generation single-cell technologies for the comprehensive characterization of the main sources of human HSPC and of different engineering conditions.

3:20 Optimizing Viral Vector Process Development

Stephen Soltys, PhD, Vice President, Process Development, Kriya Therapeutics

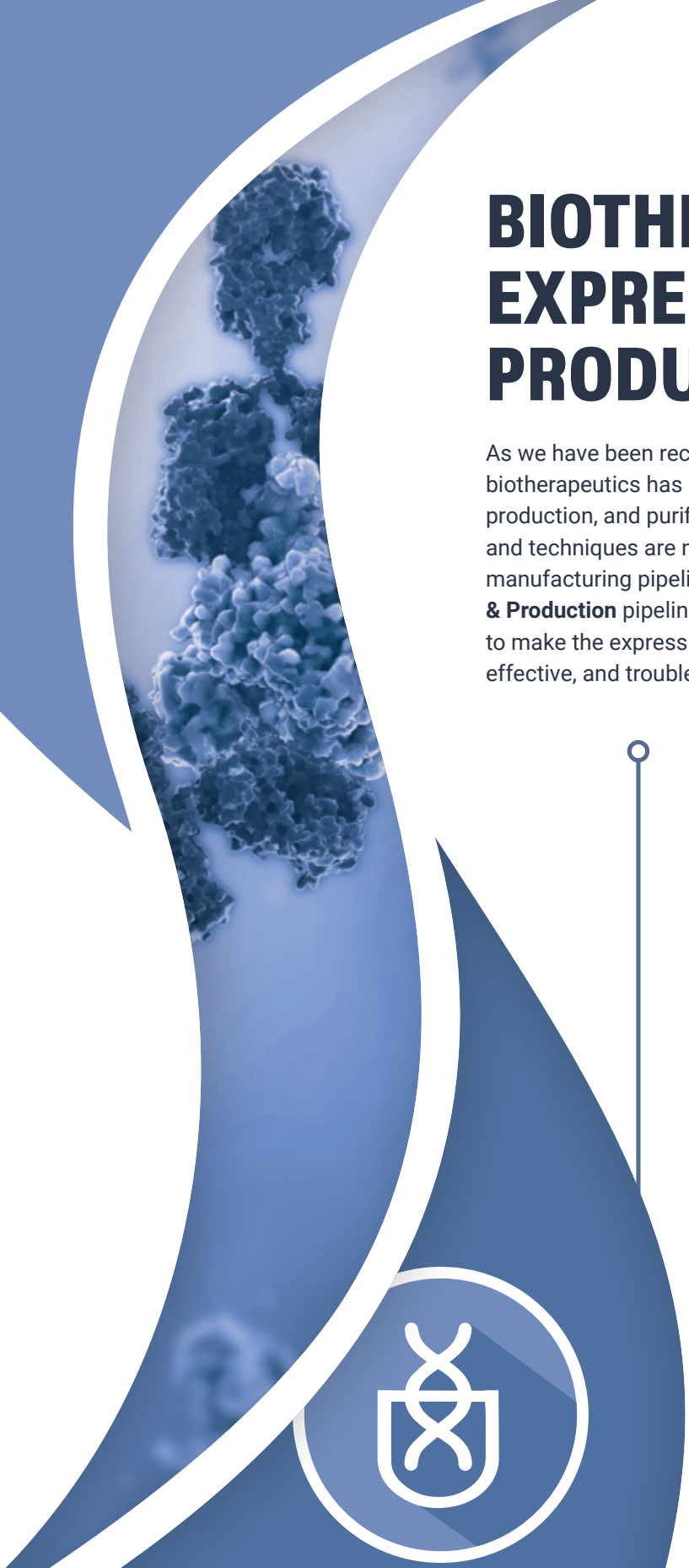
Our cGMP production suites and single-use systems will allow the production of multiple products simultaneously at up to 3,000-liter bioreactor scale. We are developing reliable and robust production systems that can deliver higher amounts of AAV product per batch.

3:50 Current Challenges in Gene Therapy Technical Development

Mark Galbraith, PhD, Former Head, Quality Control and Analytical Sciences, Spark Therapeutics

Implementation of a manufacturing process that assures a predefined quality of the product is a critical requirement for the licensing and marketing of every CGT product. This presentation will discuss the current challenges in gene therapy technical development to ensure safe, well-characterized products.

4:20 Close of Conference



BIOTHERAPEUTIC EXPRESSION & PRODUCTION

As we have been recently reminded, the demand for high-quality biotherapeutics has never been greater. Higher-throughput protein expression, production, and purification as well as more flexible expression systems and techniques are necessary to meet the demands for both research and manufacturing pipelines. Throughout the week, the **Biotherapeutic Expression & Production** pipeline explores the newest data, innovations, and strategies to make the expression and production of therapeutic proteins more efficient, effective, and trouble-free.

JANUARY 17-18

Cell Line Engineering and Development

AGENDA

JANUARY 18-19

Recombinant Protein Expression and Production

AGENDA

REGISTER EARLY & SAVE!

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SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

EMERGING TOOLS FOR EXPANDING THE EXPRESSION TOOL KIT

Session Room: Sapphire 410

9:00 Organizer's Welcome Remarks

Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks

John Dresios, PhD, Executive Director, Biological Innovations Center; Leidos Technical Fellow & Solutions Architect, Applied Science Division, Leidos Innovations Center, Leidos Inc.

9:10 FEATURED PRESENTATION: Synthetic Glycobiology: Designing and Engineering Glycomolecules Inside and Outside of Cells

Matthew P. DeLisa, PhD, William L. Lewis Professor of Engineering, Chemical & Biomolecular Engineering, Cornell University

There remains an urgent need for new tools that can overexpress structurally uniform glycans and glycoconjugates. To address this technology gap, cell-free synthetic glycobiology has emerged as a simplified and highly modular framework to investigate, prototype, and engineer pathways for glycan biosynthesis and biomolecule glycosylation outside the confines of living cells. This talk will describe how we are leveraging cell-free platforms to produce human therapeutic glycoproteins and conjugate vaccines.

9:40 Building Protein Networks in Artificial Bacteria for Biomedical Applications

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

It is challenging to create artificial cellular systems that rival the dynamic chemical-biological response and resilience of natural cells. The artificial cellular systems are hybrid material-bacteria systems with superior applications in drug discovery, disease treatment, and basic biological study. Dr. Tan will present his work on controlling the information processing of artificial cellular systems. The work has broad impact on biotechnology applications and disease treatment.

10:10 Engineered Regulon to Enable Autonomous Azide Ion Biosensing, Recombinant Protein Production, and *in vivo* Glycoengineering

Shishir P. S. Chundawat, PhD, Associate Professor, Department of Chemical and Biochemical Engineering, Rutgers University

The biological importance of carbohydrates (or glycans) can be better understood and exploited by creating a robust toolkit. Here, we highlight recent advances in glycoengineered microbial strains/plasmids and enzymes development for ***in vivo*** conversion of azido sugars to designer glycans (e.g., human milk oligosaccharides). We further discuss how such a toolkit can be used for efficient recombinant protein production as well as directed evolution of carbohydrate-active enzymes (e.g., glycosynthases).

10:40 Networking Coffee Break (Sapphire West Foyer)

11:00 Assessing Optimal: Inequalities in Codon Optimization Algorithms

Jeffrey Li, Graduate Researcher, Laboratory of Dr. Rachel Green, Johns Hopkins School of Medicine

Non-native synthetic DNA sequences have become a common resource in recombinant protein work due to the low cost of DNA synthesis. Many of these DNAs are "optimized" through commercial tools despite there being little guidance for what defines an optimal sequence. We surveyed nine optimization algorithms and found significant variability between their optimized DNAs, leading us to propose a set of best practices when designing synthetic sequences.

11:30 Synthetic Biology Strategies for Robust Production of Active Proteins

John Dresios, PhD, Executive Director, Biological Innovations Center; Leidos Technical Fellow & Solutions Architect, Applied Science Division, Leidos Innovations Center, Leidos Inc.

Production of high-value protein targets often faces significant challenges due to their poor and variable levels of expression and active folding, as well as the long turnaround times required for their end-to-end manufacturing and testing. This presentation describes strategies for robust production of active proteins that are applicable to a wide range of DNA and mRNA expression formats in the context of cell-free, cell-based and gene therapy platforms.

12:00 pm Effective Cell Line Development: Reducing Risk, Decreasing Timelines, and Optimizing Outcomes SARTORIUS

Ademola Kassim, Product Specialist, Cell Line Development, Cell Line, Media and Testing Solutions, Sartorius

When it comes to the commercialization of biologics, effective, high-quality cell line development (CLD) is essential for success. The key to minimizing risk and optimizing outcome is having a reliable partner that offers experience, expertise, and a comprehensive portfolio of products and services. This presentation will highlight the key challenges and points to consider during biopharmaceutical CLD and the impact early decision-making can have at later stages of the development process.

12:30 Session Break

12:40 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:10 Session Break

CELL LINE DEVELOPMENT: INCREASING PRODUCTIVITY

Session Room Change: Sapphire 400

1:45 Chairperson's Remarks

Bjørn Voldborg, MSc, Head, National Biologics Facility, DTU Bioengineering, Technical University of Denmark

1:50 Subcellular Proteomics Unveils New Regulatory Mechanisms Controlling mAb Expression along the Secretory Pathway of CHO Cells

Saumel Pérez Rodriguez, Universidad Nacional Autónoma de México

Genetic engineering of the classical secretion pathway (CSP) offers an alternative for obtaining more productive CHO cells. Since few CSP targets have been detected, subcellular proteomics was used to identify CSP proteins associated with productivity. Differentially expressed proteins (DEP) participate in protein synthesis, autophagy, proteasomal degradation, calcium regulation, vesicular transport, ER stress and UPR. Modulation of these DEP will have a positive impact on current bioprocesses. Supported by IN210419.

2:20 Host and Product-Specific Determinants of Recombinant Protein Yield in CHO

Helen Masson, Research Scientist, Nathan Lewis Laboratory, Pediatrics and Bioengineering, University of California, San Diego

Decades of cell line development and media optimization of CHO cell lines has led to notable improvements in recombinant protein (rProtein) production yield. However, the expression of some rProteins results in little to no yield and remains a challenge. Our lab has taken a systems biology approach, including machine learning and network analyses, to elucidate host and protein-specific properties that act as determinants of rProteins yield in CHO.

2:50 Find Your Table and Meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

CO-PRESENTATION: BuzZ Table 7: Common Issues with Transient Protein Production

Richard Altman, Field Application Scientist, Life Science Solutions, Thermo Fisher Scientific

Henry C. Chiou, PhD, Director, Cell Biology, Life Science Solutions, Thermo Fisher Scientific

- What are the current challenges to transient protein production?
- How has the COVID-19 pandemic affected your workflow and productivity?
- How do we optimize the whole protein expression workflow process?
- How can we maintain volumetric yields while scaling transient expression up or down?
- What cell line(s) should we use and when?
- What parameters can impact the quality or physical attributes of transiently produced proteins?

CELL LINE DEVELOPMENT: INCREASING PRODUCTIVITY

4:00 Apoptosis-Resistant CHO Cell Lines Significantly Improve Culture Viability and Titer in Intensified Fed-Batch Culture Process

Shahram Misaghi, PhD, Principal Scientist, Cell Culture and Bioprocess Operations (CCBO), Genentech, Inc.

Process intensification strategies in CHO production cultures can potentially increase productivity, lower cost of goods, and improve facility utilization. However, process intensification often triggers apoptotic cell death in the later phases of intensified production process. Here we show that apoptosis-resistant CHO cell lines counteract this undesired outcome, resulting in not only better viability but also enabling extended productivity that significantly improve volumetric productivity without affecting product quality.

4:30 Novel CHO Host for Improved Recombinant Protein Production

Lina Chakrabarti, PhD, Senior Manager, R&D, AstraZeneca

With the aim of increasing protein productivity, we generate a novel CHO host with favorable biomanufacturing phenotypes and improved functionality. Producer pools and clones generated from the new host outperformed the standard host by displaying (1) improvement in productivity, (2) reduced product aggregation, (3) enhanced cell viability, (4) low lactate production and (5) improved cell cloning efficiency. The new host exhibited multifaceted protection against mitochondrial dysfunction and ER stress.

5:00 Prediction of Amino Acid Consumption in Chinese Hamster Ovary Cell Fed-Batch Cultures by Coupling a Genome-Scale Metabolic Network Model with Machine Learning

Wei Wei, PhD, Principal Scientist, Cell Line Development, Biotherapeutics Pharmaceutical Sciences, Pfizer Inc.

Genome-scale metabolic modeling offers a promising approach for ***in silico*** monitoring and predicting the consumption of proteinogenic amino acids, which is critical for bioprocess control. However, the prediction accuracy is challenged by the discrepancy between the model assumption and the biological variances in CHO cultures. We demonstrate such challenge can be addressed by integrating a CHO-specific metabolic network model with machine learning to achieve accurate prediction throughout the fed-batch process.

5:30 Digital Twins for Improved Bioprocess Operation: Opportunities and Roadblocks

Krist V. Gernaey, PhD, Professor, Chemical & Biochemical Engineering, Danish Technical University

Digital twins, virtual copies of a process, will play an important role in transforming biomanufacturing towards Industry 4.0. Two major building blocks of a digital twin, data and models, are highlighted. Data characteristics and collection strategies are examined; new methods and tools for data processing are highlighted. Furthermore, different modelling approaches are presented in view of their use in a digital twin. Potential roadblocks for digital twin implementation are discussed.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

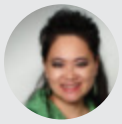
7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

GENOME ENGINEERING TOOLS: ENGINEERING EFFICIENCY

Session Room: Sapphire 410



9:05 KEYNOTE PRESENTATION: Cell Engineering Efficiency and Quality

Zhimei Du, PhD, Vice President, Process Sciences, Atara Biotherapeutics

The efficiency of generating bi-allelic gene-knockout cell lines using conventional protocols is very low. This significantly affects clone screening efficiency and reduces the chance of identifying robust knockout host cell lines. In this study, we improve the genome editing process resulting in improved GS-knockout efficiency of up to 20 folds. Furthermore, we developed an integrated end-to-end process yields robust host cells with desired growth and recombinant protein expression characteristics.

9:35 CHO Cell Engineering to Improve Therapeutic Antibody Production

Cai Guo, PhD, Scientist, Mammalian Expression & Biologics Optimization, Amgen Inc.

Bispecific antibodies can be difficult to express (DTE) with much lower productivity than classical monoclonal antibodies. Here, we analyzed the transcriptome of cells expressing various DTE proteins and identified genes that were differentially transcribed in bispecific antibody expressing cells. The effects of these genes on productivity were subsequently evaluated. Our results indicate that proper host cell engineering is one solution to improve recombinant therapeutic protein production.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:00 FEATURED PRESENTATION: Gain Control over Your Protein Expression: Glycosylation, Titer and Development

Bjørn Voldborg, MSc, Head, National Biologics Facility, DTU Bioengineering, Technical University of Denmark

Based on engineered CHO cell lines generated over the past 9 years, we offer cell lines for quick and robust production of recombinant proteins of high quality and controlled glycosylation. The cell lines can now be accessed by industrial and academic partners through our newly established National Biologics Facility, where we offer establishment of robust production cell lines, protein production, cell line development and cell line engineering.

11:30 Improvements to the Baculovirus Insect Cell Expression System to Support Structural Biology and Drug Discovery

Dominic Esposito, PhD, Director, Protein Sciences, Frederick National Laboratory

Insect cell systems are a major tool for the production of pharmaceutically relevant protein targets including multiprotein complexes for structural biology and drug discovery. We have developed a number of process and technology improvements which permit increased protein yield, protein quality, virus stability, and efficiency of protein complex formation. We will discuss the enhancements to the system and how they can be applied to high-level production of clinically relevant proteins.

12:00 pm Leap-In Transposase Platform - Past, Present and Future

ATUM

Oren Beske, PhD, Amalgamator of Business and Biology, ATUM

Launched only a few years ago, the Leap-In Transposase platform has rapidly become an industry standard technology for the generation of CHO cells for the manufacturing of antibodies and other biologics. This presentation will highlight achievements and case studies of the platform including high titer mAb manufacturing, rapid anti-COVID responses, and some novel, next generation, applications.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Boosting Transient Productivity in Genetic Code Expanded CHO Cells for Engineered Precision Biologics

MaxCyte

Mingchao Kang, PhD, Group Leader, Platform Technology, Ambrx Biopharma

Ambrx's EuCODE™ platform utilizes engineered CHO cells with an expanded genetic code to produce engineered precision biologics. Quick material delivery with high productivity is critical for rapid project development. MaxCyte's STX electroporation system enables systemic optimization of transient expression conditions and a facile scale-up to support material delivery need at different stages of projects.

1:10 Close of Cell Line Engineering and Development

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

WHEN RAPID RESPONSE IS REQUIRED

Session Room: Sapphire 410

2:00 Organizer's Welcome Remarks

Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

2:10 FEATURED PRESENTATION: Toolkit for Rapidly Generating and Characterizing Molecular Probes towards Nucleoproteins of Emerging RNA Viruses to Bolster Pandemic Preparedness

Andrew Hayhurst, Professor, Disease Intervention and Prevention, Texas Biomedical Research Institute

Whether natural spillovers, geographic migrants or unfortunate laboratory escapees, emerging RNA viruses pose grave threats to human health and socioeconomic progress. We combine responsive and forward capable strategies to deliver nanobodies specific to one species or cross-reactive to all species of a viral genus. The conserved and polymeric nature of viral nucleoproteins enable even modest nanobodies to be useful long-term molecular probes especially when produced as enzymatic and fluorescent fusions.

2:40 CyDisCo Production of Functional Recombinant SARS-CoV-2 Spike Receptor Binding Domain

Gloria Borgstahl, PhD, Professor, Biochemistry & Molecular Biology & Pharma Sciences, University of Nebraska Omaha

We have developed a bacterial strategy for the rapid expression and purification of a SARS-CoV-2 spike protein receptor binding domain (RBD). Bacterial cytoplasm is reductive and this is problematic when the recombinant protein of interest requires complicated folding and/or processing. The use of the CyDisCo system bypasses this issue by pre-expressing a sulfhydryl oxidase and a disulfide isomerase, allowing the correct folding with disulfide bonds for protein integrity and functionality.

3:10 Optimized Expression and Scale-Up of Rylaze™ Enabled by Pelican Expression Technology™ Platform

Diane Retallack, Senior Vice President, Platform Tech & Innovation, Pelican Expression Technology

Rapid and comprehensive strain selection and an early process development program utilizing the Pelican Expression Technology™ were key to establishing the foundation for late-stage success for Rylaze™, a recombinant Erwinia chrysanthemi asparaginase for the treatment of acute lymphoblastic leukemia or lymphoblastic lymphoma in patients who have developed hypersensitivity to *E. coli*-derived asparaginase. Pelican Expression Technology™, a Pseudomonas fluorescens-based protein expression system is a robust and scalable platform for recombinant protein production.

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

4:30 Expression of SARS-CoV-2 Surface Glycoprotein RBD in *E. coli*, and Its Refolding and Purification

Maria Kireeva, Director, R&D, VirIntel, LLC

Cost-effective methods of expression and purification of SARS-CoV-2 spike and its fragments that preserve antigenic properties are essential for development of COVID-19 serology tests. We developed a method of purification of S319-640 fragment containing RBD expressed in *E. coli* from the inclusion bodies. The antigenic properties of the resulting product are similar to those of the RBD-containing fragment expressed in human cells.

5:00 Panel Discussion: Protein Production Lab Challenges: Methodologies, Strategies, and the Art of Managing Multiple Projects

Moderator: Richard Altman, Field Application Scientist, Life Science Solutions, Thermo Fisher Scientific

This panel will focus on the following topics:

- Lessons learned from managing a protein production workflow during a pandemic.
- Strategies on how to manage multiple "top priority" projects.
- Strategies for supporting the professional growth and career development of direct reports.
- How do we make time for technical development and process optimization?
- Troubleshooting strategies or how much time should be spent before moving to the next option?

Panelists:

Dominic Esposito, PhD, Director, Protein Sciences, Frederick National Laboratory

Balaji Somasundaram, PhD, Strategy & Operations Manager, Protein Expression Facility, University of Queensland

Elizabeth Stangle, Senior Research Associate, Protein Engineering, Zymeworks Inc.

Bjørn Voldborg, MSc, Head, National Biologics Facility, DTU Bioengineering, Technical University of Denmark

Jessica A. Williamson, PhD, Protein Production Lead, UCB

6:00 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

CO-PRESENTATION: BuzZ Table 6: Multidisciplinary and Inter-institutional Collaborations, How to Succeed?

Bjørn Voldborg, MSc, Head, National Biologics Facility, DTU Bioengineering, Technical University of Denmark

Nathan Lewis, PhD, Associate Professor, Pediatrics and Bioengineering, University of California, San Diego (UCSD)

- How to start-up projects
- Identifying and involving collaborators
- Managing expectations (IP, Funding, commitment, etc..)
- Ensuring efficient and smooth collaboration

BuzZ Table 9: Why is it so Difficult to Engineer CHO Cells for Improved Expression and Product Quality?

Rene Hubert, PhD, Director, Biologics Optimization, Amgen Inc.

- How do we get the most out of transcriptomics?
- How do we leverage the secretome and surfaceome in generating improved CHO hosts?
- What's the best way to generate and validate candidate genes?

EFFECTIVE EXPRESSION AND PRODUCTION OF UNIQUE BIOPRODUCTS

Session Room: Sapphire 410

9:05 Bioengineering RNAs for Targeted Therapy

Aiming Yu, PhD, Professor, Biochemistry & Molecular Medicine, University of California Davis

RNAs have emerged as a novel class of medications with unique mechanisms of actions. Current RNA research and development are restricted to the use of chemo-engineered RNA mimics made ***in vitro***, which are different from natural RNAs produced and folded ***in vivo***. In this talk I will present our novel RNA bioengineering technology for high-yield, large-scale and cost-effective ***in vivo*** fermentation production of biologic RNA agents carrying payload RNAi molecules.

9:35 A Novel Recombinant Soluble Complement Receptor 1 Fragment with Enhanced Therapeutic Potential

Matthew Hardy, PhD, Associate Director, Recombinant Proteins, CSL Research

We have generated and characterized CSL040, a recombinant soluble and truncated form of human Complement Receptor 1 (CR1) that potently inhibits all three pathways of the complement system and represents a new and attractive therapeutic candidate for complement-mediated disorders. CSL040 attenuates disease development in multiple animal models, and we demonstrate that sialylation-dependent pharmacokinetics and differential complement pathway inhibition are hallmarks of CSL040 activity ***in vivo***.

10:05 Enabling the Discovery and Production of Next-Generation Biologics via Synthetic Biology and Artificial Intelligence

Matthew Weinstock, PhD, Chief Technology Officer, Absci

Recent advances in synthetic biology and artificial intelligence promise to dramatically impact the way that pharmaceuticals are developed. In this presentation I will discuss how Absci is leveraging the power of these technologies to address key pain points in both how protein-based biologics are discovered as well as how cell lines for manufacturing are designed.

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 A Novel Platform to Create Multi-Functional Immunotherapeutic for Cancer

Hing C. Wong, PhD, CEO & Founder, HCW Biologics Inc.

We developed a novel platform (TOBI) centered upon an inert tissue factor scaffold for production of heteromeric and multi-functional fusion protein complexes for therapeutic uses. We will present our characterization of HCW9218 (a bifunctional TGF-ß trap/IL-15 protein complex) and HCW9201 (a fusion complex combining IL-2, IL-15, and IL-18), created based on the TOBI platform, to demonstrate the versatility and potential utilities of these fusion proteins as immunotherapeutic against cancer.

11:45 FEATURED PRESENTATION: Engineering Fc Domains on the Surface of CHO Cells

Jennifer A. Maynard, PhD, Henry Beckman Professor, McKetta Department of Chemical Engineering, Cockrell School of Engineering, University of Texas Austin

Fc engineering is gaining interest as a strategy to tune antibody functions but bacterial and mammalian display systems are limited by their inabilities to provide the native glycosylation that supports binding to classical Fc receptors. To address this, we adapted our mammalian CHO display system to engineer human IgG1 Fc for pH-selective FcgRIIIa binding that preferentially activates cellular cytotoxicity at the low pH common to the tumor microenvironment.

12:15 pm Flexibility of the SUREtechnology Platform to Overcome Phenotypic and Genetic Changes in CHO Cells

Pierre-Alain Girod, PhD, Chief Science Officer, Science, Selexis S.A.

CHO cell volumetric productivity has significantly increased in the past two decades. However, turning these cells into high-producing factories has created an overall metabolic burden. In response to transgene expression pressure, CHO cells undergo phenotypic and genetic changes for continuous improvement. Selexis' SUREtechnology Platform™ provides a solution for overcoming the challenges of high productivity tied to metabolic adaptability.

12:45 Session Break

12:55 LUNCHEON PRESENTATION: Overcoming the Challenges for High-Throughput Production of Diverse Custom Proteins Used in Discovery Applications

Jiansheng Wu, PhD, Vice President, Protein Sciences, WuXi Biologics

We discuss the challenges in high-throughput protein production for small and large molecule drug discovery. We demonstrate the parameters and design space required to generate high-quality proteins for HTS, antibody discovery, ***in vivo*** and developability studies. Supported by our industry-leading platforms, the Protein Sciences department at WuXi Biologics provides production services utilizing various expression systems for the generation of monoclonal, bispecific and multispecific antibodies, and other recombinant proteins.

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

EFFECTIVE EXPRESSION AND PRODUCTION OF ANTIBODIES

2:15 Chairperson's Remarks

Nathan Lewis, PhD, Associate Professor, Pediatrics and Bioengineering, University of California, San Diego (UCSD)

2:20 KEYNOTE PRESENTATION: Lessons Learned from Expression Liabilities in a Four-Chain Bispecific

Rene Hubert, PhD, Director, Biologics Optimization, Amgen Inc.

Multispecific antibodies are increasingly relevant in biotherapeutic pipelines and significant effort exists in engineering the molecules in addition to optimizing vectors, cells, and processes to improve productivity and quality. Key to successful multispecific platform development is understanding the expression liabilities in challenging molecules. To understand the causes and effects of chain mispairing impurities in a difficult-to-express four-chain multispecific hetero-IgG, we investigated consequences of individual and pairwise chain expression.

2:50 Elucidating the Host Cell Machinery Supporting Efficient Therapeutic Protein Secretion through Systems and Synthetic Biology

Nathan Lewis, PhD, Associate Professor, Pediatrics and Bioengineering, University of California, San Diego (UCSD)

Each protein secreted by a cell depends on up to hundreds of different host cell proteins for its synthesis, folding, post-translational modification, and transport. However, this secretory pathway machinery required can differ considerably. Using computational modeling and omics data integration, we have developed a pipeline to identify the host machinery that can be augmented to improve secretion of diverse recombinant biotherapeutics of interest.

3:20 Membrane Mimetics to Facilitate Antibody Screening

Christy A. Thomson, PhD, Principal Scientist, Amgen, Inc.

The ability to identify and characterize therapeutic antibodies targeting multi-pass membrane proteins is hampered by their often-difficult expression and purification. Historically membrane proteins have been extracted from cell membranes using detergents, however the presence of detergent can hamper many downstream applications. We examined novel methods for membrane protein stabilization, including SMALPs, nanodiscs and amphipols, to isolate a model multi-pass membrane protein and evaluated their utility in lead antibody identification.

3:50 One-Step Engineering the Affinity, Stability and Expression of a Bispecific Molecule

Renhua Ray Huang, PhD, Scientist III, Antibody Engineering, MacroGenics Inc.

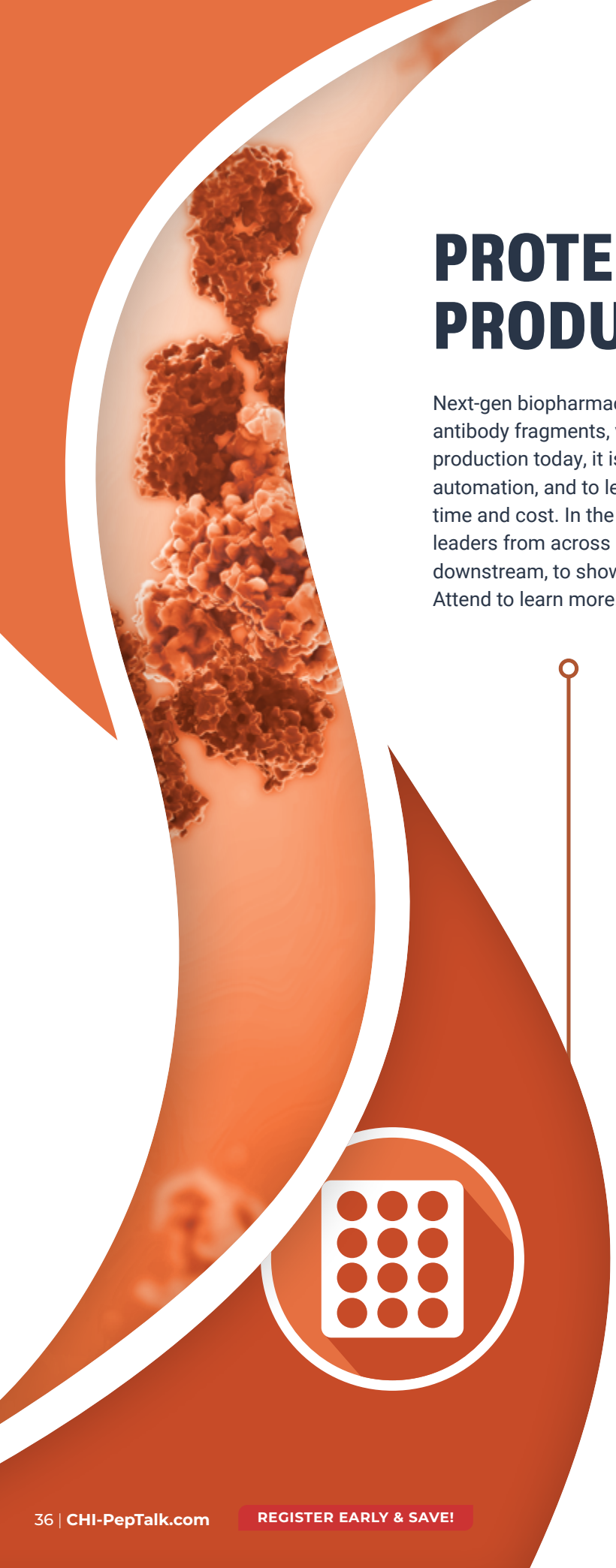
Bispecific antibodies are an emerging class of biologics that have shown great promise in cancer treatment. Yet often during preclinical development, many lead molecules fail due to poor biophysical/biochemical properties. Here a phage-display method has been developed, in which engineering of the cyno cross-reactivity, stability and expression of a bispecific molecule was tackled simultaneously, generating multiple lead molecules that showed significant improvement in all three properties.

4:20 Optimization of a Transient Antibody Expression Platform towards High Titer and Efficiency

Elizabeth A. Greene, Scientist IV, Biotherapeutics Molecule Discovery, Boehringer Ingelheim Pharmaceuticals, Inc.

Chinese Hamster Ovary (CHO) cells are one of the major workhorses for Transient Gene Expression (TGE) of recombinant antibodies. Through a matrix evaluation of multiple factors including inoculum, transfection conditions, amount and type of DNA used (including filler DNA), and post-transfection culture conditions, we arrived at an uniquely optimized TGE process with higher titer and reduced costs and time, thus increasing the overall efficiency of early antibody material supply.

4:50 Close of Conference



PROTEIN PRODUCTION & HTP

Next-gen biopharmaceuticals are increasingly complex, including, ADCs, antibody fragments, vaccines, gene therapies and beyond. In protein production today, it is imperative to aim for higher-throughput, to drive automation, and to leverage digital tools to increase productivity, and minimize time and cost. In the **Protein Production & HTP** pipeline we will bring together leaders from across biopharmaceutical development, from both upstream and downstream, to showcase innovation and discuss challenges and solutions. Attend to learn more.

JANUARY 17-18

Higher-Throughput Protein Production

AGENDA

JANUARY 18-19

Optimizing Bioproduction & Processing

AGENDA

REGISTER EARLY & SAVE!

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HIGHER-THROUGHPUT PROTEIN PRODUCTION

SUNDAY, JANUARY 16

4:00 pm Conference Registration Open (Sapphire West Foyer)

MONDAY, JANUARY 17

7:00 am Registration and Morning Coffee (Sapphire West Foyer)

AUTOMATION AND ANALYTICS

Session Room: Sapphire 400

9:00 Organizer's Welcome Remarks

Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks

Stefano Menegatti, PhD, Assistant Professor, Chemical & Biomolecular Engineering, North Carolina State University

9:10 FEATURED PRESENTATION: End-to-End High-Throughput Protein Production Using a Reimagined Automated Platform

Sarah M. Rue, PhD, Associate Director, Advanced Automation Technologies, Genomics Institute of the Novartis Research Foundation

For 10+ years, we have used our in-house-built Protein Production and Purification Platform (PEPP) to support hybridoma, transient HEK, and transient and stable CHO workflows. Here, we describe our new automated platform, PEPP2. We detail how PEPP2 has increased speed and throughput compared to the original PEPP system, how new hardware enables automated magnetic bead-based protein purification, and how PEPP2 will be used to build the Secretomics 2.0 protein collection.

9:40 3D Printed Convective Media for the Separation of Small and Large Biomolecules

Gregory Dutra, PhD Student, Department of Biotechnology, BOKU

Based on computational fluid dynamics we fabricated precisely ordered three-dimensional chromatography columns with a pore structure relevant for chromatography. The novel material was generated by 3D printing and the advantages for separation of large and small biomolecules, including bionanoparticles like viruses and virus like particles will be presented.

10:10 Modeling Approaches in High-Throughput Systems

Stefan Haider, PhD, Scientist, Process Science & Downstream Development, Boehringer Ingelheim RCV GmbH & Co KG

The fully-automated fermentation platform at Boehringer Ingelheim in Vienna has been developed to the point that it can routinely carry out up to 100 fed-batch fermentation runs per week. Huge amount of data is generated, which in turn paves the way for implementing both mechanistic and statistical modeling approaches. Such models help accelerate process development and build knowledge to reduce developmental efforts, ensuring deeper process understanding and better manufacturing processes.

10:40 Networking Coffee Break (Sapphire West Foyer)

11:00 Accelerating Higher-Throughput Discovery Workflows with Informatics Advances and Next-Gen Predictive Tools

Daniel Yoo, Senior Scientist, Therapeutic Discovery, Amgen Inc.

As biologic therapeutics continue to increase in complexity, innovative approaches to candidate screening, characterization and development are more important than ever. Our approaches to high-throughput protein production incorporate advanced analytics, automation and high-quality informatics to enable robust molecule screening, selection and scale-up. These enhancements enable advances in the speed, quality and productivity of our biologics development pipeline.

11:30 In/At-Line Analytics for Rapid Assessment of Titer and Critical Quality Attributes of Therapeutic mAbs

Stefano Menegatti, PhD, Assistant Professor, Chemical & Biomolecular Engineering, North Carolina State University

With dozens of monoclonal antibodies (mAbs) in production, accurate in/at-line mAb quantification is vital to biomanufacturing. Current mAb quantification is time-/labor-intensive. Therefore, we developed the "Dual-Affinity Ratiometric Quenching" (DARQ) assay for rapid quantification of mAb titer and glycosylation, and host cell protein (HCP) titer. The assay is reproducible (variation <1%) and rapid (5 min), and offers excellent sensitivity (<0.5 ng/mL), limit of detection (<100 ng/mL), and dynamic range (100-1600 ng/mL).

12:00 pm Novel Solution For High Throughput Antibody And Protein Purification Using Magnetic Bead

GenScript

Nishant Saxena, PhD, Product Manager, Catalog Product, GenScript

Protein purification using traditional chromatography is limited by throughput and requires labor-intensive sample preparation processes. Magnetic beads-based purification permits the incubation of the beads directly into cell culture or crude lysates regardless of sample volume. This provides a simplified approach to direct target capture while minimizing preparation steps and potentially improving the quality of final product. The tools and their application to simplify protein purification, screening cost-effectively will be described.

12:30 Session Break

12:40 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:10 Session Break

MONITORING, MODELING AND NETWORK ANALYSIS

1:45 Chairperson's Remarks

Bjørn Voldborg, MSc, Head, National Biologics Facility, DTU Bioengineering, Technical University of Denmark

1:50 Subcellular Proteomics Unveils New Regulatory Mechanisms Controlling mAb Expression along the Secretory Pathway of CHO Cells

Saumel Pérez Rodriguez, Universidad Nacional Autónoma de México

Genetic engineering of the classical secretion pathway (CSP) offers an alternative for obtaining more productive CHO cells. Since few CSP targets have been detected, subcellular proteomics was used to identify CSP proteins associated with productivity. Differentially expressed proteins (DEP) participate in protein synthesis, autophagy, proteasomal degradation, calcium regulation, vesicular transport, ER stress and UPR. Modulation of these DEP will have a positive impact on current bioprocesses. Supported by IN210419.

2:20 Host and Product-Specific Determinants of Recombinant Protein Yield in CHO

Helen Masson, Research Scientist, Nathan Lewis Laboratory, Pediatrics and Bioengineering, University of California, San Diego

Decades of cell line development and media optimization of CHO cell lines has led to notable improvements in recombinant protein (rProtein) production yield. However, the expression of some rProteins results in little to no yield and remains a challenge. Our lab has taken a systems biology approach, including

machine learning and network analyses, to elucidate host and protein-specific properties that act as determinants of rProteins yield in CHO.

2:50 Find Your Table and Meet the BuzZ Sessions Moderator

3:00 BuzZ Sessions with Refreshments (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 9: Future Platforms for Future Modalities

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

- Are columns here to stay, or is it time to reconsider other approaches?
- What about cleavable tags? Is the risk justified by the need for platforms?
- What kinds of products will be driving this innovation?
- How open are companies to trying disruptive technologies? Are the innovations in the products enough for now, so we should play it safe on the methods?

CO-PRESENTATION: BuzZ Table 10: BuzZ Session: Automated Cell Culture and Protein Production: Are We There Yet?

Sarah M. Rue, PhD, Associate Director, Advanced Automation Technologies, Genomics Institute of the Novartis Research Foundation

Michelle R. Gaylord, M.S., Senior Scientist II, Genomics Institute of the Novartis Research Foundation

Automated solutions for cell culture and protein production seem to be simultaneously becoming more complex and more critical to drug discovery. Here, we discuss current challenges with automation, and opportunities for new technology development.

PROCESS ENHANCEMENT STRATEGIES

4:00 Apoptosis-Resistant CHO Cell Lines Significantly Improve Culture Viability and Titer in Intensified Fed-Batch Culture Process

Shahram Misaghi, PhD, Principal Scientist, Cell Culture and Bioprocess Operations (CCBO), Genentech, Inc.

Process intensification strategies in CHO production cultures can potentially increase productivity, lower cost of goods, and improve facility utilization. However, process intensification often triggers apoptotic cell death in the later phases of intensified production process. Here we show that apoptosis-resistant CHO cell lines counteract this undesired outcome, resulting in not only better viability but also enabling extended productivity that significantly improve volumetric productivity without affecting product quality.

4:30 Novel CHO Host for Improved Recombinant Protein Production

Lina Chakrabarti, PhD, Senior Manager, R&D, AstraZeneca

With the aim of increasing protein productivity, we generate a novel CHO host with favorable biomanufacturing phenotypes and improved functionality. Producer pools and clones generated from the new host outperformed the standard host by displaying (1) improvement in productivity, (2) reduced product aggregation, (3) enhanced cell viability, (4) low lactate production and (5) improved cell cloning efficiency. The new host exhibited multifaceted protection against mitochondrial dysfunction and ER stress.

5:00 Prediction of Amino Acid Consumption in Chinese Hamster Ovary Cell Fed-Batch Cultures by Coupling a Genome-Scale Metabolic Network Model with Machine Learning

Wei Wei, PhD, Principal Scientist, Cell Line Development, Biotherapeutics Pharmaceutical Sciences, Pfizer Inc.

Genome-scale metabolic modeling offers a promising approach for ***in silico*** monitoring and predicting the consumption of proteinogenic amino acids, which is critical for bioprocess control. However, the prediction accuracy is challenged by the discrepancy between the model assumption and the biological variances in CHO cultures. We demonstrate such challenge can be addressed by integrating a CHO-specific metabolic network model with machine learning to achieve accurate prediction throughout the fed-batch process.

5:30 Digital Twins for Improved Bioprocess Operation: Opportunities and Roadblocks

Krist V. Gernaey, PhD, Professor, Chemical & Biochemical Engineering, Danish Technical University

Digital twins, virtual copies of a process, will play an important role in transforming biomanufacturing towards Industry 4.0. Two major building blocks of a digital twin, data and models, are highlighted. Data characteristics and collection strategies are examined; new methods and tools for data processing are highlighted. Furthermore, different modelling approaches are presented in view of their use in a digital twin. Potential roadblocks for digital twin implementation are discussed.

6:00 Welcome Reception in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

7:30 Close of Day

TUESDAY, JANUARY 18

8:30 am Registration and Morning Coffee (Sapphire West Foyer)

HIGHER-THROUGHPUT PURIFICATION

Session Room: Sapphire 400

9:00 Chairperson's Remarks

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

9:05 Building Higher-Throughput, Multi-Host, Automated, Mid-Scale, Protein Screening Platform for Drug Discovery

Kanika Bajaj Pahuja, PhD, Scientific Manager, Protein Sciences, Genentech Inc.

We are building higher-throughput multi host system mid-scale protein expression and screening platform to accelerate drug discovery research at Genentech. This platform is built to perform quick triage of high-quality recombinant proteins for structural and biochemical screens. Our semi-automated workflow leverages affinity in tip technology and size exclusion chromatography integrated with liquid robotic handlers to purify multiple samples in parallel.

9:35 Next-Generation Integrated Antibody Capture Process Based on Magnetic Beads from High Cell Density Cultures

Kristofer Eriksson, PhD, CTO, MAGic Bioprocessing

Cell clarification represents a major challenge for processing suspensions with very high cell densities. By using high-capacity protein A magnetic beads, we have developed an integrated affinity process where cell clarification and antibody recovery is performed in a single step. Using this approach on suspensions with 100 million cells/ml, we achieve adsorptions larger than 95% and yields over 90% with a logarithmic host cell protein clearance of 2-3.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

HIGHER-THROUGHPUT PROTEIN PRODUCTION CONTINUED

11:00 KEYNOTE PRESENTATION: Advances in High-Throughput Protein Purification at Different Scales

John K. Kawooya, PhD, Director, Biologics Optimization and Therapeutic Discovery, Amgen, Inc.

Currently, protein engineering is the major gateway to biotherapy discovery. Protein engineering starts with ***in silico*** generation of multi-constructs panels. These constructs are cloned, expressed, purified and analyzed for efficacy and manufacturability. In this workflow, protein purification remains the major bottle neck in accelerating lead identification from multi-construct panels. Here, I present new concepts of the next-generation magnetic and non-magnetic high-throughput parallel systems for de-bottlenecking panel purification.

11:30 FEATURED PRESENTATION: A Self-Cleaving Affinity Tag to Bridge Research and Manufacturing: Concept to Commercialization

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

A practical self-removing affinity tag now exists that can bridge tag-based high-throughput methods for basic research with clinical manufacturing processes to produce tagless products. The development and commercialization of this tag, with a focus on its practicality for a variety of applications is presented. Case studies demonstrate rapid purification of proteins for research, as well as the potential for large-scale manufacturing of biosimilars and new biopharmaceuticals in the future.

12:00 pm New Approaches to De-Risking Early Selection of Microbial Strains for Recombinant Protein Expression

Nigel Shipston, Director - Technical Marketing, FUJIFILM Diosynth Biotechnologies

Lead strain selection is a critical step during microbial process development, initially based on product titer because product quality evaluations are challenged by the timely availability of sufficiently purified material. The capability of a well-proven ***E. coli*** expression platform has been enhanced through the use of a scale down/high throughput approach to protein purification using robotics, to enable strain selection based on parallel evaluation of product titer and quality.

12:30 Session Break

12:40 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:10 Close of Higher-Throughput Protein Production

TUESDAY, JANUARY 18

1:00 pm Registration (Sapphire West Foyer)

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

CONTINUOUS AND NOVEL PURIFICATION

Session Room: Sapphire 400

2:00 Organizer's Welcome Remarks

Edel O'Regan, Vice President, Production, Cambridge Healthtech Institute

2:05 am Chairperson's Remarks

James Ware, Director, Purification Development & Tech Transfer, Ligand Pharmaceuticals, Inc.

2:10 KEYNOTE PRESENTATION: High Performance Countercurrent Membrane Purification (HPCMP) for Continuous Downstream Processing

Andrew Zydney, PhD, Bayard D. Kunkle Chair & Professor, Chemical Engineering, Pennsylvania State University

This presentation examines a new downstream processing technology, High Performance Countercurrent Membrane Purification (HPCMP), which exploits highly selective diffusive transport across the thin walls of a hollow fiber membrane. Experiments were performed using several model systems. HPCMP achieved greater than 98% product yield for with purification factors >100-fold over 96 hours of continuous operation. These results clearly demonstrate the potential of using HPCMP for protein purification in downstream processing.

2:40 A Novel Protein A-Based Purification Matrix for Mild Purification of Antibodies

Sophia Hober, PhD, Professor, School of Biotechnology, KTH Royal Institute of Technology

Antibodies are widely used affinity molecules in many fields of biological science and their use in therapy is constantly growing. The most common tool used for purification of antibodies is Protein A affinity chromatography. However, when eluting the captured antibodies from the column, low pH is needed which can be deleterious for certain antibodies and Fc-fusion proteins. We have addressed this issue by protein engineering.

3:10 Osmotic Shock: A Viable Primary Recovery Option for Biopharmaceutical Manufacturing from a Microbial Host

James Ware, Director, Purification Development & Tech Transfer, Ligand Pharmaceuticals, Inc.

Microbial manufacturing has advantages over traditional CHO systems and differences in primary recovery provide opportunities to explore techniques leveraging the physical properties of the organism. High titers generated in the Pelican Expression Technology platform are retained within the cell and release methods vary depending on the strain and product stability. We demonstrated that a unique approach using osmotic shock is viable for manufacturing and a beneficial method of protein release.

3:40 Refreshment Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

INNOVATION IN CELL CULTURE PROCESS, BIOREACTORS & MODELING

4:30 The Use of a High-Throughput, One-Step Transient-to-Stable Cell Line Generation Process for Accelerated Delivery of Proteins in Early Discovery

Marina Alvi, PhD, Senior Research Scientist, Mammalian Protein Expression, Eli Lilly & Co.

There is a constant need in the pharmaceutical industry to accelerate the production of antibodies and other large molecules in the early stages of R&D. Here we describe a high-throughput cell line generation process that negates the need to perform multiple transfections per expressed protein. Our results show that this process can be applied to a large number of samples with high protein yield and protein quality.

5:00 Continuous Production with *E. coli*

Gerald Striedner, PhD, Associate Professor, Biotechnology, University of Natural Resources & Life Sciences, Vienna (BOKU), Austria

Genome-integrated as well as growth-decoupled ***E. coli*** expression systems enable continuous protein production. Efficient implementation requires suitable process strategies for cultivation and product recovery and purification. The presentation will show two case studies inclusive an economic evaluation with standard fed batch as benchmark.

5:30 Close of Day

WEDNESDAY, JANUARY 19

7:30 am Registration (Sapphire West Foyer)

8:00 BuzZ Sessions with Continental Breakfast (Sapphire Foyer)

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

BuzZ Table 7: Buzz Session: Balancing Speed of Development with the Quality of the Product in the Race to an IND Filing

James Ware, Director, Purification Development & Tech Transfer, Ligand Pharmaceuticals, Inc.

BuzZ Table 8: CMC Strategies for Successful Manufacturing of Drugs and Novel Modalities

Brian O'Mara, Associate Director, Downstream Process Development, Ambrx, Inc.

PROCESS DEVELOPMENT & BIOMANUFACTURING

Session Room: Sapphire 400

9:05 Production and Purification of Non-mAb Proteins by Platform Processes Using Affinity Tags

Alois Jungbauer, PhD, Professor & Head, Biotechnology, Institute of Bioprocess Science and Engineering, University of Natural Resources and Life Sciences (BOKU)

The conventional His tag often leads to reduced expression level and cleavage is expensive, slow and often the required N-terminus is not achieved. An expression and purification system based on a circular permutated Caspase which generates an authentic N-terminus irrespective of the amino acid is presented.

9:35 Panel Discussion: Protein Tag Technologies

Moderator: Richard Altman, Field Application Scientist, Life Science Solutions, Thermo Fisher Scientific

- How do you select an affinity tag?
- How do you know whether it's best to cleave the tag or not?
- Are there regulations (FDA, EMA) regarding cleaving affinity tags?
- When does it make sense not to cleave the tag? Are there complications?
- Is it possible to introduce a universal approach for protein production and purification?

Panelists:

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

Dennis Karthaus, MSc, Director, Protein Products & Assays, IBA Lifesciences

John K. Kawooya, PhD, Director, Biologics Optimization and Therapeutic Discovery, Amgen, Inc.

Dominic Esposito, PhD, Director, Protein Sciences, Frederick National Laboratory

Barbara J Kaboord, PhD, Manager, R&D, Thermo Fisher Scientific Inc

10:35 Coffee Break in the Exhibit Hall with Poster Viewing (Sapphire Ballroom)

11:15 Challenges and Solutions for mAb Process Development and Manufacturing

Yanhuai Richard Ding, PhD, Director, Downstream Process Development & Manufacturing Operations, AnaptysBio, Inc.

This presentation will highlight some challenges and effective solutions from early to late stages of mAb development. Some major challenges related to cell line development, upstream development, downstream development, analytical methods, DS/DP stability are discussed. Effective solutions are assessed and applied.

11:45 Hybrid Modeling and Intensified Design of Experiments to Significantly Accelerate Upstream Process Development

Mark Duerkop, CEO, Novasign GmbH, Austria

The cost and required time to conduct reliable process understanding and characterization limits the bioprocess understanding. The talk highlights several upstream showcases in which the combination of hybrid modeling and advanced design space screening methods increased process understanding while simultaneously significantly reduced the required experiments by up to 70%. The chosen model structure also enabled the usage of those models during up-scaling and easy implementation for process monitoring and control.

12:15 pm Session Break

12:55 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:25 Refreshment Break in the Exhibit Hall and Last Chance for Poster Viewing (Sapphire Ballroom)

DOWNSTREAM PROCESS DEVELOPMENT

2:15 Chairperson's Remarks

Naveenkumar Singh, PhD, Scientist II, Downstream Process Development, Ambrx, Inc.

2:20 Optimizing the Design of Single Pass Tangential Flow Filtration (SPTFF) Processes for Continuous Antibody Purification

Andrew Zydney, PhD, Bayard D. Kunkle Chair & Professor, Chemical Engineering, Pennsylvania State University

Single Pass Tangential Flow Filtration (SPTFF) systems can provide inline concentration of monoclonal antibodies and other biotherapeutics, both to resolve bottlenecks in existing processes and as part of the development of integrated continuous downstream processes. We have developed a model that can be used to optimize the design of SPTFF modules.

2:50 Evolution of a Disruptive Downstream Processing Technology Based on Magnetic Materials

Sonja Berensmeier, PhD, Professor, Bioseparation Engineering Group, Mechanical Engineering, Technical University of Munich

Chromatography has been established as a central step in the purification of proteins, although this is often cost-determining. As an alternative, magnetic separation is presented here, in which magnetic nanoparticles serve as a separation phase that can bind the target molecule directly in unclarified cell culture supernatants or cell lysates. In our case, cost-intensive functionalization of the particles can be omitted and a pilot-scale technical implementation is presented.

3:20 Increasing the Dynamic Binding Capacity of Hydrophobic Interaction Chromatography (HIC) Resins Using a Dual Salt System

Dhanesh Gadre, Scientist I, Purification Process Sciences, AstraZeneca

HIC is typically used as a polishing step to remove impurities in a non-platform protein purification process. In select instances, it has been employed as a capture step for novel biotherapeutics. In this work, we demonstrated that combining two kosmotropic salts can increase the DBC on HIC resin significantly compared to single salt systems. We demonstrated this improvement with three different dual salt systems using two model proteins.

3:50 Host Cell Protein Challenges in the Downstream Process Development of Non-Antibody Processes

Naveenkumar Singh, PhD, Scientist II, Downstream Process Development, Ambrx, Inc.

In this case study, host cell protein reduction challenges were encountered with a recombinant protein conjugate expressed in CHO cells. A baseline process using conventional chromatography and filtration techniques was rapidly developed to support toxicology and Phase 1 production. Here we discuss the systematic approach to reduce HCP levels to within specification using strategies amenable to manufacturing.

4:20 On-Demand and *in situ*: Continuous Reconstitution of Media and Buffers Directly from Solids

Daniel Komuczki, MMMSc, PhD Candidate, Biotechnology, University of Natural Resources & Life Sciences

The transformation from batch to integrated continuous bioprocessing only "shrinks" the unit-operations while necessary auxiliaries are drastically increased. This leads either to necessarily large hold tanks or high personal costs. To solve this bottleneck, we developed a device for a continuous on-demand reconstitution of media and buffers directly from solids.

4:50 Close of Conference

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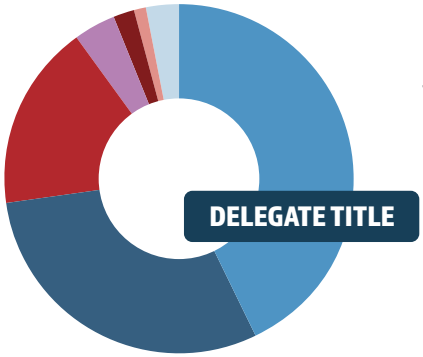

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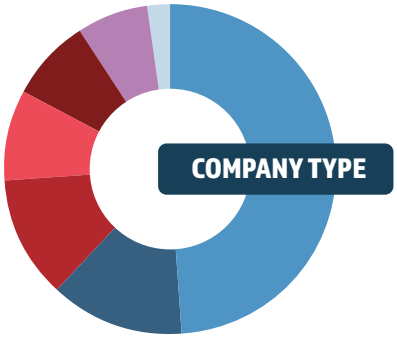

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WHAT'S THE BUZZ ABOUT?

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. This is a moderated discussion with brainstorming and interactive problem-solving between 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.

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