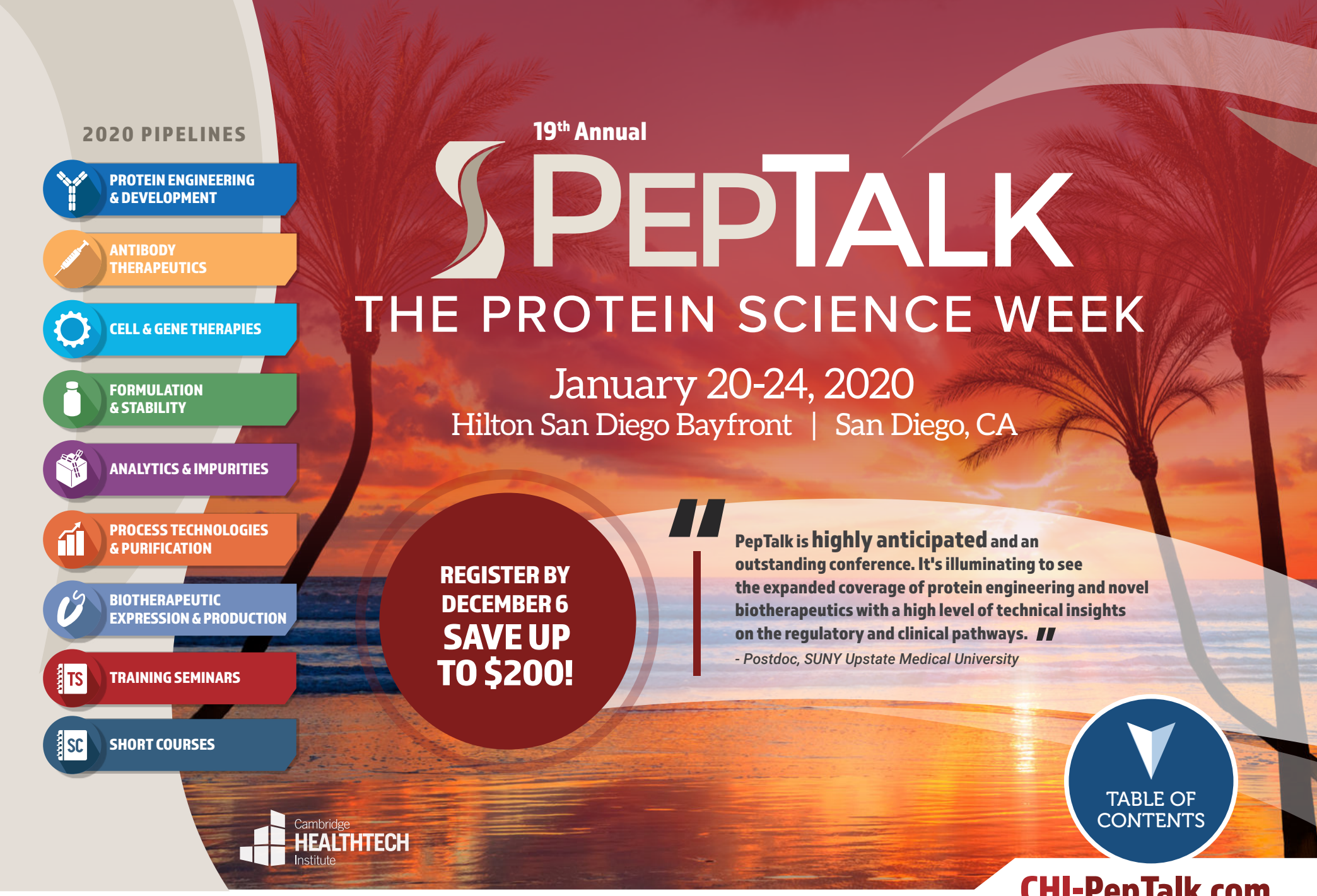
2020 PIPELINES
PROTEIN ENGINEERING & DEVELOPMENT
ANTIBODY THERAPEUTICS
CELL & GENE THERAPIES
FORMULATION & STABILITY
ANALYTICS & IMPURITIES
PROCESS TECHNOLOGIES & PURIFICATION
BIOTHERAPEUTIC EXPRESSION & PRODUCTION
TS
TRAINING SEMINARS
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January 20-24, 2020
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THE PROTEIN SCIENCE WEEK

JANUARY 20-24, 2020
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19th Annual

PEPTALK 2020

THE PROTEIN SCIENCE WEEK

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More than 1,300 leaders from academia, biotech and pharma gather at PEPTALK: THE PROTEIN SCIENCE WEEK for intensive learning and networking, to discover new opportunities, apply alternative solutions, and develop promising partnerships.

- Hear from some of the most influential and thought-provoking speakers in the biotherapeutics industry.
- Gain insight into emerging strategies, the latest innovative technologies, and best practices to move your research to the next level.
- Network with world renowned industry experts, collaborate with your peers and build your network in a friendly atmosphere.

Conference Programs feature keynote presentations, case studies and new unpublished data from influential leaders in academia and industry.

Training Seminars offer focused instruction in topics related to your field using a mix of lecture and interactive discussion formats and are led by experienced instructors. These may be combined with conferences to customize your week at PepTalk.

Dinner Short Courses offer a unique, intimate setting to delve into a particular topic. Each course provides a great introduction for those who are new to a discipline or a helpful refresher for those who want to brush up on their knowledge or expand their horizons.

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EVENT AT-A-GLANCE

JANUARY 20-24, 2020

Hilton San Diego Bayfront | San Diego, CA

	PART A Mon. - Tue. AM | Jan. 20-21	PART B Tue. PM - Wed. | Jan. 21-22	PART C Thu. - Fri. | Jan. 23-24
PROTEIN ENGINEERING & DEVELOPMENT	Recombinant Protein Therapeutics	Lead and Candidate Selection for Therapeutic Proteins	Deep Sequencing and Single Cell Analysis for Antibody Discovery
ANTIBODY THERAPEUTICS	Engineering Next-Generation Cancer Immunotherapies	Antibody-Drug Conjugates	Bispecific Antibody Therapeutics
CELL & GENE THERAPIES	Vector Design and Development for Gene and Cell Therapies	Gene Therapy Analytics and Manufacturing	Cell Therapy Analytics and Manufacturing
FORMULATION & STABILITY	Optimizing Biologics Formulation Development	Lyophilization and Emerging Drying Technologies	Protein Aggregation and Emerging Analytical Tools
ANALYTICS & IMPURITIES	Characterization of Biotherapeutics	Detection and Characterization of Particulates and Impurities	Protein Aggregation and Emerging Analytical Tools
PROCESS TECHNOLOGIES & PURIFICATION	Bioprocess Data Management and Analysis	Protein Purification and Recovery	Higher-Throughput Protein Production and Characterization
BIOTHERAPEUTIC EXPRESSION & PRODUCTION	Engineering Genes, Vectors, Constructs, and Clones	Recombinant Protein Expression and Production	Optimizing Expression Platforms
TRAINING SEMINARS / SHORT COURSES	Protein Aggregation and Formulation Optimization ——— Introduction to Antibody Engineering	Next-Generation Approaches to Antibody Screening and Discovery ——— GMP and Validation Requirements for Biologics Processes – Phase I through to Commercial Manufacturing	Introduction to Analytical Characterization and Method Validation for Protein Therapeutic Drugs

Tue. PM Dinner Short Courses

WEDNESDAY, JANUARY 22 | 1:45 - 3:05 PM

PLENARY KEYNOTE PANEL

R&D Challenges in an Era of Innovation

The PepTalk Plenary Keynote Panel convenes a group of leading scientists working across novel therapeutic modalities and R&D technologies to explore the many challenges associated with discovering, developing, and advancing today's novel biotherapeutics. The Panel, via a highly interactive format, encourages discussion among both the panelists and the audience members. Please come prepared with your questions and ideas for this spirited discussion.

- Advances and challenges in expression and production for novel modalities
- Implementing next-generation informatics: data collection, standardization, analysis, ML/AI, and considerations for IP landscape and protection
- Implementing R&D and production capacity for gene and cell therapies – where are we heading?
- Modality-specific challenges: multi-specifics for cancer, improving the ADC therapeutic window, improved safety and pharmacology, novel delivery/targeting
- Preclinical and clinical development of drug combinations with focus in IO: How do we select the right combination dose so we can accelerate clinical development?

Moderator:

Mohammad Tabrizi, PhD
Senior Director, Pharmacology, Ascendis Pharma A/S

Panelists:

Edward Kraft, PhD
Senior Scientific Manager, Biomolecular Resources, Genentech

Ilya Shestopalov, PhD,
Associate Director, Cell Analytics, bluebird bio

David E. Szymkowski, PhD
Vice President, Cell Biology, Xencor, Inc.

Alayna George Thompson, PhD
Senior Scientist I, Drug Discovery Science & Technology, AbbVie

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Students must present a valid/current student ID to qualify for the student rate.

To secure a poster board and inclusion in the conference materials, your abstract must be submitted, approved and your registration paid in full by November 22, 2019.

Training SEMINARS

By Cambridge Healthtech Institute

Please visit CHI-PepTalk.com to view detailed agendas for each Training Seminar

Cambridge Healthtech Institute Training Seminars offer real-life case studies, problems encountered and solutions applied, along with extensive coverage of the academic theory and background. Each Training Seminar offers a mix of formal lecture and interactive discussions and activities to maximize the learning experience. These Training Seminars are led by experienced instructors who will focus on content applicable to your current research and provide important guidance for those new to their fields.

SUNDAY, JANUARY 19 | PRE-CONFERENCE REGISTRATION 4:00 - 6:00 PM

MONDAY, JANUARY 20 - TUESDAY, JANUARY 21

DAY 1: 9:00 AM - 6:00 PM | **DAY 2:** 8:45 AM - 12:30 PM

TS8A: Protein Aggregation and Formulation Optimization

Molecular interactions are central to protein discovery, development, and formulation. This training seminar allows a fundamental, but very practical, understanding of protein interactions, solution behavior, aggregate formation, and its application to formulation optimization. Building on a review of central energy concepts, the framework allows a deeper understanding of protein structural stability, interactions with small molecules, surfaces, itself, other proteins, and other macromolecules. A deeper insight is afforded into the binding, solubility, viscosity, detection, and characterization of protein aggregates.

Instructors:

Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire

Kevin Mattison, PhD, Principal Scientist, Malvern Pananalytical, Inc.

Matthew Brown, PhD, Applications Manager, Bioscience, Malvern Panalytical, Inc.

TS9A: Introduction to Antibody Engineering

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, providing students with ample opportunities to discuss technology with instructors.

Instructors:

Andrew R.M. Bradbury, MB BS, PhD, CSO, Specifica, Inc.

James D. Marks, MD, PhD, Chief of Performance Excellence, Zuckerberg San Francisco General Hospital and Trauma Center; Professor of Anesthesia, UCSF Department of Anesthesia and Perioperative Care

TUESDAY, JANUARY 21 - WEDNESDAY, JANUARY 22

DAY 1: 2:00 - 5:30 PM | **DAY 2:** 8:15 AM - 6:05 PM

TS8B: Next-Generation Approaches to Antibody Screening and Discovery

Over the space of a few years, DNA sequencing and data analysis, DNA synthesis, single-cell isolation, and genome engineering using CRISPR/Cas9 have improved greatly in both capability and affordability, and have now been adapted to enhance the discovery and development of antibodies and other immunotherapies.

This training seminar will evaluate these new developments and their applications in antibody and immunotherapy discovery and development.

Instructor:
David Bramhill, PhD, Founder, Bramhill Biological Consulting, LLC

TS9B: GMP and Validation Requirements for Biologics Processes – Phase I through to Commercial Manufacturing

This seminar looks at the current requirements and expectations for GMP manufacturing and testing at all stages of the product lifecycle from Phase I through all clinical phases to commercial manufacturing and maintaining validated status. It will cover phase-appropriate GMP and the evolution of the pharmaceutical quality system to address the requirements at different phases of development and of the commercial product lifecycle. It will also look at how the challenges can vary for different types of biological products.

Topics covered will include the regulatory background, process and analytical development, process knowledge, and the impact of single-use systems, process qualification, continuous process verification, and specific considerations for challenging and/or unusual processes, including live vaccines and cell therapy products.

Instructor:
Trevor Deeks, PhD, QA/QC and GMP Consultant, Deeks Pharmaceutical Consulting Services, LLC

THURSDAY, JANUARY 23 - FRIDAY, JANUARY 24

DAY 1: 8:10 AM - 5:15 PM | **DAY 2:** 9:00 AM - 12:30 PM

TS7C: Introduction to Analytical Characterization and Method Validation for Protein Therapeutic Drugs

This seminar will review analytical method development and validation in the context of IND regulatory filing of therapeutic proteins, including monoclonal antibodies and recombinant proteins. The curriculum will provide a broad overview of biologics analytical and characterization methods and is beneficial to individuals involved in biologics drug development, analytical development, quality control, quality assurance, regulatory affairs, project management, process development, formulation development, or related functional areas. Attendees will learn the practical aspects of the commonly used analytical panel not only for DS/DP release and stability but also for monitoring the manufacturing process and facilitating formulation development. New real-world case studies and common pitfalls will be presented.

Instructor:
Kevin Zen, PhD, Executive Director, Analytical Characterization, Formulation Development and Biologics Manufacturing, AnaptysBio Inc.

TUESDAY, JANUARY 21 | 5:45 - 8:45 PM

DINNER SHORT COURSES*

SC2: The Safety of Immunotherapy and ADCs: How to Mitigate Risk and Adverse Effects

This short course examines safety issues surrounding immunotherapies and particularly Antibody-Drug Conjugates in an intimate setting with two of the world's leading ADC experts. Following a review of current cancer immunotherapies in development, including CAR T cells, CD-3 T cell-based bispecifics, and immune checkpoint inhibitors and agonists, the safety of ADCs will be explored in depth. ADC design and translational strategies for safety risk mitigation will be discussed, along with conjugation, payload, and engineering impacts on the therapeutic window.

Instructors:
Rakesh Dixit, PhD, DABT, President & CEO, Bionavigen, LLC
Stephanie Voss, PhD, Group Leader, Bioconjugation & Protein Chemistry, Heidelberg Pharma Research GmbH

SC3: Structure-Based Optimization of Antibodies

This 3-hour course offers a quick overview of the concepts, strategies, and tools of structure-based optimization of antibodies. This lecture will cover structure-based techniques to modulate affinity, create novel constructs (such as Fc-fusions, bispecifics, etc.), along with increasing the manufacturability of a biologic. The class is directed at scientists new to the industry, academic scientists, and career protein engineers wanting a quick overview about how structure can aid in guiding experimental design.

Instructor:
Traian Sulea, PhD, Principal Research Officer, Human Health Therapeutics, Biotechnology Research Institute, National Research Council Canada

SC5: Protein Aggregation: Mechanism, Characterization, and Consequences

Protein aggregation is recognized by regulatory agencies and the biopharmaceutical industry as a key quality attribute of biotherapeutics. Various aggregates hold the potential for adversely impacting production and patients in a variety of ways. This in-depth course reviews the origins and consequences of aggregation in biotherapeutics, and then examines strategies for predicting and quantifying aggregation in biopharmaceuticals. It benefits scientists engaged in the development, production, analytical characterization, and approval of biotherapeutics, and those who require a good working knowledge of protein aggregation.

Instructors:
Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire
Kevin Mattison, PhD, Principal Scientist, Malvern Pananalytical, Inc.

SC6: Assembling an Effective Toolbox of Expression Systems to Support Your Drug Discovery Efforts

This course will discuss the systems necessary to support the expression of both traditional (mAbs) and next-generation formats of proteins to support all aspects of drug discovery. This includes therapeutic candidates, assay reagents, immunogens, and proteins for structural studies.

Instructors:
Richard Altman, Field Application Scientist, Protein Expression, Biosciences Division, Life Sciences Solutions Group, Thermo Fisher Scientific
Henry C. Chiou, PhD, Director, Cell Biology, Life Science Solutions, Thermo Fisher Scientific
Dominic Esposito, PhD, Director, Protein Expression Laboratory, Frederick National Laboratory for Cancer Research

**Separate registration required*

PROTEIN ENGINEERING & DEVELOPMENT

As biologics gain greater prominence, protein engineers are adapting to new indications, new advances in targeting science, new product formats, and products that are truly differentiated in the marketplace. The Protein Engineering & Development pipeline offers a weeklong exploration of state-of-the-art approaches for developing safe and effective protein and antibody-based therapeutics, including improving product qualities, optimizing lead and candidate selection, and the application of deep sequencing and single cell analysis.

January 20-21

AGENDA Recombinant Protein Therapeutics

January 21-22

AGENDA Lead and Candidate Selection for Therapeutic Proteins

January 23-24

AGENDA Deep Sequencing and Single Cell Analysis for Antibody Discovery

RECOMBINANT PROTEIN THERAPEUTICS

Fusion Proteins & Beyond

Cambridge Healthtech Institute's RECOMBINANT PROTEIN THERAPEUTICS conference presents the latest developments in non-antibody therapeutics from international leaders. The conference focuses on the varying designs of fusion protein-based therapies and the latest data from R&D to post-approval, including case studies. By combining modular building blocks that can reach targets not accessible to antibodies, fusion protein therapies possess advantages over antibody-based therapies; their customizable functionality translates into lower patient dosing, reduced production costs, and improved product homogeneity. This conference will demonstrate how these molecules are being engineered to form more efficacious therapeutics that offer specificity with enhanced stability and longer half-life.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

ENGINEERING & PRODUCING THERAPEUTIC FUSION PROTEINS

9:00 Organizer's Welcome Remarks
Mary Ruberry, MA, Senior Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Joachim Feldswich, PhD, Director, Preclinical Development, Affibody AB

KEYNOTE PRESENTATION

9:10 From Cytokine Traps to Antibodies to Antibody-Protein Fusions

Aris N. Economides, PhD, Vice President, Research, Regeneron Pharmaceuticals, Inc.
Antibodies, endowed by nature with desirable properties, have provided an excellent starting point for engineering protein-based therapeutics. Even preceding the ability to generate human (or humanized) mAbs, the constant region of antibodies was used to generate Immunoadhesins and Cytokines Traps, a good number of which became approved drugs. The ability to generate human mAbs has enabled the exploration of many novel formats. A select set of these will be discussed in the context of relevant therapeutic applications.

9:50 Strategic and Technical Considerations on Designing, Manufacturing and Using Complex Protein Therapeutics
Stefan Schmidt, PhD, MBA, COO/Head, Operations, BioAtrium AG
Triggered by the tremendous success of antibodies, complex and multifunctional proteins represent a current trend in therapeutic modalities. Here several elements are combined in a single molecule to optimize on-target activities, simplify the manufacturing process and improve administration schemes. This presentation connects these different approaches and gives recommendations supported by examples from case studies and a review of the current fusion protein pipeline.

10:20 Networking Coffee Break

TARGETING THE BRAIN WITH FUSION PROTEINS AND ONCOLOGY BREAKTHROUGHS

10:45 Targeting the Brain with IgG-Bifunctional Fusion Proteins: Preclinical and Clinical Update
Ruben J. Boado, PhD, Co-Founder, ArmaGen, Inc.
Protein therapeutics can be re-engineered as brain-penetrating IgG-bifunctional fusion proteins for the treatment of CNS disorders. The IgG domain targets a specific endogenous receptor-mediated transporter system within the blood-brain barrier (BBB), i.e., insulin or transferrin receptor, respectively. The therapeutic domain of the fusion protein exerts the pharmacological effect in brain once across the BBB. Preclinical and first in human clinical trials will be discussed.

11:15 A Brain-Penetrating Erythropoietin-Transferrin Receptor Antibody Fusion Protein for Alzheimer's Disease
Rachita Sumbria, PhD, Associate Professor, Biopharmaceutical Sciences, Keck Graduate Institute
Erythropoietin (EPO) is a promising neurotherapeutic for Alzheimer's disease (AD). However, blood-brain barrier (BBB) penetration and negative hematopoietic effects are the challenges for the therapeutic development of EPO for AD. A BBB-penetrating EPO is engineered by fusing EPO to a monoclonal antibody targeting the BBB transferrin receptor (TfRMAb) to ferry EPO into the brain. The talk will focus on the therapeutic effects of this BBB-penetrating EPO in AD mice.

11:45 ALPN-202, a Novel Tri-Functional Immuno-Oncology Biologic
Mark Rixon, PhD, Senior Director, Protein Therapeutics, Alpine Immune Sciences
ALPN-202 is an Fc-fusion protein of a human CD80 variant immunoglobulin domain (vIgD™) designed to block PD-L1 and CTLA-4, and to provide PD-L1-dependent T cell activation via the CD28 costimulatory receptor. ALPN-202 has potent single agent immunomodulatory activity in mouse tumor models that is superior to single PD-L1 blockade and elicits a unique proinflammatory gene signature in the tumor microenvironment.

12:15 pm Sponsored Presentation *(Opportunity Available)*

12:45 Session Break

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

NEXT-GENERATION CANCER THERAPEUTICS

2:00 Chairperson's Remarks
Stefan Schmidt, PhD, MBA, COO/Head, Operations, BioAtrium AG

FEATURED PRESENTATION

2:05 Engineered Fc-Fusion Proteins as Next-Generation Cancer Therapeutics
Jennifer Cochran, PhD, Professor, Bioengineering and Chemical Engineering, and Shriram Chair, Bioengineering, Stanford University
We create novel engineered ligands and receptors as therapeutic candidates to address limitations of their antibody counterparts, such as the need to achieve ultra-high target binding affinity or the ability to modulate multiple receptors. Within these constructs, we utilize antibody Fc domain fusions to increase circulation half-life, achieve avidity effects, or recruit immune cell effector function. My talk will describe several examples of clinical and pre-clinical stage Fc-fusion proteins against emerging targets in oncology.

2:35 HERA-CD40L: A Unique Hexavalent CD40 Agonist for Cancer Immunotherapy
Katharina Billian-Frey, PhD, Senior Scientist, Protein Engineering, Drug Discovery, Apogenix AG
HERA-CD40L is a member of a novel class of TNFR superfamily agonists for immuno-oncology therapies. The engineering is based on a trivalent, but single-chain mimic of the natural CD40L fused to a dimerization scaffold, leading to a potent crosslinking-independent hexavalent agonist. HERA-CD40L is superior to other agonistic formats regarding activation and maturation of distinct immune cells, and demonstrates anti-tumor activity as single agent in tumor mouse models.

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.
Click here for details.

FORTIFYING THE IMMUNE SYSTEM TO FIGHT TUMORS

4:30 Preconditioning the Tumor Microenvironment to Enable Effective Immunotherapy Using Antibody Fusion Proteins
Alan Epstein, MD, PhD, Professor, Pathology, Keck School of Medicine, University of Southern California (USC)
As surrogates for patient investigations, syngeneic murine tumor models are being treated with antibody and Fc-fusion proteins to precondition the tumor microenvironment and rearm the immune system. When used in combination with suppressor cell inhibition, tumor eradication can be achieved even in the face of high tumor burden. For solid tumors, where tumor heterogeneity is the norm, the induction of innate immunity, antigen spreading, and immunologic memory are especially important to prevent the reoccurrence of tumor growth and treatment failure.

5:00 T Cells Engineered with Immunomodulatory Fusion Proteins Enhance Adoptive Cell Therapy of Liquid and Solid Tumors
Shannon K. Oda, PhD, Research Associate, Philip D. Greenberg Laboratory, Program in Immunology, Clinical Research Division, Fred Hutchinson Cancer Research Center
To improve the efficacy of adoptive cell therapy (ACT), we have developed immunomodulatory fusion proteins (IFPs) that combine an inhibitory ectodomain with a costimulatory signal to "replace a brake with an accelerator." IFP-engineered T cells exhibit enhanced function, metabolic reprogramming, and *in vivo* persistence, significantly improving survival in murine models of leukemia and pancreatic cancer. Human primary IFP-T cells also exhibit increased antitumor function, supporting clinical translation of this strategy.

5:30 Antibody-Cytokine Fusion Proteins to Promote Proliferation of Tumor-Reactive T Cell Subsets
Elissa Leonard, PhD, Postdoctoral Research Fellow, Biomedical Engineering, Johns Hopkins University
Many solid tumors are allowed to proliferate due to suppression of T effector cells (Teffs) by T regulatory cells (Tregs). We have engineered and optimized an antibody-cytokine fusion in which the antibody blocks key interactions with the high affinity domain of the Tregs' IL-2 receptor, while still permitting signaling through the moderate affinity IL-2 receptor expressed on Teffs. This promotes a more proinflammatory T cell response that reduces tumor growth.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

NEXT-GEN ENGINEERING FOR THERAPEUTIC FUSION PROTEINS

8:45 Chairperson's Remarks
Shannon K. Oda, PhD, Research Associate, Philip D. Greenberg Laboratory, Program in Immunology, Clinical Research Division, Fred Hutchinson Cancer Research Center

8:50 Novel Fc Platform Development and Applications for Fc-Fusion Proteins
Qing Li, PhD, Scientist, Antibody Discovery & Protein Engineering, AstraZeneca
Monovalent fusion proteins are often a necessary drug format for optimal structure and activity profiles. We present our novel monovalent fusion platform in target validation and lead discovery.

9:20 Molecular Landscape of Anti-Drug Antibodies Reveals the Mechanism of the Immune Response following Treatment with TNFα Antagonists
While therapeutic mAbs hold significant promise for improving human health, repeated administration of mAbs often leads to the induction of undesirable Anti-Drug Antibodies (ADA) that reduces drug efficacy. The mechanisms that lead to the generation of ADA and their molecular composition are unknown. ADA repertoire analysis reveals the possible mechanism involved in generation of ADA following infusion with TNFα antagonists. The data suggests that mAb administration elicits a vaccine-like response in the marginal zone that is a T cell independent (TI) response.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

FUSION PROTEINS TO FIGHT DISEASE

11:00 *In vitro* Evolution of a Vaccine-Elicited Antibody Identifies New Capabilities for Effective Fusion Peptide-Based HIV Neutralization
Bharat Madan, PhD, Postdoctoral Researcher, Pharmaceutical Chemistry, University of Kansas
We present a new platform for interrogating the functional landscape of somatic hypermutation pathways for antibody improvement. We leveraged precision antibody library generation with yeast surface display and NGS to identify a comprehensive set of beneficial mutations across the entire antibody variable region. This work has identified multiple independent pathways for antibody therapeutic improvement and provided new insights on the developmental dynamics of antibody immune responses.

11:30 Affibody Molecules in Psoriasis, Autoimmune Disease, and Cancer: From Lab Bench to Patient Outcomes
Joachim Feldswich, PhD, Director, Preclinical Development, Affibody AB
Affibody molecules are engineered affinity proteins based on a compact three-helical bundle scaffold. The molecules are ideally suited to create novel biologic therapeutics and diagnostics. Two different therapeutic clinical programs and one diagnostic (HER2) will be presented to exemplify how Affibody molecules can be used as modular building blocks to create novel innovative mono- and bifunctional therapeutics. ABY-035 is a best in class IL-17A blocking ligand trap with femtomolar binding affinity that translates to high therapeutic efficacy in patients with psoriasis.

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

12:30 Session Break

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

1:10 Close of Recombinant Protein Therapeutics Conference

LEAD AND CANDIDATE SELECTION FOR THERAPEUTIC PROTEINS

Strategies and Best Practices for Key Early Decision Gates

The screenings and studies that comprise a company's lead and candidate selection funnel are an essential stage of biopharmaceutical R&D. Good selections not only ensure that the best quality molecules are chosen for advancement, but that these match target profile for efficacy, safety, and pharmacology. PepTalk's new LEAD AND CANDIDATE SELECTION FOR THERAPEUTIC PROTEINS meeting presents a wide range of strategies, models and technologies used for these evaluations, and considers the best practices in this field. Case studies from both large and small organizations will showcase the innovative ways organizations have employed these tools to help ensure rapid progression through subsequent development steps and the prospects for success in the clinic.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

IMPROVING THE QUALITY OF LEAD AND CANDIDATE SELECTIONS

2:00 Chairperson's Opening Remarks
Max Vásquez, PhD, Head, Computational Biology, Adimab LLC

KEYNOTE PRESENTATION

2:05 Chemical and Physical Properties of Drug-Like Antibodies

Peter M. Tessier, PhD, Professor, Pharmaceutical Sciences, Chemical Engineering and Biomedical Engineering, University of Michigan

Monoclonal antibodies display variable and difficult-to-predict levels of non-specific (heterotypic) and self (homotypic) interactions that lead to various drug development challenges, including antibody aggregation, abnormally high viscosity and fast antibody clearance. In this presentation, we will report novel experimental and bioinformatics methods for identifying, engineering and predicting antibody variants with drug-like specificity for diverse panels of preclinical and clinical antibodies.

2:45 Designing Better Therapeutics by Understanding the Complexity of the Target Ortholog in Nonhuman Primates
Ramkrishna (Ramu) Sadhukhan, PhD, Principal Research Scientist, Global Protein Sciences, AbbVie Bioresearch Center

Nonhuman primates (NHP) exhibit genetic variation due to allelic drift resulting from geographic separation and environment, including diet and microbiome. These genetic differences may affect drug targets and thereby impact the outcome of the studies. In my presentation, I will describe a comprehensive approach that we have adopted at AbbVie to interrogate polymorphisms of our target molecules in NHP. Case studies will be used to illustrate the impact of such investigations.

Sponsored by

3:15 Antibody Protein Sequencing with Mass Spectrometry
Anthony Stajduhar, Business Development Manager, Rapid Novor, Inc.

Many applications in antibody engineering require the direct sequence of antibody proteins. At Rapid Novor (www.rapidnovor.com) we have developed a robust workflow and routinely sequence antibody proteins. Here we share our success stories, examine common mistakes novices make and present our practices to ensure the correctness of every amino acid.

3:30 Sponsored Presentation *(Opportunity Available)*

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

4:30 Exploiting an Achilles Heel on Lassa Virus Glycoprotein to Improve Antibody Therapeutics and Vaccine Design
Kate Hastie, PhD, Instructor, La Jolla Institute for Immunology

Lassa virus causes ~5000 deaths from viral hemorrhagic fever every year in West Africa. The trimeric surface glycoprotein, termed GPC, is critical for infection, is the target for neutralizing antibodies, and is a major component of vaccines. Structural analysis of Lassa GPC bound to antibodies from human survivors reveals a major Achilles heel for the virus and provides the needed template for development of immunotherapeutics and improved vaccines.

5:00 Chemical Liability Analysis of the Therapeutic Antibody Sequence Landscape
Max Vásquez, PhD, Head, Computational Biology, Adimab LLC

Asparagine deamidation and aspartate isomerization are among the most common modes of degradation observed in therapeutic antibodies. Here, we produced 131 mAb samples with sequences from clinical-stage mAbs, subjected these to low and high pH stresses, and identified the resulting modifications at amino acid-level resolution via tryptic peptide mapping. Amassing data across this diverse antibody set enabled us to identify regions and sequence features prone or resistant to chemical modification.

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*
Click here for details.
**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

SAFETY AND EFFICACY PREDICTION

8:15 Chairperson's Remarks
Karl Griswold, PhD, Associate Professor, Engineering, Dartmouth College

8:20 Engineering Molecules with Complex Modes of Action by Improved Understanding of Drug Biology
Hubert Kettenberger, PhD, Senior Principal Scientist, Protein Engineering, Roche, Germany

Next-generation therapeutics often require proteins which can do more than just bind a target, e.g., *in situ* activation, pH-dependent binding, penetration through barriers, etc. This increased complexity makes it difficult to find molecules with exactly the right properties (e.g., activation kinetics) to be fit for purpose. We will present a DOE-type simulation of the envisaged mode of action in order to guide protein engineering towards optimal drug properties.

8:50 Preclinical Risk Assessment Tools to Support Probability of Immunogenicity Risk in the Clinic
Vibha Jawa, PhD, Director, Risk Assessment and Clinical Immunogenicity, Merck

The risk assessment approaches have evolved over the past decade with multiple approaches that rely on both algorithms and cell-based assays. This talk will provide recent advances in several cell-based assay formats to address specific questions around immune modulation, next-generation biologics and gene therapy/cell-based and nucleic acid-based therapies. The questions around antigen processing and the T cell repertoires to react with the biologics will be presented.

Sponsored by ABZENA

9:20 ADCascade: A New Clinically Based Approach for Target Validation, Lead Design and Selection
Mark Frigerio, PhD, VP Design and Development, Abzena
Current focus of ADC development is complex conjugation chemistry. Some ADC are approved and marketed but clinical efficacy and safety concerns continue. A new approach, ADCascade is needed for target validation, lead selection and conjugation chemistry. Augment target validation with clinically characterized tissues to identify patient subgroup of interest. Rational design with augmented with binding studies to clinically characterized off-target.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

LEAD CHARACTERIZATION AND LIABILITY MITIGATION

10:35 Robust Computational Algorithms for *de novo* Design of Functional Proteins
Daniel-Adriano Silva, PhD, Vice President, Head of Research, Neoleukin Therapeutics, Inc.
Neoleukin-2/15 is the first entirely *de novo* protein with biological activity, and it combines the signaling properties of IL-2 and IL-15. Neoleukin 2-15 has been computationally engineered to have optimized therapeutic properties, is thermally hyper-stable, and has higher potency and reduced side effects compared to natural IL-2 or IL-15. We foresee that the technology behind the creation of Neoleukin-2/15 will enable the development of a next generation of protein-based therapeutics optimally engineered to treat disease.

11:05 Quest for Quality Drug: The Application of Early Screening Biophysical Assays to Select Manufacturable Molecules
Sathya Venkataramani, PhD, Associate Director, Biophysics, Janssen Biotherapeutics
One of the major factors that has commonly impacted the success rate of Phase I drugs to progress for FDA approval is poorly behaved molecules. To save cost and to expedite development that will enable a higher success rate, it is undoubtedly critical to characterize the intrinsic properties of molecules early on. This talk is designed to highlight few high-throughput assays and first principle-based biophysical tools to select molecules that are risk-free from manufacturing challenges.

11:35 Preemptive Mitigation of Biotherapeutic Immunogenicity via Optimized Library Design
Karl Griswold, PhD, Associate Professor, Engineering, Dartmouth College
Protein therapeutics can elicit detrimental antidrug antibody responses (ADA) in patients, and the safety and financial ramifications of clinical ADA have begun to prompt earlier consideration of immunogenicity risk during drug development. Here, we describe the use of advanced protein design technologies that enable ensemble "deimmunization" of entire recombinant protein libraries. Our strategy is to mitigate immunogenicity risk during the earliest phase of drug discovery, thereby producing preemptively deimmunized candidates for lead selection.

12:05 pm Session Break

Sponsored by BIOCYTOGEN

12:15 LUNCHEON PRESENTATION: RenMab™ Mouse and *In Vivo* Efficacy-based Solution for Fully Human Antibody Drug Discovery
Benny Yang, Director, Antibody Discovery, Biocytogen

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

LEAD CHARACTERIZATION AND LIABILITY MITIGATION *(Cont.)*

4:00 Chairperson's Remarks
Rajiv Panwar, PhD, Principal Scientist, Magenta Therapeutics

4:05 An *in vitro* Transcytosis Assay for Predicting *in vivo* Clearance of Therapeutic Antibodies in Humans
Chang Liu, PhD, Associate Scientist, BioAnalytical Sciences, Genentech
Proper evaluation of candidate drugs for desirable pharmacokinetic (PK) properties is imperative to successful biotherapeutic development. We have developed an *in vitro* cell-based assay to measure transcytosis of monoclonal antibodies (mAbs), which showed a notable correlation between the transcytosis readouts of more than 50 mAbs and their clearance in humans. This assay may serve as a screening tool for predictive assessment of non-specific clearance of antibody-based drug candidates in humans.

4:35 Selection and Characterization of a Lead Antibody for an Antibody-Drug Conjugate to Achieve Non-Genotoxic Conditioning for Bone Marrow Transplant
Rajiv Panwar, PhD, Principal Scientist and Head, Analytical and Formulation Development, Magenta Therapeutics
Antibody-Drug Conjugates (ADCs) are an emerging class of biotherapeutics that are starting to find applications in areas other than oncology. This talk will focus on selection, characterization and developability analysis of a lead antibody from a panel of molecules obtained from discovery and affinity maturation campaigns. The lead antibody was further engineered and optimized to enable site-specific conjugation of the linker-payload and tuning of Fc-receptor interactions.

IMPROVING THE QUALITY OF DEVELOPABILITY PREDICTION

5:05 Benchmarking to Validate Developability Risk Assessment
Jonathan Kingsbury, PhD, Senior Director, Developability & Preformulation Science, Sanofi
Successful screening of pre-candidate molecules requires reliable, well-characterized developability tests and accurate projection of development risk from the results. Benchmarking against process experience, proof-of-concept datasets, and precedent data provides the context needed to enable valid risk assessments. An overview of the strategy for benchmarking a developability workflow will be described and illustrated with several examples.

5:35 Improved AC-SINS Assay to Remove the Hurdles of Salt Dependency in Formulation Screening
Samantha Phan, Consultant Biologist, Protein BioSciences, Eli Lilly and Company
Affinity-capture self-interaction nanoparticle spectroscopy (AC-SINS) is a high-throughput screening assay to evaluate antibody self-interaction propensity. One challenge has been instability of gold nanoparticles under low salt and incompatibility with histidine-based buffers. We have improved the assay to perform robustly in multiple formulation conditions, including histidine buffer in low salt environment. The optimized assay format further enables the screening of molecules under relevant formulation conditions critical for downstream development.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Lead and Candidate Selection for Therapeutic Proteins Conference

DEEP SEQUENCING AND SINGLE CELL ANALYSIS FOR ANTIBODY DISCOVERY

Best Practices and Technologies for Applying Repertoire Analysis to the Discovery of Therapeutic Proteins

The rapid adoption of deep sequencing and single B cell analysis has given discovery scientists an extraordinary view into human and animal immune repertoires that is now informing all aspects of biopharmaceutical R&D. This dynamic field is bringing together the disciplines of immunology, structural and computational biology, informatics, and microfluidics to offer previously unimaginable perspectives that will drive discovery of the next generation of biologic drugs. PepTalk's 2nd Annual DEEP SEQUENCING AND SINGLE CELL ANALYSIS FOR ANTIBODY DISCOVERY conference explores new science and technology in this field and how these advanced capabilities are being implemented and integrated with platforms, workflows, and traditional discovery methods.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

ANTIBODY DISCOVERY APPLICATIONS

8:10 Organizer's Welcome Remarks
Kent Simmons, Senior Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Vu Truong, PhD, CSO & CEO, R&D, Aridis Pharmaceuticals, Inc.

KEYNOTE PRESENTATION

8:20 Deep Genetic Analysis of Human Antibody Repertoires

Bryan Briney, PhD, Assistant Professor, Immunology and Microbiology, The Scripps Research Institute
Exceptionally deep genetic analysis of antibody repertoires has revolutionized our understanding of humoral responses to infection and immunization. Emerging high-throughput single cell analysis techniques now allows us to link repertoire genetics with cell phenotype, allowing us to study the development and maturation of the antibody repertoire at a scale and depth that has not previously been possible.

9:00 Discovery 2.0: Creating (Almost) Unlimited Diversity Using a Novel Nano-Scale B Cell Culturing System and a High-Throughput Platform for Bispecific Antibody and Format Combinations
Elke Glasmacher, PhD, Head, Immunobiology, Roche, Germany
The applications of standard therapeutic antibodies created with conventional lead generation processes have reached their limitations. Rare epitopes or bispecific combinations in different formats that can find broader applications in various disease areas are urgently needed. We generate maximal diversity to identify truly next-generation biologics using novel high-throughput techniques, including a nano-scale single cell imaging and selection technology and a combinatorial platform to rapidly generate bispecific antibodies in differing formats.

9:30 How to Find What is Rare: Natural Immunity and Antibodies Targeting Complex Membrane Proteins
Marta Szabat, PhD, Project Leader, Abcellera
Antibodies offer significant selectivity advantages over small molecules to target complex membrane proteins. Yet, few have made it to clinic, primarily due to discovery challenges. Over the years, AbCellera has successfully completed several antibody discovery programs targeting GPCRs and ion channels. We will share lessons and insights that were instrumental to those successes, centred on deep screening and a suite of cutting-edge technologies that includes intelligent antigen formats, strategic immunizations, machine learning, and data visualization.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 Deep Sequencing Analysis of Phage Selection Outputs: Leaving Conventional Screening Behind
Stefan Ewert, PhD, Senior Investigator, Novartis Pharma AG, Switzerland
We will show adaptations to library design and panning strategies exploiting the full potential of deep sequencing analysis of phage selection output pools to identify specific and high affine antibodies without conventional screening.

11:30 Advancing Cancer Immunotherapy One Cell at a Time
Navin Varadarajan, PhD, Associate Professor, Chemical and Biomolecular Engineering, University of Houston
The engineering of genetically modified immune cells has enabled unique challenges in the design and manufacture of these products. I will describe single-cell technology platforms and molecular engineering approaches that we have developed to identify the potency of immune cells, and how these are being implemented to improve the efficacy of cancer immunotherapy.

12:00 pm Accelerate Your Drug Discovery with Nicoya's Alto: The World's First Digital, High-Throughput, Benchtop SPR System
Sponsored by nicoya
Ryan Denomme, CEO, Co-Founder, Nicoya
Nicoya believes in empowering scientists. We know how important SPR data is for your next big discovery. That's why we are awarding one accomplished scientist a New Product Grant for a free Alto SPR system. Come by to learn about the world's first fully automated, high-throughput, benchtop SPR system. Enter to win at alto.nicoyalife.com/slas2020/ - limited spots available! You must be present to win. The future of drug discovery is digital. Join the movement.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Screening Broad B Cell Diversity to Accelerate Therapeutic Antibody Lead Candidate Selection Using the Beacon Platform
Sponsored by BERKELEY LIGHTS
Anupam Singhal, PhD, Technology Development, Marketing, Berkeley Lights, Inc.
Antibody discovery against difficult targets is hampered by the lack of available technologies for functional screening of B cell repertoires. The Berkeley Lights' BeaconTM platform enables users to generate large, genetically-diverse hit panels by screening multiple B cell compartments. Lead candidate down-selection is performed in 1 day by performing functional characterization during primary screening. Case studies will highlight how Beacon users are dramatically accelerating development of next-generation antibody therapeutics.

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

RAPID SCREENING AND MACHINE LEARNING

2:15 Chairperson's Remarks
Stefan Ewert, PhD, Senior Investigator, Novartis Pharma AG, Switzerland

2:20 Combining Single Cell TCR Sequencing and Transcriptomics to Discover Tumor-Specific T Cells by Unsupervised Learning
Alexander Yermanos, Researcher, Biosystems Science and Engineering, ETH Zurich, Switzerland
Identifying tumor-reactive T cells from cancer patients would be highly valuable in promoting TCR-based cell therapies. Recent advancements in single cell sequencing (scSeq) technologies have increased the resolution to which we can profile tumor-infiltrating lymphocytes. We thereby performed scSeq of both TCR repertoires and whole transcriptomes of ~9,000 tumor-infiltrating T cells arising from a patient with lung carcinoma. We employed unsupervised learning to identify tumor-specific T cells and tested their specificity to tumor cells.

2:50 NGS-Enabled Synthetic Ab Discovery
Jarrett Adams, PhD, Associate Director, Toronto Recombinant Antibody Center, Canada
Phage-displayed antibody repertoires are powerful resources for the discovery and optimization of therapeutic antibodies. By utilizing Illumina sequencing technologies, we are able to interrogate phage-Fab populations to fully map paratope distributions and rapidly identify rare but functional antibodies with minimal screening. This approach has provided a simple means of minimizing epitope bias from antibody discovery campaigns, while enhancing our ability to target antigens in context of cell.

3:20 Networking Refreshment Break

3:45 Long Read Next-Generation Sequencing and Machine Learning for Antibody Discovery
Andrew R.M. Bradbury, MB BS, PhD, CSO, Specifica, Inc.
Selection of potential antibody leads from display libraries is usually carried out by random colony picking. This approach is biased by dominant clones and explores rare clones inefficiently. We have developed an unsupervised machine-learning approach to PacBio sequencing of selection outputs to maximally explore epitope space to generate highly diverse antibody panels against specific targets.

4:15 High-Throughput Functional Screening of Immune Repertoires
Bob Chen, PhD, Director, Engineering; Co-founder, xCella Biosciences
Here we present xPloration, an innovative drug discovery platform that enables high-throughput and high-content screening of millions of antibody-secreting cells. This image-based micropore array technology is compatible with a wide variety of assay formats, including cell surface binding assays, reporter cell stimulation, and cross-reactivity screening. When combined with single cell sequencing at scale, this platform is enabling deep functional profiling of immune repertoires.

4:45 ANTAEUS: Next-Generation Antibody Discovery and Repertoire Analysis
The ANTAEUS (Antibody Accelerated Engineering by a Universal Selection) platform integrates three major technological innovations in order to enable unprecedented scale, ease and fidelity of functional antibody repertoire interrogation: 1) Our rapid, novel antibody-antigen interaction reporting method, PRIMP; 2) Next-generation barcoding for massively parallel NGS-based data analysis; and 3) A humanized yeast strain capable of reliable population-wide display of native Fab fragments.

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

NEXT-GENERATION APPLICATIONS

9:00 Chairperson's Remarks
Aude Segaliny, PhD, Group Leader, Assay Biology & Scientific Liaison, Amberstone Biosciences

9:05 High-Throughput Interrogation of Cancer Patient Repertoires for Discovery of Anti-Tumor Antibodies
Sean Carroll, PhD, Associate Director, Molecular Biology, Atreca
Patient antibody repertoires can be the source of potent anti-tumor antibodies that bind novel targets. ATRC-101 (Ph1 ETA early 2020) is a recent example of a patient-derived antibody that exhibits potent anti-cancer activity in pre-clinical models. In this presentation, we will demonstrate advances in display-based interrogation of cancer patient antibody repertoires in a target-agnostic manner for the high-throughput discovery of anti-tumor antibodies.

9:35 B Cell Repertoire Screening Using Nanoculture Arrays and Rapid Production of mAb Using Cell Fusion
Vu Truong, PhD, CSO & CEO, R&D, Aridis Pharmaceuticals, Inc.
We developed a nanoculture array that is able to comprehensively screen the B cell repertoire and assess mAb binding at single cell level, and also engineered a fusion partner cell line designed to immortalize the selected B cell, effectively enabling mAb production without the need for a recombinant step.

10:05 Single-Cell Droplet Microfluidics for Discovery of Therapeutic Antibodies
Aude Segaliny, PhD, Group Leader, Assay Biology and Scientific Liaison, Amberstone Biosciences
Discovery of functional antibody leads for therapeutic targets remains challenging. Several bottlenecks of conventional methods prevent users to efficiently and rapidly screen for antibody function, such as screening time, cost and inability to recover precious rare clones. Here, we present case studies to show the power of AmberFlow™ in overcoming those challenges, a cutting-edge microfluidic-based, single-cell platform technology used for discovery of functional antibodies against immunotherapeutic targets.

10:35 Networking Coffee Break

11:00 Continuous Evolution of Affinity Reagents with an Orthogonal Replication System in Yeast
Alon Wellner, PhD, Postdoctoral Research, Biomedical Engineering, University of California, Irvine
We have engineered a system that enables continuous evolution of affinity reagents in yeast. The gene encoding the antibody is orthogonally replicated on a cytoplasmic linear plasmid that has an error rate 100,000x higher than the nuclear DNA. We demonstrated conformationally selective nanobody affinity maturation against the AT1R GPCR. A library of computationally designed CDR3 variants was cloned into the system and allows for discovery and affinity maturation of tight binders against a plethora of antigens without the need for *ex vivo* sequence diversification.

11:30 Bioinformatics Approaches for Analyzing Adaptive Immune Systems through Profiling of Antibody Repertoires with Immunosequencing Data
Yana Safonova, PhD, Postdoctoral Fellow, Computer Science and Engineering Department, University of California San Diego
Rapid development of DNA sequencing technologies opened new avenues for analyzing adaptive immune systems through deep interrogation of antibody repertoires. Recent immunoinformatics studies revealed poorly understood properties of antibody immune response. In this talk, I will show how computational analysis of antibody repertoires can be used in estimating efficacy of vaccines and designing antibody drugs. We will also discuss the future of immunoinformatics as a high-priority direction of personalized medicine.

12:00 pm Conference Wrap-Up

12:30 Close of Conference

ANTIBODY THERAPEUTICS

The weeklong Antibody Therapeutics pipeline reveals the exciting developments in next-generation antibody therapeutics, including Antibody-Drug Conjugates, Bispecific Antibody Therapeutics, and Cancer Immunotherapies. Along with engineering breakthroughs, this pipeline also explores successful R&D strategies, translational case studies, clinical results, and efficacy data for these promising molecules as they seek to conquer cancer and other diseases and promote human health.

January 20-21

AGENDA Engineering Next-Generation Cancer Immunotherapies

January 21-22

AGENDA Antibody-Drug Conjugates

January 23-24

AGENDA Bispecific Antibody Therapeutics

ENGINEERING NEXT-GENERATION CANCER IMMUNOTHERAPIES

New Protein Engineering Science to Support the Development of Novel Immunotherapeutics and Treatment Combinations

Based on the clinical successes of checkpoint inhibitors, the industry is now directing its attention to combination treatments, single agent therapeutics with multiple modes of action, confronting resistance mechanisms, reducing toxicity and the persistent challenge of solid tumors. Cambridge Healthtech Institute's 6th Annual ENGINEERING NEXT-GENERATION CANCER IMMUNOTHERAPIES conference provides a forum in which research scientists can discuss the contributions of protein engineering to the discovery and development of novel biotherapeutics in the IO space.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

DISCOVERY OF IO COMBINATIONS

9:00 Organizer's Welcome Remarks
Kent Simmons, Senior Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Govinda Sharma, PhD, Postdoctoral Fellow, Genome Sciences Center, BC Cancer Research Center, Canada

KEYNOTE PRESENTATION

9:10 Defining T Cell States Associated with Response to Combination Immunotherapy

Shahram Salek-Ardakani, PhD, Senior Director, Cancer Immunology Discovery, Pfizer
It has remained unclear how simultaneous blockade of PD-1 and costimulation of OX40 and 4-1BB receptors synergize for potent T cell-driven anti-tumor efficacy. Using high-dimensional analysis, we examined the dynamics of effector CD4 and CD8 T cell responses in the tumor microenvironment (TME) in response to anti-PD-1/OX40/4-1BB treatment. Our findings provide insight into T cell states and biomarkers that underlie the synergy between OX40/4-1BB agonism and PD-1 blockade.

9:50 Enhancing Tumor-Targeting Antibodies through CD27 Immunostimulation
Sean H. Lim, MBChB, PhD, Associate Professor, Haematological Oncology, Center for Cancer Immunology, University of Southampton, United Kingdom
Agonistic antibodies, such as those against the TNFR superfamily member, CD27, can be used to enhance the anti-tumor efficacy of direct targeting antibodies through bystander myeloid cell activation. Here, we will present our recent data on the factors that govern the potency of CD27 agonistic antibodies.

10:20 Networking Coffee Break

ENGINEERING CONSIDERATIONS FOR NEW IO MODALITIES

10:45 Engaging Multiple T Cell Targets with Bispecific Antibodies for Selective Immune Stimulation in the Tumor Microenvironment
Michael Hedvat, PhD, Group Leader, Cell Biology, Xencor
The XmAb® bispecific platform has enabled clinical development of TIL-targeting agents, including XmAb20717 (combining PD1 and CTLA4 blockade), XmAb22841 (CTLA4 and LAG3 blockade), and XmAb23104 (PD1 blockade with ICOS agonism). Xencor has also engineered an IL15/IL15Rα-Fc complex to create the clinical candidate, XmAb24306, thus establishing a tunable format for rapid generation of targeted immune activators. I will also discuss development of a TME-directed IL-15 achieved via coupling to an anti-PD1-moiety.

11:15 Directing T Cell Phenotype and Metabolism during Large-Scale Expansion
Kathryn Henckels, PhD, Senior Scientist, Process Development, Amgen
T cell therapy involves treating patients with live T cells engineered to recognize tumor-specific antigens. Efficacy depends on persistence, which is mainly driven by T cell phenotype; an effector cell will quickly become exhausted, whereas a stem cell memory T cell-type can survive for months or years. A manufacturing process that controls the differentiation of T cells throughout the expansion process will result in a final product that is more efficacious.

11:45 Rapid Selection and Identification of Functional CD8+ T Cell Epitopes from Large Peptide-Coding Libraries
Govinda Sharma, PhD, Postdoctoral Fellow, Genome Sciences Center, BC Cancer Research Center, Canada
We have developed a novel methodology for high-throughput, function-based T cell epitope profiling that is capable of identifying T cell antigens from libraries of peptide-coding sequences much larger than would be feasibly tractable using conventional plate-based assays. Currently, we are mobilizing this technology towards performing unbiased neoantigen screenings for discovering novel targets of T cell immunotherapy and for assessing potential off-target cross-reactivity of designer TCR therapeutics.

Sponsored by Benchling

12:15 pm Centralize, Standardize and Automate Antibody and Cell Therapy R&D Data
Wendy Ochoa, PhD, Scientific Solutions Consultant, Benchling
Benchling is a biologics-native informatics platform used by over 180,000 scientists to configure biologics workflows and run day-to-day R&D. This presentation will highlight how Benchling has helped leading antibody and cell therapy R&D organizations to centralize, standardize and automate their R&D data.

12:30 Sponsored Presentation *(Opportunity Available)*

12:45 Session Break

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

TUMOR SPECIFICITY AND REGIONAL DELIVERY

2:00 Chairperson's Remarks
Mitchell Ho, PhD, Senior Investigator, National Cancer Institute, NIH

2:05 A Coiled-Coil Masking Domain for Selective Activation of Therapeutic Antibodies
Matthew Levengood, PhD, Principal Scientist, Protein Sciences, Seattle Genetics
To enhance the selectivity of monoclonal antibodies for tumors over healthy tissues, we have developed an antibody masking system that utilizes coiled-coil peptide domains to sterically impede antigen binding. On exposure to tumor-associated proteases, the coiled-coil domains can be cleaved and antibody function restored. The coiled-coil domain is a generalizable approach for antibody masking that results in antibody therapeutics with improved circulation half-lives, minimized systemic effects, and improved tumor targeting.

2:35 Novel Antibody Engineering to Improve the Therapeutic Index of Solid Tumor-Targeting Antibodies
Hitoshi Katada, PhD, Research Scientist, Biologics Discovery, Chugai Pharmaceutical Co., Ltd., Japan
One of the remaining issues of antibody therapeutics is on-target, off-tumor toxicity induced by binding to target antigens expressed in normal tissues. To overcome this problem, we have established novel antibody engineering to enable antibody binding to the antigen selectively at tumor site, but not at normal tissues.

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.

Click here for details.

ENGINEERING CHALLENGES FOR NOVEL CAR T CONFIGURATIONS AND COMBINATIONS

4:30 GPC3 as a CAR T Cell Therapy Target in Cancer
Mitchell Ho, PhD, Senior Investigator, National Cancer Institute, NIH
In the past decade, we have studied the role of glypican-3 (GPC3) as a therapeutic target in hepatocellular carcinoma. We have created new CAR T cells based on our antibodies that are specific for the N-lobe and C-lobe of GPC3 and tested them in mice. Using single cell-based analysis, we have identified a small subset of polyfunctional T cells that exhibit highly persistent T cell expansion in the tumor microenvironment.

5:00 Expanding the Functionality of CAR T Cells Through Meditope Engineering
Christine Brown, Ph.D., Professor Hem/HCT; Deputy Director, T Cell Therapeutics Research Laboratories, Beckman Research Institute, City of Hope

CAR T cell therapy has shown clinical success against hematological malignancies, nevertheless frequently accompanied by diverse adverse events. To enhance the safety profile of CAR-T therapy, we developed a conditionally-activatable, single-module CAR architecture, in which the cytotoxicity is specifically modulated by a small-molecule drug. The resulting CAR-Ts demonstrated specific cytotoxicity of tumor cells comparable to a traditional CAR, but the cytotoxicity could be reversibly attenuated by the addition of the small-molecule.

5:30 Use of CD19-Directed CAR T Cells to Kill Any Tumor
Roy Lobb, PhD, Director and Cofounder, Aleta Biotherapeutics
We reprogram CAR T cells to CD19 (CAR19s) to kill any heme or solid tumor, using CD19 fused to an antibody fragment. Such CD19-binding proteins (CD19-BPs) can 'coat' any tumor and direct CAR19-dependent cytotoxicity while targeting two or more antigens with potency and selectivity. By placing the CD19-BPs within the CAR19 itself, the CAR19s secrete the CD19-BPs locally, providing 'on-demand' tumor killing combined with inherent long-term persistence.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

TARGETING THE TUMOR MICROENVIRONMENT WITH THERAPEUTIC PROTEINS

8:45 Chairperson's Remarks
Traian Sulea, PhD, Principal Research Officer, Human Health Therapeutics, National Research Council Canada

8:50 Reengineering the Physical Microenvironment of Tumors to Improve Treatment Response
Lance L. Munn, PhD, Associate Professor, Department of Radiation Oncology, Massachusetts General Hospital
As tumors grow in a confined space, fibrosis and unchecked proliferation result in a highly abnormal physical microenvironment. Tumor mechanopathologies, including increased tissue stiffness and accumulation of solid stresses, fuel tumor progression and treatment resistance by altering extracellular matrix (ECM) production and blood flow. Reengineering the tumor microenvironment to normalize the tumor vasculature and ECM can improve treatment and is already showing promise in the clinic.

9:20 Engineering pH-Dependent Antibody Binding for Selective Targeting of Solid Tumors
Traian Sulea, PhD, Principal Research Officer, Human Health Therapeutics, National Research Council Canada
Development of monoclonal antibodies as anti-cancer agents requires further optimization of their safety for use in humans. Among the optimization avenues for specific tumor targeting is the slightly higher acidity of solid tumors relative to normal tissues. A structure-based computational approach was applied here to engineer antibody fragments with selective binding in acidic environments relative to physiological pH. Designed, full-size antibodies exhibit binding selectivity between tumor and normal cell models.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 Exploiting the ECM as a Therapeutic Target in Disease
Noor Jailkhani, PhD, Postdoctoral Research Scientist, Koch Institute for Integrative Cancer Research, MIT
To exploit the ECM as an imaging and therapeutic target, we developed recombinant single domain antibodies called "nanobodies" against disease-associated ECM proteins. We demonstrated their specificity for tumors, metastatic sites and early lesions by immuno-PET/CT imaging in multiple models of cancer. Their properties make nanobodies promising candidates for therapeutic applications and we showed that nanobody-based CAR T cells were able to inhibit the growth of solid tumors.

11:30 Epitope and Fc-Mediated Cross-Linking are Critical for MoA of 4-1BB Antibodies: Anti-Tumor Efficacy vs. Liver Toxicity
Hamsell Alvarez, PhD, Principal Research Scientist, Immuno-Oncology Discovery, AbbVie
4-1BB agonist antibodies have demonstrated potent anti-tumor activity, but cause severe hepatotoxicity in mouse models. We identified a new class of 4-1BB antibodies that bind unique epitopes, retain anti-tumor efficacy, and result in significantly less liver toxicity. T cell costimulation activity only occurs when these antibodies are crosslinked, and anti-tumor efficacy was lost in FcγRIIB-deficient mice. This highlights the importance of epitope and isotype selection and suggests that 4-1BB biotherapeutics with improved safety profiles can be developed.

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

12:30 Session Break

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

1:10 Close of Engineering Next-Generation Cancer Immunotherapies Conference

JANUARY 21-22, 2020 | 7TH ANNUAL

ANTIBODY-DRUG CONJUGATES

Next-Gen Engineering

Antibody-Drug Conjugates have demonstrated their ability to deliver cytotoxic small-molecule drugs through a selective and targeted mechanism in the fight against cancer. In recent years, ADCs have entered almost 600 clinical trials with more than 60 distinct ADC molecules currently under development. Despite the enormous promise, a low therapeutic index has plagued ADC development, particularly for treating solid tumors.

Cambridge Healthtech Institute's ANTIBODY-DRUG CONJUGATES conference explores the engineering finesse required to achieve the crucial balance between efficacy and safety, thus leading the way to more potent and targeted molecules. Case studies and data will be shared that illustrate the ongoing efforts to engineer ADCs, move them into the clinic, and conquer cancer.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

THE PROMISE OF ADCs AND LESSONS LEARNED

2:00 Chairperson's Opening Remarks
Ian Schwartz, MS, Global Technology Consultant, Bioconjugation, Sartorius Stedim North America, Inc.

KEYNOTE PRESENTATION

2:05 Learnings from Successes and Failures of ADCs and Cancer Immunotherapies

Rakesh Dixit, PhD, DABT, President & CEO, Bionavigen, LLC

Learning from failures & enabling innovations in ADCs and immunotherapies to fight against deadly cancers; what are common features among clinically successful ADCs and immunotherapies? What went wrong with some clinically unsuccessful ADCs? Why have some immunotherapies failed? Top five lessons learned from the development of ADCs and immunotherapies in the last two decades; next-generation ADCs and immunotherapies meeting the five rights; combination of immunotherapies and ADCs: a new frontier in the fight against cancers.

2:45 Antibody-Drug Conjugates: Progress, Pitfalls, and Promises
Mark Glassy, PhD, Chairman, Nascent Biotech, Inc.

Antibody-drug conjugates (ADCs) represent a promising and an efficient strategy for targeted cancer therapy. The therapeutic success of future ADCs is dependent on adherence to key requirements of their design and careful selection of the target antigen on cancer cells. The main components in the design of antibody-drug conjugates, improvements made, and lessons learned over two decades of research are discussed.

3:15 ADC Bioanalysis in Support of Exposure-Response (E-R) Relationships for ADC Clinical Development
Leo Kirkovsky, PhD, Director, Clinical Assay Group, Global Clinical Pharmacology, Pfizer, La Jolla

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

ADC DEVELOPMENT STRATEGIES

FEATURED PRESENTATION

4:30 Exploring the Bioanalytical Strategy for ADCs
Edit Tarcsa, PhD, Director and Research Fellow, Drug Metabolism & Pharmacokinetics, Abbvie Bioresearch Center, AbbVie

ADCs are complex therapeutic modalities with the possibility of forming multiple analytes *in vivo*. A wide variety of assays on multiple analytical platforms has been utilized for their characterization. How does one choose what is appropriate for decision making at the various project stages while balancing speed, quality, and reagent availability? A few case studies with bioanalytical decision trees will illustrate the issues and solutions.

5:00 Novel Approaches to Modeling Preclinical Activity of ADCs and Informing Biomarker Strategy
Tony D'Alessio, PhD, Senior Research Investigator, Oncology Biotherapeutics, Novartis Institutes for Biomedical Research

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*

Click here for details.

**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

ADCs FOR CANCER THERAPY

8:15 Chairperson's Remarks
Edit Tarcsa, PhD, Director and Research Fellow, Drug Metabolism & Pharmacokinetics, Abbvie Bioresearch Center, AbbVie

8:20 Antibody-Drug Conjugates for Immunology (iADC)
Adrian Hobson, PhD, Research Fellow, Global Biologics – Antibody Drug Conjugates, AbbVie Bioresearch Center, AbbVie

Antibody-Drug Conjugates (ADC) combine the targeting of an antibody with the potency of a small molecule. Pioneered for oncology, there are 4 marketed oncology antibody-drug conjugates (oADC) and many in clinical development. This talk will describe the technology behind oADCs, then the efficacy and safety challenges faced when modifying these novel therapeutic agents for immunology to enable an immunology antibody-drug conjugate (iADC) to progress to the clinic.

8:50 Amanitin-Based Antibody-Drug Conjugates as New Therapeutic Modalities for Cancer Therapy
Stephanie Voss, PhD, Group Leader, Bioconjugation & Protein Chemistry, Heidelberg Pharma Research GmbH

Antigen-Targeted Amanitin-Conjugates (ATACs) represent a new class of ADCs using the payload Amanitin. This payload introduces a novel mode of action into oncology therapy, the inhibition of RNA polymerase II. The technology platform includes Amanitin supply, site-specific conjugation, demonstrated safety profile and biomarker. HDP-101 is the first ATAC directed against BCMA entering Phase I trials by the end of 2019.

9:20 Developing Site-Specifically Modified ADCs using a Chemoenzymatic Approach
David Rabuka, PhD, CEO and President, Acrigen Biosciences, Inc.

We will present recent data on our SMARTagTM technology platform and its application to generating novel bioconjugates,

including ADCs, utilizing our new conjugation chemistries and linkers. The application of these chemistries to the generate site-specifically modified bioconjugates with improved efficacy against numerous targets and safety profiles will be presented. Additionally, we will highlight progress in developing conjugates with a focus on preclinical studies as well as highlight our progress with the SMARTagTM technology in the clinic.ADCs Targeting the Urokinase Receptor (uPAR) as a Possible Treatment of Aggressive Breast Cancer

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

TARGETING TUMORS IN THE FIGHT AGAINST CANCER

10:35 Peptide Nucleic Acid (PNA)-Mediated Pretargeting for Radionuclide Therapy
Amelie Eriksson Karlström, PhD, Professor, Protein Sciences, Engineering Sciences in Chemistry, Biotechnology and Health, KTH Royal Institute of Technology
Radioimmunotherapy utilizes tumor-specific radiolabeled antibodies to deliver cytotoxic radiation to tumor cells. To avoid unwanted exposure of non-tumor organs, we use pretargeting to uncouple the tumor-targeting step from the delivery of the toxic radionuclide. We have developed and evaluated a system for pretargeting based on the high selectivity and high affinity of PNA:PNA (peptide nucleic acid) hybridization. The primary agent is administered first, and the secondary, radiolabeled agent is administered after the primary agent has accumulated in the tumor and cleared from non-tumor tissue.

11:05 Probody Therapeutics in the Treatment of Cancer
Siew Schleyer, PhD, Director, Oncology Research, CytomX Therapeutics, Inc.
ProbodyTM therapeutics are fully recombinant antibody-based prodrugs designed to remain largely inactive in circulation until proteolytically activated in the tumor microenvironment. They are designed to protect normal tissues while increasing the concentration of active antibody in tumors, thus widening the therapeutic index. Probody technology can be applied to multiple antibody-based therapies. Examples will include probodies based on checkpoint inhibitor antibodies, T cell-engaging bispecifics, and will focus on antibody-drug conjugates.

11:35 SELECTED POSTER PRESENTATION
A Different "ADC": Albumin-Drug Conjugates with Controlled Loading for Improved Antitumor Efficacy
Debadyuti Rana Ghosh, PhD, Assistant Professor, Molecular Pharmaceutics & Drug Delivery, University of Texas at Austin

12:05 pm Session Break

12:15 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

BREAKTHROUGH ENGINEERING & DESIGN

4:00 Chairperson's Remarks
Jonathan van Dyck, Scientist, Analytical Sciences, Seattle Genetics

4:05 Antibody-Drug Conjugates as Targeted Conditioning Agents for Bone Marrow Transplant Patients
Bradley Pearse, PhD, Director, Biotherapeutics, Magenta Therapeutics
Current regimens for patient preparation, or conditioning, prior to bone marrow transplant in malignant and non-malignant settings are non-selective and toxic, limiting the use of this curative procedure due to regimen-related morbidities and mortality. To address this, we developed antibody-drug conjugates (ADCs) that specifically deplete recipient target cell populations to enable robust donor cell engraftment. Thus, ADCs may enable curative treatment through safer and targeted conditioning prior to transplant.

4:35 Characterizing Antibody-Drug Conjugate CQAs Considering Multiple Mechanisms of Action
Jonathan van Dyck, Scientist, Analytical Sciences, Seattle Genetics
Defining and understanding the critical quality attributes (CQAs) of antibody-drug conjugates (ADCs) is a necessary and integral part of product development. This assessment is more complex when multiple mechanisms of action (MOA) are present, since quality attributes that impact safety and efficacy must be understood within the context of each MOA. Typically, ADCs are understood to act through cellular delivery of a cytotoxic small molecule payload via specific antibody/antigen interactions. However, additional MOAs driven by antibody effector function, such as ADCC and ADCP, may be present and quality attributes that influence them should be well understood and characterized. Here we present results from experiments to characterize how drug-load and N-glycan product variants impact the effector function and overall MOA of MMAE conjugates.

5:05 Identification of Engineered Methionines and Oxaziridines for Antibody-Drug Conjugates
Susanna Elledge, MSc, Scientist, Chemistry and Chemical Biology, University of California, San Francisco (UCSF)
In this presentation, we will discuss the systematic scan of methionines throughout the trastuzumab antibody scaffold for a new kind of site-specific antibody engineering and drug conjugation. We will describe how expression, labeling, and stability varied at each methionine site and discuss *in vitro* and *in vivo* potency of methionine-based antibody-drug conjugates.

5:35 Improved Tumor Growth Inhibition of Diabody-Drug Conjugates Achieved by Half-Life Extension
Qing Li, PhD, Scientist, Antibody Discovery & Protein Engineering, AstraZeneca
Half-life extension technologies, such as PEGylation and albumin-binding domains (ABDs), have been widely used to improve the pharmacokinetics of many different types of biologics. In this study, we used an anti-5T4 diabody conjugated with a highly potent cytotoxic pyrrolobenzodiazepine (PBD) warhead to assess and compare the effects of PEGylation and albumin binding on the *in vivo* efficacy of antibody fragment drug conjugates.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Antibody-Drug Conjugates Conference

BISPECIFIC ANTIBODY THERAPEUTICS

Combination Therapy & Engineering Multi-Specificity

Cambridge Healthtech Institute's BISPECIFIC ANTIBODY THERAPEUTICS conference explores the challenges of engineering multi-specificity to achieve more effective therapies that bind to at least two targets simultaneously. The conference examines how these molecules are used to fight a wide array of diseases, as well as in combination therapy for enhanced effects in the fight against cancer. Along with increased efficacy, Bispecific Antibody Therapeutics can also optimize expenses by reducing the cost of development and clinical trials. Case studies highlight novel engineering approaches and platform constructs that improve safety, stability, enhanced targeting, and manufacturability.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

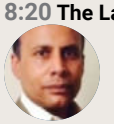
FULFILLING THE PROMISE OF MULTI-SPECIFIC ANTIBODY THERAPEUTICS

8:10 Organizer's Welcome Remarks
Mary Ruberry, MA, Senior Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Steffen Goletz, PhD, Professor and Deputy Head, Biotechnology and Biomedicine, and Vice Director, Institute of Bioengineering, Technical University of Denmark

KEYNOTE PRESENTATION

8:20 The Landscape of Multi-Specific Antibodies



Partha S. Chowdhury, Senior Director, Biologics Research, Sanofi Genzyme

Etiology and progression of diseases usually involves an intricate interplay of a number of molecular entities. Targeting and modulating activities of two or more of these molecules or homing an effector component, such as a cell to the disease site or bridging two components in the pathologic site, serves an important therapeutic mechanism of action (MOA). This talk will be a synopsis of the different designs and their associated biological MOA.

FEATURED PRESENTATION

9:00 Bispecific Antibodies: Combinatorial and Activatable Functionalities
Ulrich Brinkmann, PhD, Expert Scientist and Scientific Director, Roche Pharma Research & Early Development, Roche Innovation Center Munich

9:30 Dealing with the Combinatorial Complexity of Protein Engineering: Bi- and Multi-specifics, TCRs and CAR Ts
Sebastian Kolinko, PhD, Scientific Consultant, Biologics, Genedata

We present a new technology platform to fully automate both molecular design, as well as the integrated assessment of potency, efficacy, and developability profiling of large panels of bispecific candidates. We will present use cases showing how the platform allows for the systematic cloning, expression, purification, and characterization of complex multi-specific, CAR T and TCR modalities, with a focus on immuno-oncology applications.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

NEXT-GEN ENGINEERING & DESIGN

11:00 Maximizing Therapeutic Potential of Bispecific Antibodies and Cytokines by Affinity and Avidity Engineering
David E. Szymkowski, PhD, Vice President, Cell Biology, Xencor, Inc.

New immunotherapeutic modalities, such as T cell-engaging, tumor-targeted bispecific antibodies, T cell-activating cytokines, and checkpoint blockers are rapidly changing the cancer treatment paradigm. However, an unintended consequence of these biologics' high potency is a suboptimal therapeutic index due to immune-related adverse events (irAEs). I will discuss case studies showing that next-generation immunotherapeutics can be engineered by affinity- and avidity-tuning to improve efficacy while reducing irAEs, thereby increasing their therapeutic index.

11:30 Benchmarking T Cell-Redirecting Therapies for Cancer: Comparing CD3-Bispecifics and CAR T Cells
Thomas Craig Meagher, PhD, Senior Research Scientist, Regeneron Pharmaceuticals, Inc.

The two leading platforms for redirecting a patient's T cells to recognize tumors, CD3-binding bispecific molecules and chimeric antigen receptor (CAR) T cells, both show clinical activity. We have developed pre-clinical *in vitro* and *in vivo* models to mechanistically compare these two technologies and will discuss our findings, as well as the clinical implications.

Sponsored by

12:00 pm Development of "Imbalanced" CD3-bispecific Antibody with Balanced Safety, Efficacy and Developability
Yue Liu, CEO, Ab Studio, Inc.

Applying computer aided antibody design (CAAD), we were able to develop novel IgG like CD3-BsAbs with "imbalanced" binding to cancer and T cell and balanced safety, efficacy and developability *in vitro* and *in vivo*. One case study, a CD20/CD3 "imbalanced" BsAb (ABS BsAb), served as a proof of concept.

12:15 Sponsored Presentation *(Opportunity Available)*

12:30 Session Break

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

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

T CELL-ENGAGING BISPECIFICS

2:15 Chairperson's Remarks
Thomas Craig Meagher, PhD, Senior Research Scientist, Regeneron Pharmaceuticals, Inc.

2:20 Advancing a Novel T Cell-Engaging Bispecific Antibody that Induces Lysis of Small Cell Lung Cancer Cells *in vitro* and Shows Potent T Cell-Redirected Anti-Tumor Activity *in Vivo*
Justin Scheer, PhD, Director, Antibody Engineering, Boehringer Ingelheim

2:50 Novel Insights into T Cell-Redirected Killing of Tumor Cells
Stephen Demarest, PhD, Senior Research Fellow, Lilly Biotechnology Center, Eli Lilly and Company

Using computational modeling and protein engineering, we generated novel agents to redirect T cells to fight cancer. We created a novel platform for robust production of these novel agents and demonstrate interesting novel geometrical constraints for redirected lysis.

3:20 Networking Refreshment Break

FIGHTING CANCER WITH MULTI-SPECIFIC ANTIBODIES

3:45 Engineered Multi-Specific Antibodies for Targeted Inhibition of Cancer Metastasis
Jamie B. Spangler, PhD, Assistant Professor, Biomedical Engineering and Chemical & Biomolecular Engineering, Whiting School of Engineering, Johns Hopkins University
Metastasis is responsible for 90% of all cancer-related deaths, yet current anti-cancer therapies are designed to inhibit growth of the primary tumor and fail to address or sometimes even exacerbate metastasis. We leverage our recent discovery of a biochemical pathway that drives tumor cell migration to engineer multi-specific antibodies that potently block metastasis. This new approach presents an exciting opportunity for targeted therapeutic design that synergizes with current anti-cancer therapies.

4:15 Modulating the Immune System with Multi-Specific Antibodies in Cancer
Nathan Trinklein, PhD, Chief Technology Officer, TeneoBio, Inc.
Using a unique sequence-based discovery approach, we have created a large collection of fully human antibodies targeting a variety of tumor antigens and activating receptors on immune cells. Using machine learning tools, we rapidly establish sequence-activity relationships and identify key residues and variable region positions in the antibody repertoire with desired agonist behavior. Our lead program, TNB383B (BCMAxCD3) is currently in phase 1 clinical studies. In summary, we have created a platform for tunable immune activation at the site of the tumor that works with a variety of tumor antigens.

4:45 Revision of RTK Tumor Targeting: How to Design Truly Potent Bispecific and Biparatopic Agents
Rastislav Tamaskovic, PhD, Head, TCL Tumor Targeting, Biochemistry, University of Zurich
Due to adaptiveness of oncogenic networks, tumors driven by hyperactivated RTK receptors readily develop resistance against targeted therapies. We developed multivalent chimeric vehicles devoid of toxic payloads, which achieve their tumoricidal activity by trapping tumor-driving receptor tyrosine kinases in inactive conformations and/or supramolecular assemblies. Using analogous construction scheme, we build a new platform for tumor RTK fingerprinting aimed at identification of prospective therapeutic leads or truly synergistic combination therapies.

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

PLATFORM TECHNOLOGIES

9:00 Chairperson's Remarks
David E. Szymkowski, PhD, Vice President, Cell Biology, Xencor, Inc.

9:05 Utility of the ADAPTIR Platform to Build Stable, Bispecific Proteins with Novel Mechanisms of Action
David Bienvenue, PhD, Senior Director, Protein Sciences, Aptevo Therapeutics
The ADAPTIR™ bispecific platform offers key advantages due to its flexible and modular nature. Preclinically, potent biological activity has been demonstrated with ADAPTIR bispecifics designed to engage the immune system via several different mechanisms while retaining antibody-like manufacturing characteristics. An update on advanced preclinical and clinical bispecific candidates will be covered. The presentation will include a discussion of developability criteria to consider during the selection and development of bispecific antibodies.

9:35 CB213: A Second-Generation Checkpoint Inhibitor Optimally Configured for Therapeutic Efficacy
James Legg, PhD, Senior Vice President, Research, Crescendo Biologics, Ltd.
Crescendo has a proprietary transgenic mouse platform for generation of fully human VH domains (Humabody VH). The talk will describe the identification and characterisation of CB213, a tetravalent, trispecific therapeutic delivering dual checkpoint blockade through dual inhibition of PD-1 and Lag3.

10:05 Targeted and Conditional Biologics
Wendy Ritacco, MSc, Senior Scientist III, Global Biologics, AbbVie
Targeted and locally activated biologics, such as the bi-specific conditional dual variable domain immunoglobulins (cDVD-Igs), offer new opportunities for engineering efficacy while sparing systemic side effects. We will describe preclinical examples of tissue targeting in normal and disease *in vivo* models as part of a new generation of locally acting "regio-specific" biologics therapies.

10:35 Networking Coffee Break

ENGINEERING BREAKTHROUGHS

11:00 Development of NM21-1480, a Trispecific Anti-PD-L1x4-1BBxhSA Antibody Fragment
Timothy Egan, PhD, Vice President, Business Development, Numab Therapeutics AG
NM21-1480 is a molecule that potently blocks PD-L1/PD-1 signaling and elicits T cell activation through its costimulatory domain solely in the proximity of cells that overexpress PD-L1. Preclinical data show efficacy on tumor growth in combination with an enhanced intratumoral CD8+ T cell activation when compared to the combination of the PD-L1 and 4-1BB modalities. Next to NM21-1480, Numab advances several immune-modulatory products targeting specific tumor antigens based on its proprietary antibody fragment technology.

11:30 Engineering Multi-Specific Antibodies Leveraging Patients' Active B Cell Responses
Shaun Lippow, PhD, Director, Protein Engineering, Atreca, Inc.
Atreca discovers novel cancer-specific targets and native human antibodies to those targets, through examination of the active B cell responses of cancer patients. Antibodies that specifically bind non-autologous human tumor are advanced through our drug discovery pipeline, including standard IgG formats and next-generation multi-specifics. I will discuss our selection of multi-specific formats for cell engagement and the engineering of potent anti-tumor molecules.

12:00 pm Conference Wrap-Up
Steffen Goletz, PhD, Professor and Deputy Head, Biotechnology and Biomedicine, and Vice Director, Institute of Bioengineering, Technical University of Denmark

12:30 Close of Conference

CELL & GENE THERAPIES

The inaugural Cell & Gene Therapies pipeline features three back-to-back conferences exploring the challenges, advances, and opportunities in gene and cell therapies. The conferences on Vector Design and Development for Gene and Cell Therapies, Gene Therapy Analytics and Manufacturing, and Cell Therapy Analytics and Manufacturing will discuss critical and hot topics like engineering and development of safer and more efficacious vectors, CMC and characterization, manufacturing, scale-up, next-generation production technologies, automation, supply chain, commercialization, and many more practical issues for the success of cell and gene therapies.

January 20-21

AGENDA Vector Design and Development for Gene and Cell Therapies

January 21-22

AGENDA Gene Therapy Analytics and Manufacturing

January 23-24

AGENDA Cell Therapy Analytics and Manufacturing

JANUARY 20-21, 2020 | INAUGURAL

VECTOR DESIGN AND DEVELOPMENT FOR GENE AND CELL THERAPIES

Engineering Safer and More Efficacious Vectors

The recent success in gene and cell therapies has necessitated a resurgence in vector engineering. Research and development efforts focusing on vectors to combine low genotoxicity and immunogenicity with efficient delivery have shown promise. However, numerous delivery challenges must be overcome, including developing techniques to evade preexisting immunity to ensure more efficient transduction of therapeutically relevant cell types, to target delivery, and to ensure genomic maintenance. Cambridge Healthtech Institute's Inaugural VECTOR DESIGN AND DEVELOPMENT FOR GENE AND CELL THERAPIES conference convenes clinicians, along with engineers and a variety of scientists from biotech and pharma companies, who are driving the advancement of gene and cell therapies into the clinic.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

rAAVs

9:00 Organizer's Welcome Remarks
Mary Ann Brown, Executive Director, Conferences & Team Lead, PepTalk, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Christopher Tipper, PhD, Vice President of Discovery, Touchdown Therapeutics

KEYNOTE PRESENTATION

9:10 Adeno-Associated Virus-Based *in vivo* Gene Therapy: Capsid Discovery, Therapeutic Payload Design, and Product Characterization

Guangping Gao, PhD, Co-Director, Li Weibo Institute for Rare Diseases Research; Director, Horae Gene Therapy Center and Viral Vector Core; Professor, Microbiology and Physiological Systems, University of Massachusetts Medical School

Since the first proof-of-concept human application in the early 90's, the field of Gene Therapy has now entered a stage of unprecedented revolution for clinical translation and commercialization. The progress of human gene therapy has been primarily driven by vector platform technologies. This presentation will focus on AAV *in vivo* gene therapy, showcasing capsid discovery and engineering, therapeutic gene expression cassette design and optimization, and preclinical and clinical evaluations.

9:50 The Development of Recombinant Adeno-Associated Virus/Human Bocavirus Vector Production System
Ziying Yan, PhD, Research Associate Professor, Department of Anatomy and Cell Biology, The University of Iowa

Recombinant adeno-associated virus vector (rAAV) has low tropism for airways, while Human bocavirus 1 (HBoV1) naturally infects the human respiratory tract. Cross-genera packaging of the rAAV2 genome into the HBoV1 capsid created a hybrid parvoviral vector rAAV2/HBoV1, which is highly tropic for human airways with an increased packaging capacity of up to 5.8 kb. Understanding the transcriptions of HBoV1 proteins facilitated the development of an efficient rAAV2/HBoV1 production system.

10:20 Networking Coffee Break

10:45 Multiplex and Clonal Assessment of Production Yield of *in silico* Designed AncAAVs
Christopher Tipper, PhD, Vice President of Discovery, Touchdown Therapeutics

DNA barcoding and terabyte-depth NGS have enabled the ability to track and contrast the basic behavior of multiple AAV capsids in a single experiment. Our rationally designed libraries, combined with the multiparametric data generated from our NGS process, drive us to develop tools that allow us to discover optimal vectors for patient and industry issues, such as targeting and manufacturability. Recent results from our platform around manufacturability will be discussed.

11:15 Strategies for Engineering Adeno-Associated Virus Capsids with Novel Properties
Andrew Mercer, PhD, Principal Scientist, Gene Transfer Technologies, REGENXBIO

Recombinant Adeno-associated virus (rAAV) has proven to be a safe and efficacious option for gene therapy. Despite success in gene transfer in numerous animal models, clinical trials, and more recently in approved therapeutics, none of the currently described rAAV serotypes display tropism and infectivity for all possible applications. To overcome these limitations, we are interrogating AAV capsids from nature, attempting rational engineering based on structure-function relationships, and using directed evolution to create the next generation of rAAV vectors.

11:45 High-Throughput Screening of Adenovirus Infectivity for Accelerated Development
Annicka Evans, PhD, Scientist I, Analytical Development, Gene Therapy, Biogen

Adenovirus (Ad) is commonly used as a helper to produce Adeno-associated Virus (AAV)-based vectors for gene therapy. Throughout optimization of upstream and downstream processes associated with Ad-dependent AAV production, large numbers of samples will need to be tested for Ad presence and infectivity. Here we will present and discuss our screening method that allows for higher sample throughput and analytical efficiency than gold standard methods.

12:15 pm Sponsored Presentation *(Opportunity Available)*

12:45 Session Break

Sponsored by charles river

12:55-1:25 LUNCHEON PRESENTATION: Considerations in the Use of Analytical Ultracentrifugation for Characterization of AAV Gene Delivery Vectors
Christopher Sucato, PhD, Associate Director, Biophsical Characterization, Charles River

Analytical Ultracentrifugation (AUC) in the biopharmaceutical industry has traditionally been employed in the analysis of aggregation and higher order structure in protein drug products. More recently, gene delivery vectors have opened new avenues for AUC-based characterization and QC lot release methodologies. We discuss here the parameters of an AUC method which conform to the objectives of an ICH/cGMP validation, and suggest gap-bridging strategies to maintain a high-quality AUC platform for use in AAV programs.

EXPLORING GENE THERAPIES

2:00 Chairperson's Remarks
Douglas Jolly, PhD, Executive Vice President, Research & Pharmaceutical Development, Tocagen, Inc.

2:05 Dual AAV Vectors for Inner Ear Delivery of Large Genes
Tyler Gibson, PhD, Scientist II, Decibel Therapeutics

Genetic causes of hearing loss offer an ideal indication for gene therapy. However, the inner ear has a disproportionately high number of large genes that exceed the 4.7 kb carrying capacity of

standard adeno-associated viruses (AAV). To deliver large genes to the inner ear we are using a dual vector approach. Here we demonstrate recombination of two halves of a gene *in vitro*, *ex vivo*, and in the inner ear.

2:35 Design Considerations and Testing of Proposed Solutions for a Retroviral Replicating Vector, Toca 511, as an Anticancer Agent in Humans
Douglas Jolly, PhD, Executive Vice President, Research & Pharmaceutical Development, Tocagen, Inc.
Features in a vector designed for anti-cancer activity are partly universal and partly mechanism-specific. Universal features include the use of amplification mechanisms. Toca 511 amplifies its effect by selectively replicating in tumors without significant inflammation then starting an anti-tumor immune response by administration of well-tolerated small molecule drug as a "trigger" for induction of anti-tumor immunity. In animal models and clinical trials this treatment leads to durable complete responses and extended survival.

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments

Join your peers and colleagues for interactive roundtable discussions.

Click here for details.

ALTERNATIVE VECTORS

4:30 A Nuclear Genetic Sensor to Measure and Optimize Delivery of Non-Viral DNA into Human Cells
Karmella Haynes, PhD, Assistant Professor, Wallace H. Coulter Department of Biomedical Engineering, Emory University
The small fraction of DNA that reaches the nucleus during non-viral gene delivery is often silenced by mechanisms that are not well understood. Viral transduction is a robust alternative, but has critical limitations, such as cargo size, and side effects, such as immunogenicity. We developed a genetically encoded sensor to track the fate of unlabeled non-viral DNA in live cells and to support efficient screening for interventions to improve gene delivery.

5:00 Development of Pediatric Gene Therapy Using Nuclease-Free Genomic Editing Technology, GeneRide
Jing Liao, PhD, Associate Director, Discovery Biology, LogicBio Therapeutics
GeneRide is a promoterless, nuclease-free genome editing technology. Combined with highly liver-tropic AAV vectors, GeneRide harnesses the natural process of homologous recombination to integrate the therapeutic gene site specifically into the *Albumin* (*Alb*) locus in a non-disruptive manner. Following GeneRide treatment, expression of the therapeutic gene is linked to that of Albumin via a 2A peptide and can be applied to treat the pediatric disease.

5:30 Bioresponsive Liposomes – Modulating the Trigger to Improve Site-Specific Delivery
Francis C. Szoka, PhD, Professor of Bioengineering, Therapeutic Sciences and Pharmaceutical Chemistry, University of California, San Francisco
Four decades since the original publications of pH-triggered liposomes, improved chemistries and a much better understanding of the cell biology of endocytosis/phagocytosis have provided components that can be used for the intracellular delivery of macromolecules. I'll describe modified lipids that can be incorporated into liposomes and that are activated by changes in pH, redox potential, or phosphatase activity during the delivery phase to enable intracellular content delivery.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

EXPLORING CELL THERAPIES

8:45 Chairperson's Remarks
Peter Yingxiao Wang, PhD, Professor, Bioengineering, Institute of Engineering in Medicine, University of California, San Diego

8:50 Precision Engineering to Advance Adoptive T Cell Therapies
Justin Eyquem, PhD, Principal Investigator, Department of Microbiology and Immunology, University of California San Francisco
We showed that targeting a CAR transgene into the TRAC locus improves the safety, the manufacturing, and the performance of CAR T cells, defining it as an optimal landing pad for adoptive T cell therapy. I will discuss our latest developments using the TRAC platform, including scaling up the TRAC-CAR T cells clinical manufacturing.

9:20 Engineering Genetic Circuits for Controllable CAR T Immunotherapy
Peter Yingxiao Wang, PhD, Professor, Bioengineering, Institute of Engineering in Medicine, University of California, San Diego
Cell-based immunotherapy is a paradigm-shifting therapeutic approach to treatment. However, life-threatening non-specificity and off-target activity against normal, non-malignant cells, as well as cytokine release syndrome, are major problems. To mitigate these, we genetically engineered immune cells to allow precise control of these engineered cells against target tumors.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 mRNA Reprogramming for cGMP iPSC Generation
Jiwu Wang, PhD, President and CEO, Allele Biotech
iPSC-based cell therapy has a very promising future. In order to achieve its full potential, reprogramming must be safe, proficient, and compliant with cGMP production standards. mRNA-based cell fate manipulation is a highly efficient, footprint-free method for both iPSC reprogramming and differentiation. Our process allows for precise stoichiometric control of factors in a controlled environment ensuring the processes are repeatable, scalable, safe, effective, and USFDA cGMP Compliant.

11:30 PANEL DISCUSSION: Current Strategies and Emerging Progress for Cell & Gene Therapies
Cell and gene therapies have emerged as promising therapeutic tools to target a variety of disease. However, there are also well-established biotherapeutics that have delivered therapeutic results, including antibodies, recombinant proteins, and antibody-drug conjugates. Panelists will discuss the current and emerging landscape for these therapies. Ultimately, the patient is the winner.
Moderator:
Peter Yingxiao Wang, PhD, Professor, Bioengineering, Institute of Engineering in Medicine, University of California, San Diego
Panelists:
Justin Eyquem, PhD, Principal Investigator, Department of Microbiology and Immunology, University of California San Francisco
Douglas Jolly, PhD, Executive Vice President, Research & Pharmaceutical Development, Tocagen, Inc.
Jiwu Wang, PhD, CEO and President, Allele Biotech

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

12:30 Session Break

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

1:10 Close of Vector Design and Development for Gene and Cell Therapies Conference

JANUARY 21-22, 2020 | INAUGURAL

GENE THERAPY ANALYTICS AND MANUFACTURING

Strategies, Analysis, Process Development, and Scale-Up of Vector-Based Gene Therapies

Cambridge Healthtech Institute's Inaugural GENE THERAPY ANALYTICS AND MANUFACTURING conference will take an in-depth look at the challenges facing the formulation development, characterization, analysis and scale-up of gene therapies. The conference will examine critical challenges facing the analytical characterization, issues of aggregation and impurities, quality control, specifications, bioproduction process development and scale-up of viral vector-based gene therapies such as AAV, lentivirus and retrovirus.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

OPPORTUNITIES, REGULATIONS, AND CHALLENGES

2:00 Chairperson's Opening Remarks
Jim Richardson, PhD, Senior Science and Standards Liaison, Global Biologics, United States Pharmacopeia

KEYNOTE PRESENTATION

2:05 Living in the World of RNAi Therapeutics

Muthiah (Mano) Manoharan, PhD, Senior Vice President, Drug Discovery, Alnylam Pharmaceuticals, Inc.
The approval of ONPATTRO® by the US FDA in 2018 paves the way for a new class of RNA-based medicines that can be available for needy patients soon. This talk will discuss current challenges and opportunities in RNAi delivery. Furthermore, we will discuss the case study of ONPATTRO, talk about the challenges faced during discovery and development and how they were overcome.

2:45 Regulation and Challenges in Developing Vector-Based Gene Therapies
Mo Heidaran, PhD, Vice President, Technical, PAREXEL Consulting, PAREXEL International
While it is assumed that regulatory approval often leads to commercial success, this may not necessarily become an overwhelming trend in the field of gene therapy. The major reasons for this potential disconnect will be discussed in my presentation, but full understanding of how these products work (knowledge of the product in context of applicable CGMPs) and how these products could be consistently manufactured at commercial scale sustainably remain to be fully demonstrated or established.

3:15 Sponsored Presentation *(Opportunity Available)*

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

FORMULATION DEVELOPMENT AND STABILITY

4:30 Lyocycle Development for AAV-Based Gene Therapy Applications
Tanvir Tabish, MSc, Head of Formulation Development, Formulation, Fill and Finish, Takeda
Biopharmaceuticals show varying levels of stability in aqueous solutions for short periods of time. Lyophilisation is a technique commonly used to improve the stability profile of biomolecules through the removal of water resulting in the increasingly restricted mobility of the reacting species. The Factor IX (FIX) gene therapy product was formulated and lyophilized. A stability study was established with the lyophilized material to determine its stability profile at the accelerated temperature of 5°C.

5:15 Extended Q&A with the Speaker

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*
Click here for details.
**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

ANALYTICAL STANDARDS, TOOLS, CMC, AND CHARACTERIZATION STRATEGIES

8:15 Chairperson's Remarks
Lake N. Paul, PhD, President, BioAnalysis, LLC

8:20 USP Standards for Gene Therapy
Jim Richardson, PhD, Senior Science and Standards Liaison, Global Biologics, United States Pharmacopeia
This presentation will provide updated information on existing USP Standards relevant for developers of Gene Therapies, such as Chapter <1047> Gene Therapy Products as well as Chapter <1043> Ancillary Materials for Cell, Gene, and Tissue-Engineered Products. It will also cover USP's development of new physical reference materials to aid developers of Gene Therapies.

8:50 Beyond Empty Capsids: Biophysics in Gene Therapy Manufacturing
Lake N. Paul, PhD, President, BioAnalysis, LLC
Currently the gene therapy space is underutilizing the power of biophysics, specifically Analytical Ultracentrifugation (AUC). Besides the quantitation of empty capsids, AUC can also be used to evaluate the physicochemical properties along establishing the CQA of the viral vector. From QC and IPC (decision point) perspectives, AUC can be an invaluable tool for evaluating the DP during the entire manufacturing process.

Sponsored by WYATT TECHNOLOGY

9:20 Measure AAV Quality Attributes with SEC-UV-MALS-dRI
Michelle Chen, PhD, Vice President, Analytical Services, Wyatt Technology
In this presentation, we discuss a size exclusion chromatography (SEC) method coupled with UV, multi-angle light scattering (MALS), and differential refractive index (dRI) detectors to measure the following three important AAV quality attributes: total number of viral capsid particles, relative capsid content, and percentage of monomer or aggregates.

9:35 Sponsored Presentation *(Opportunity Available)*

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

10:35 Strategy in Building In-House Analytical Capability for Gene Therapy Products
Jichao (Jay) Kang, PhD, RAC, Director, Analytical Development, Amicus Therapeutics
Compared with the traditional biologic products, gene therapy products are extremely heavy in CMC development. With limited

CMO capacity and high requirements for quality and timeline, it is critical for a serious gene therapy company to develop its in-house development and manufacturing capability. This presentation will share Amicus Therapeutics Inc.'s experience in building its in-house analytical development capability, including the key requirements, strategy, priority, and examples of success and lessons.

11:05 Analytical Ultracentrifugation to Assess Critical Quality Attributes of Viral Vectors for Gene Therapy
Klaus Richter, PhD, Group Leader, Analytical Ultracentrifugation (AUC) Group, Coriolis Pharma Research
Viral vectors are far more complex than other biopharmaceuticals. As part of drug development, it is required to monitor infectious virus titers, total number of virus particles, filled and empty virus particles, the functional envelope surface proteins (if applicable), virus aggregation and viral particle morphology. The talk focuses on how analytical ultracentrifugation (AUC) can be integrated as a powerful method for assessing critical quality attributes of viral vectors.

11:35 Manufacturing Lentiviral Vector for Gene Therapy Against RAG1-SCID
Alfred Luitjens, Director Cell Technology, Operations, Batavia Biosciences
We will present a case study on the process development and subsequent GMP production of lentivirus-based gene therapy against severe combined immunodeficiency syndrome. Our partner, Leiden University Medical Center transferred a lab-scale process to Batavia Biosciences, which was subsequently implemented and further developed to a GMP production process to be able to deliver material for clinical trials.

12:05 pm Session Break

12:15 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

MANUFACTURING CHALLENGES, AGGREGATES, AND IMPURITIES

4:00 Chairperson's Remarks
Lisa Lundberg, Bioassay & Cell Culture Lead, Spark Therapeutics, Inc

4:05 Monitoring and Control of Aggregates and Impurities in Large Scale AAV Production
Lisa Lundberg, Bioassay & Cell Culture Lead, Spark Therapeutics, Inc
Monitoring and control of aggregates and impurities are important for successful large-scale production of gene therapies. In this presentation, we will discuss various aggregates and different types of impurities that can be encountered in a large-scale AAV production, what tools and techniques can be used to monitor and characterize them, consideration for setting specification, etc.

4:35 Characterization and Quantification of Empty and Full AAV Capsids
Qin Zou, PhD, Associate Research Fellow and Group Leader, Analytical Research and Development, Pfizer, Inc.
This presentation can highlight various analytical methods for AAV empty and full capsids and emphasize the proper use of analytical ultracentrifugation for this purpose. AAV empty and full capsids is a product-related impurity and a critical quality attribute. Careful consideration of using appropriate analytical techniques to control that is important for a successful product.

5:05 Analytical Solutions for AAV Manufacture
Tristan Thwaites, PhD, Lead Technical Scientist, Industrialization, Cell and Gene Therapy Catapult
With a push towards more sophisticated pipelines, we need to develop systems that can help us understand the interaction between the complex bioproduct and the process tools so that we can scale and control the manufacturing process. In this presentation, we will discuss different analytical solutions for AAV manufacturing.

5:35 Predicting Viral Clearance: DOE, HTS and AAV Case Studies Utilizing a Non-Infectious MVM Surrogate during Downstream Development
David Cetlin, Founder & CEO, MockV Solutions LLC
Viral clearance studies are expensive and logistically challenging. This presentation will highlight data from the use of a non-infectious MVM surrogate in a variety of downstream applications and processes.

POSTER PRESENTATION: Detection of AAV Capsid Proteins by CE-SDS as an Alternative to Silver Stain SDS-PAGE
April Blodgett, MS, LAT, Biotherapeutics Senior Sales Specialist, PerkinElmer, Inc.
SDS-PAGE followed by silver staining has typically been used to visualize the VP1, VP2, VP3 ratio. This approach is labor and time-intensive but yields only qualitative data with poor reproducibility. Here, we describe the use of microfluidic CE-SDS for the characterization of capsid proteins from AAV serotype 8 as the rapid, quantitative, reproducible alternative to SDS-PAGE with silver stain.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Gene Therapy Analytics and Manufacturing Conference

JANUARY 23-24, 2020 | INAUGURAL

CELL THERAPY ANALYTICS AND MANUFACTURING

Analysis, Process Development, Scale-Up, and Commercialization of Cell Therapies

Cambridge Healthtech Institute's Inaugural CELL THERAPY ANALYTICS AND MANUFACTURING conference will discuss opportunities, advances, and challenges facing the analysis and manufacture of autologous and allogenic cell therapies. The conference will discuss analytical, CMC, and quality control challenges of cell therapies. The conference will also discuss commercialization aspects, such as manufacturing, scale-up, bioreactors, next-generation production technologies, automation, supply chain, and other manufacturing-related issues.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

STRATEGIES, REGULATIONS, AND GUIDANCE

8:10 Organizer's Welcome Remarks
Nandini Kashyap, Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Mo Heidaran, PhD, Vice President, Technical, PAREXEL Consulting, PAREXEL International

KEYNOTE PRESENTATION

8:20 Manufacturing Challenges for the Commercialization of Cell and Gene Therapy Products

Mo Heidaran, PhD, Vice President, Technical, PAREXEL Consulting, PAREXEL International

Achieving and meeting the requirements of manufacturing control for Cell and Gene Therapy product at commercial scale prior to licensure necessitates intensive focus and resources throughout the product development lifecycle. In my talk, I will attempt to highlight key challenges in consistent manufacturing of Cell and Gene Therapy products at commercial scale and provide possible solutions to some of these challenges, particularly as it is related to the collection of starting materials, establishing manufacturing control, and dealing with manufacturing changes during the product development lifecycle.

9:00 USP Standards for Cell Therapy
Jim Richardson, PhD, Senior Science and Standards Liaison, Global Biologics, United States Pharmacopeia

USP Standards Development for Cell Therapies - This presentation will provide updated information on existing USP Standards relevant to developers of Cell Therapies, such as Chapter <1046> Cell and Gene Therapy Products, as well as Chapter <1043> Ancillary Materials for Cell-, Gene-, and Tissue-Engineered Products. It will also cover USP's development of new physical reference materials to aid developers of Cell Therapies.

9:30 Novel Luciferase Based Assays for Determining the Expression of CAR-T Cells and Cytotoxicity of Adoptive Cell Therapies
Preet Chaudhary, MD, PhD, Professor of Medicine and Chief Hematology, Blood & Marrow Transplant, Keck School of Medicine, Univ of Southern California

The talk will describe novel non-radioactive marine luciferase based assays (Topanga and Matador Assays) for detection of CAR-T cells and for measuring the cytotoxicity of CAR-T cells and other forms of adoptive cell therapies.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

SOLID TUMORS

11:00 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.

11:30 PANEL DISCUSSION: Next-Generation Production Technologies and Process Development

Discussion Points:

- Next-Gen Cell Therapy Pipeline
- Next-Gen Processes for Better and Faster Optimization
- Next-Gen Scale-Up and Production Technologies

Moderator:
Mo Heidaran, PhD, Vice President, Technical, PAREXEL Consulting, PAREXEL International
Panelists:
Jim Richardson, PhD, Senior Science and Standards Liaison, Global Biologics, United States Pharmacopeia
Kuldip Sra, PhD, Senior Director, Crispr Therapeutics
Preet Chaudhary, MD, PhD, Professor of Medicine and Chief Hematology, Blood & Marrow Transplant, Keck School of Medicine, Univ of Southern California
Kelly Kemp, PhD, Director, Process Development, ViaCyte
Ilya Shestopalov, PhD, Associate Director, Cell Analytics, bluebird bio

12:00 pm Enjoy Lunch on Your Own

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

ANALYTICAL TOOLBOX AND CMC STRATEGIES

2:15 Chairperson's Remarks
Sandro Matosevic, PhD, Assistant Professor, Department of Industrial and Physical Pharmacy, Purdue University

2:20 Characterization and Qualification of Cell Banks and Other Critical Reagents Used in Potency Assays
Kelly Bowen, M.S., Sr. Associate Scientist, Analytical Development, bluebird bio

Cells are highly critical and complex reagents that are the foundation for any cell-based assay. To ensure operational consistency and limit the variability in cell-based assays, cell banks and cell lines require stringent characterization and control strategies. This presentation will focus on strategies to characterize, qualify, and manage cell banks used in potency assays.

2:50 Analytical Methods and CMC for Cell Therapies
Kuldip Sra, PhD, Senior Director, Crispr Therapeutics

For autologous cell therapy products, each patient is a product batch. Manufacturing is a very tedious and manual process. The urgency to release the product quickly to the patient is very high. The presentation will cover the implementation of rapid analytical methods to release the final product in the desired timeframe to patients.

3:20 Networking Refreshment Break

3:45 Outcomes of Characterization of CD34-Enriched Gene Therapy Drug Products
Ilya Shestopalov, PhD, Associate Director, Cell Analytics, bluebird bio

Cell-based drug products manufactured with lentiviral vectors (LVVs) require advances in analytical methods to characterize their safety and efficacy. This seminar will cover implementation of novel technologies to address unique challenges posed by gene therapy drug products. Approaches to identify drug product CQAs correlating with *in vivo* function will be discussed.

PROCESS DEVELOPMENT, SCALE-UP, AND MANUFACTURING

4:15 Exosomes as an Alternative for Cell Therapies: Novel Tools for Manufacturing Process and Characterization of Exosomes
Wasfi AlAzzam, PhD, Chief Scientific Officer, TechnoPharmaSphere LLC
Cell therapy provides immense hope for the treatment of diseases and regenerating pathological organs, yet has been marred by issues surrounding the effectiveness, unclear mechanisms, and survival of the donated cells. As exosomes fulfill a critical role in cellular communication with targeted message content, they become obvious candidates for an extensive range of diagnostic and therapeutic applications. However, the development of such large molecules need fast, robust and scalable purification procedure with effective analytical characterization.

4:45 CMC study of Viral Vector in CAR-T
Ben Xu, PhD, BD Director, Biologics Development, Genscript

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

PROCESS DEVELOPMENT, SCALE-UP, AND MANUFACTURING *(Cont.)*

9:00 Chairperson's Remarks
Kelly Kemp, PhD, Director, Process Development, ViaCyte

9:05 Challenges of Scaling-Up Cell-Based Processes to Meet Pivotal Trial Requirements
Kelly Kemp, PhD, Director, Process Development, ViaCyte
Product characterization and process understanding is critical when scaling a manufacturing process; for example, moving from a 2D to a 3D cell culture platform, to ensure a comparable, reliable, and robust manufacturing process. A review of the challenges, including flexibility of batch sizes to support increasing trial commercial demands, and separation of high-quality cells for cryopreservation, will be presented along with proposed solutions.

9:35 Cryopreservation Optimization of CAR T Drug Product by Utilizing a Stochastic Global Optimization Approach
John Zhao, MSc, Senior Associate Scientist II, Cellular Process Development and Gene Editing, bluebird bio
Cryopreservation is a complex process with multiple variables that can interact and impact cell viability and proliferation potential. The work at bluebird bio used a stochastic global optimization tool as a successful means to efficiently test a small number of conditions to improve the cryopreservation process (50 out of >500 combinations).

10:35 Networking Coffee Break

11:00 Evaluating Cell Settling Velocity
Danika Rodrigues, MS, Senior Associate Scientist, Research & Development, Janssen Pharmaceutical, LLC
Cell settling can occur during dose preparation and administration of cell therapies, potentially compromising homogeneity of product suspension. A model that considered cell and fluid properties was used to calculate settling velocities for cell product suspensions under varied administration conditions. Model calculations show agreement with experimental velocities and can be expanded to serve as a predictive simulation tool. We intend to optimize this model for the evaluation of clinical preparation/administration procedures.

11:30 Interactive Buzz Session Report Out
Cell and Gene therapies are a fast-growing field. As science improves, so does the complexities. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion report out. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends, which talks, and speakers motivated you, learnings during the week that you can apply in your work.

11:45 Conference Wrap-Up
Jim Richardson, PhD, Senior Science and Standards Liaison, Global Biologics, United States Pharmacopeia

12:00 Close of Conference

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.

FORMULATION & STABILITY

As the industry advances biotherapeutic development, the formulation and process development functions play important roles, supporting the selection and optimization of molecules with better developability, manufacturability, stability, safety and efficacy. The popular Formulation & Stability pipeline presents case studies of the latest tools, technologies and cutting-edge approaches related to the progression of biologics from R&D into the development of high-quality biotherapeutic products.

January 20-21

AGENDA Optimizing Biologics Formulation Development

January 21-22

AGENDA Lyophilization and Emerging Drying Technologies

January 23-24

AGENDA Protein Aggregation and Emerging Analytical Tools

Also part of **ANALYTICS & IMPURITIES**

JANUARY 20-21, 2020 | 12TH ANNUAL

OPTIMIZING BIOLOGICS FORMULATION DEVELOPMENT

Exploring the Future of Tools and Techniques for Formulating Novel Biologic Drug Products

Cambridge Healthtech Institute's 12th Annual OPTIMIZING BIOLOGICS FORMULATION DEVELOPMENT conference is an essential yearly gathering of analytical and formulation scientists from leading industry companies that provides an exchange of scientific developments and emerging technologies in an environment that encourages discussion with colleagues. For 2020, the meeting will address the formulation challenges of emerging modalities, new strategies for predictive analysis at this stage, exciting new analytical methodologies and accelerating the best practices being employed to overcome formulation challenges.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

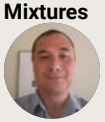
FORMULATION FOR EMERGING MODALITIES

9:00 Organizer's Welcome Remarks
Kent Simmons, Senior Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Jainik Panchal, PhD, Associate Principal Scientist, Sterile Formulation Sciences, Merck

KEYNOTE PRESENTATION

9:10 Stability Assessment of Coformulated Antibody Mixtures



Brian D. Soriano, Scientist, Discovery Attribute Sciences, Amgen Inc.

Co-formulating two or more drugs can be highly beneficial for therapeutic treatment of disease. There are unique analytical challenges for assessing stability in coformulations. In this study, we describe the stability assessment of 5 mAbs and 6 associated coformulated mAb mixtures before and after thermal stress. The observed data suggest that the stabilities of antibody coformulations were found to be comparable to the stabilities of individual parental mAbs.

9:50 Biologics Co-Formulation Product Development – Challenges and Case Studies
Jainik Panchal, PhD, Associate Principal Scientist, Sterile Formulation Sciences, Merck

Co-formulated products contain more than one drug as part of a single drug product image. The concept of coformulation is very common for small molecule drugs, which are routinely co-formulated in a single product (e.g., Delstriga®, BikTarvy®). Recently, there is an increased interest in co-formulation of biologics. However, there are significant challenges due to inherent molecular complexity of proteins. This talk highlights some of the challenges during coformulation development.

10:20 Networking Coffee Break

10:45 The Relevance of Sub-Visible Particulate Matter in Lipid Nanoparticle Products
Flaviu Gruia, PhD, Principal Scientist, Drug Product Analytical Development, Moderna Therapeutics

Lipid nanoparticles (LNP) are the leading delivery system for mRNA-based therapeutics and vaccines. They are manufactured by microfluidic mixing of a lipid-containing-ethanol-phase and an mRNA-carrying-aqueous-phase. The LNP self-assemble via a rapid antisolvent precipitation process. Although the resulting size distributions are well controlled, due to complex nature of nanoprecipitation, larger particles may develop. The presentation will focus on characterization of particulate matter in LNP formulations. Selected case studies will be included.

11:15 Drug Product Development Approach across a Multi-Modality Parenteral Product Portfolio
Jason Fernandez, Senior Scientist, Biogen

At Biogen, we are developing a diverse portfolio consisting of small molecules, proteins, antisense oligonucleotides and gene therapy to target many neurodegenerative diseases. There are differences in molecular characteristics, route of administration, and supply chain needs between these modalities. To efficiently deliver against these diverse needs, development strategies that leverage established platforms while catering to unique needs of the emerging modalities will be discussed.

11:45 Challenges in Low-Temperature Storage of Cell Therapy Drug Products
Page McAndrew, PhD, Director, Scientific Communications, West Pharmaceutical Services

Low-temperature storage of cell therapy drugs products presents challenges to achieving good packaging system container closure integrity (CCI). These challenges result from (1) differences in thermal expansion coefficients of components, and (2) permeability of gases. This presentation considers the fundamentals of these challenges and how they may be overcome, as well as differences between glass- and polymer-based systems.

12:15 pm Sponsored Presentation *(Opportunity Available)*

12:45 Session Break

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

PREDICTIVE METHODS FOR FORMULATION DEVELOPMENT

2:00 Chairperson's Remarks
Samantha Pace, PhD, Research Investigator, Bristol-Myers Squibb

2:05 Physics-Based Simulations to Predict Developability of Antibody Therapeutics
Saeed Izadi, PhD, Scientist, Genentech

This talk will provide an overview of physics-based biomolecular simulations and molecular modeling techniques to understand and predict a variety of therapeutic antibodies developability characteristics such as chemical degradation, high viscosity in concentrated solutions, effect of formulation on viscosity, and aggregation. For each category, theoretical and computational models from our group, along with their benchmarking against experimental datasets, will be presented and the models' accuracy, robustness and pitfalls will be discussed.

2:35 Development of Scale-Down Assays for Assessment of Mechanism(s) of Tangential Flow Filtration Instability of Proteins
Samantha Pace, PhD, Research Investigator, Bristol-Myers Squibb
Interfacial stresses can play a major role in unfolding and aggregation of proteins. The development of a predictive tool to access the risk of molecules when exposed to this stress can help identify the need for different formulations and handling techniques. This talk will discuss the use of Langmuir trough to measure air/water interfacial properties of several molecules and their correlation to aggregation during the ultrafiltration/diafiltration using tangential flow filtration (TFF).

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.
Click here for details.

4:30 Formulation of Stable Complexes for Intracellular Delivery of Therapeutic Antibodies
Julie Champion, PhD, Associate Professor, Chemical and Biomolecular Engineering, Georgia Tech
To enable antibody access to "undruggable" intracellular protein targets, we have developed a self-assembling protein carrier comprised of a self-assembling hexamer barrel with six antibody binding domains that bind the constant region of any antibody. We have performed extensive molecular characterization to understand the loading, dynamics and stability of our assemblies. We have demonstrated intracellular delivery of functional antibodies, and have characterized the uptake, trafficking and fate of internalized antibodies.

5:00 Calculating the Ea Activation Energy and Aggregation Propensity of mAbs Utilizing DSC Differential Scanning Calorimetry
Ralf Carrillo, PhD, Associate Principal Scientist, Pharmaceutical Science, Merck

5:30 A Split β-Lactamase Platform to Predict the Developability of Biopharmaceuticals
Jessica Ebo, Researcher, Astbury Center for Structural Molecular Biology, University of Leeds, United Kingdom
We have developed an *in vivo* platform to characterize the aggregation propensity of biopharmaceuticals that circumvents the need for recombinant expression and downstream analysis. This split beta-lactamase enzyme assay enables the identification of aggregation-prone sequences inserted between the two enzyme domains, whose function is necessary for the survival of the bacteria in which it is expressed. This platform presents a powerful tool for screening drug candidates without any prior knowledge of the mechanism of aggregation.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

OVERCOMING FORMULATION CHALLENGES

8:45 Chairperson's Remarks
Shalini Minocha, PhD, Staff Scientist, Formulation Development, Regeneron

8:50 Formulation Strategies for Labile Protein Molecules: A Bi-Specific Antibody Case Study
Xiaofeng Lu, Ph.D., Principal Research Scientist, Pharmaceutical Development, AbbVie, Inc.
Development of a bispecific protein posed significant formulation challenges due to susceptibility to aggregation in aqueous solution. In this talk, the aggregation stabilization approaches explored to develop a formulation for FIH clinical studies and potential formulations for later stage development will be presented.

9:20 Chemical Degradation of Therapeutic Protein Formulations
Krishna M.G. Mallela, PhD, Associate Professor, Pharmaceutical Sciences, University of Colorado
Methionine oxidation and asparagine deamidation are the two most common chemical modifications that occur during the shelf life of protein pharmaceuticals. I will discuss how to detect such chemical modifications and their effects on the structure, stability, and aggregation of therapeutic proteins using various spectroscopic techniques that include 2D NMR, and methods on how to prevent such chemical degradation.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 Effect of Temperature and Intermediate Packaging on Photostability of Biological Products
Shalini Minocha, PhD, Staff Scientist, Formulation Development, Regeneron
Biologic products in Prefilled Syringes (PFS) may be exposed to unintended light exposure when stored in tubs before being labelled, packaged and distributed to clinical sites. The effective light exposure to the formulation in PFS in tubs may vary depending on the orientation, type and intensity of light source and packaging material. The impact of temperature and intermediate packaging on photostability of biologics in PFS will be presented.

11:30 Best Practices for Working with Contract Organizations for Formulation and Process Development
Aniket Badkar, PhD, Director, Biologics Product Development, Allergan
Working with contract development and manufacturing organizations (CDMOs) is commonplace in the pharmaceutical industry. Outsourcing controls operating costs, streamlines internal resources and company focus, and increases efficiency; however the client will have limited control regarding scheduling, cost, quality and accountability. Data security may become an issue as intellectual property is exchanged. This presentation discusses these points and provides a comprehensive strategy and best practices for selecting and working with CDMOs.

12:30 Session Break

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

1:10 Close of Optimizing Biologics Formulation Development Conference

JANUARY 21-22, 2020 | 13TH ANNUAL

LYOPHILIZATION AND EMERGING DRYING TECHNOLOGIES

Emerging Strategies and Drying Technologies for Biologics

The popular 13th Annual LYOPHILIZATION AND EMERGING DRYING TECHNOLOGIES conference covers latest trends, advances and challenges in lyophilization and emerging drying technologies for biotherapeutics. In addition to key issues like PAT, controlled nucleation, cycle optimization, etc., this year the conference will feature in-depth case studies, new and unpublished data and discussions around lyophilization of complex formulations, cell, gene and tissue-based products. Also, we will take a deep dive into the advances and implementation of several novel and emerging drying technologies.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

DRYING TECHNOLGIES FOR COMPLEX AND NOVEL BIOLOGICS

2:00 Chairperson's Opening Remarks
Xiuling Lu, PhD, Associate Professor, Pharmaceutical Sciences, University of Connecticut

FEATURED PRESENTATION

2:05 Impact of Freeze-Drying Process and Lyoprotectants on Nanoparticle Stability
Xiuling Lu, PhD, Associate Professor, Pharmaceutical Sciences, University of Connecticut
Freeze-drying is an effective approach to improve the storage stability of nanomedicines. The optimal freeze-drying process and lyoprotectants for three types of nanoparticles (solid lipid nanoparticles, polymeric nanoparticles, and liposomes) were investigated. It was identified that various nanoparticle platforms have different behaviors in the freeze-drying process and require appropriate approaches to cope with. The impact of lyoprotectant selection and the freeze-drying process on nanoparticle stability will be presented.

2:45 Stabilization of Gene Therapy and Cell Therapy Drug Products Using Lyophilization and Vetrification Strategies
Rajiv Nayar, PhD, President, HTD Biosystems, Inc.
Currently, nucleic acid-based and cell therapy drug products are formulated as frozen drug dosage forms or liquid dosages with limited shelf life. This makes them restricted to only be available at specialized institutions and specific geographic locations. Lyophilization of such drug products would enhance their stability and increase their availability. This presentation will address issues and strategies to overcome the limitations of these next-generation biopharmaceuticals.

3:15 Dehydration Induced Structural Transition of Proteins and Its Thermal Stability in Solid/Semi Solid Formulation
Tuan Phan, PhD, Researcher, Biology, Malmo University

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

4:30 Formulation Development, Stability and Delivery for Gene Therapies
Arun Alphonse Ignatius, PhD, Principal Scientist, Pharmaceutical Research and Development, Biotherapeutics, Pfizer, Inc.

5:00 Lyocycle Development for AAV-Based Gene Therapy Applications
Tanvir Tabish, MSc, Head of Formulation Development, Formulation, Fill and Finish, Takeda
Biopharmaceuticals show varying levels of stability in aqueous solutions for short periods of time. Lyophilisation is a technique commonly used to improve the stability profile of biomolecules through the removal of water resulting in the increasingly restricted mobility of the reacting species. The Factor IX (FIX) gene therapy product was formulated and lyophilized. A stability study was established with the lyophilized material to determine its stability profile at the accelerated temperature of 5°C.

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*
Click here for details.
**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

EMERGING DRYING TECHNOLOGIES

8:15 Chairperson's Remarks
Bakul Bhatnagar, PhD, Senior Principal Scientist, Pharmaceutical R&D, BioTherapeutics Pharmaceutical Sciences, Pfizer, Inc.

8:20 Exploring Novel Drying Technologies for Generating Monoclonal Antibody Powders in Consideration of Critical Quality Attributes
Benson Gikanga, Senior Engineer, Pharmaceutical Processing and Technology Development, Genentech
Some novel spray drying technologies proved feasible in producing powders of monoclonal antibody formulations with acceptable particle characteristics (particle size distribution, morphology, moisture content, etc) while maintaining key quality attributes (cQAs), including charge and size variants. They also demonstrated stability performance comparable to freeze drying. Despite these promising data, this presentation offers insights into changes in other cQAs, which pose challenges in utilization of spray drying technologies for dehydration of biopharmaceutical products.

8:50 New Technologies for Freeze-Dried Formulations and Continuous Manufacturing
Bakul Bhatnagar, PhD, Senior Principal Scientist, Pharmaceutical R&D, BioTherapeutics Pharmaceutical Sciences, Pfizer, Inc.
While the pharmaceutical industry continues to demonstrate its creativity associated with novel compounds in development, the processing technologies utilized for their manufacture have not kept their pace. This is not a reflection of the paucity of innovation associated with processing technology. The barrier can broadly be classified as economic, logistical, technical and psychological, and all elements need to be overcome for successful implementation of a new technology.

9:20 Sponsored Presentation *(Opportunity Available)*

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

KEYNOTE PRESENTATION

10:35 New Approaches to Make Freeze Drying of Proteins Faster and Better

Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen

To improve freeze drying, two aspects have been in the focus of recent research. First, to speed up the process to reduce time, and second, to make it more homogeneous, particularly with respect to ice nucleation. We will present our newest research results on microwave assisted freeze drying, applicability of tBA in protein freeze drying and conclusive studies of stability of lyophilisated in relation to controlled or random ice nucleation.

11:35 PANEL DISCUSSION: Challenges in Developing and Implementing Drying Technologies for New and Complex Biologics

Discussion Points:

- Drying of novel biotherapeutics, cell and gene therapy products, tissues, particles, etc.
- What are standards and good starting points?
- What are some alternative drying technologies?
- How to scale up and implement for large scale continuous manufacturing

Moderator:
Rajiv Nayar, PhD, President, HTD Biosystems, Inc.
Panelists:
Benson Gikanga, Senior Engineer, Pharmaceutical Processing and Technology Development, Genentech
Evgenyi Shalaev, PhD, Executive Director, Pharmaceutical Development, Allergan plc
Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen
Justin Stanbro, PhD, Associate Principal Scientist, Novel Adjuvants, Formulation & Delivery Technologies, Merck & Co.
Tanvir Tabish, MSc, Head of Formulation Development, Formulation, Fill and Finish, Takeda

12:05 pm Session Break

12:15 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Enjoy Lunch on Your Own**

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

PAT, CONTROLLED NUCEATION, CONTAINER CLOSURE, AND CYCLE OPTIMIZATION

4:00 Chairperson's Remarks
Evgenyi Shalaev, PhD, Executive Director, Pharmaceutical Development, Allergan plc

4:05 PAT in Freeze-Drying: Detection of Secondary Crystallization of Excipient+Water
Evgenyi Shalaev, PhD, Executive Director, Pharmaceutical Development, Allergan plc

Crystallization of an excipient or an active ingredient during freeze drying could have a major impact on the product yield (e.g., vial breakage), manufacturing process (e.g., the drying rate), and quality attributes of the finished product, including appearance, reconstitution, potency, and stability. The presentation overviews main experimental tools for monitoring secondary solute crystallization during freeze drying, including product temperature, electrical resistance, spectroscopy (such as Raman), and heat-flux sensors.

4:35 Characterization of Moisture Uptake of Lyophilized Drug Product from Different Stoppers
Pauline Che, MSc, Engineer II, Pharmaceutical Development, Genentech

Post-lyophilized drug product residual moisture may increase with time from stopper-bound moisture and from water vapor permeation through stopper. This work evaluates the impact of stopper size, stopper type, initial stopper moisture content, and drug product storage conditions on residual moisture uptake rate. Data package generated will support stopper moisture specification prior to product fill and predict residual moisture of lyophilized drug product at end of shelf life.

5:05 Small-Angle Scattering of Surfactants and Protein-Surfactant Mixtures during Freeze-Thaw
Xiaoda Yuan, PhD, Scientist, Pharmaceutical Development, Allergan, Inc.

Frozen storage represents one of the most common preservation methods for biotherapeutics. Surfactant is a typical component in biopharmaceutical formulations for its protective role against interfacial stresses. This presentation will discuss phase behaviors of surfactants and protein-surfactant mixtures during freeze-thaw as studied by small-angle scattering techniques (X-ray and neutron scattering). Different surfactants (PS 20 and P 188) and surfactant concentrations were compared. Lysozyme was used as a model protein.

5:35 Evaluation of Optical Coherence Tomography – Freeze Drying Microscopy (OCT-FDM) for Lyophilization Cycle Development
Andrew Massetti, Senior Associate Scientist, Protein Pharmaceutical Development, Biogen

Traditional techniques used to estimate product collapse temperature (Tc) may not be representative of the actual drying process in vials, the most commonly used commercial container closure. Optical coherence tomography freeze drying microscopy (OCT-FDM) allows direct Tc measurement in vials and has the potential to enable development of more efficient drying process. Freeze drying cycles were developed by OCT-FDM and the resulting product quality was compared to cycles developed by traditional techniques.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Lyophilization and Emerging Drying Technologies Conference

PROTEIN AGGREGATION AND EMERGING ANALYTICAL TOOLS

Mechanism, Prediction, Immunogenicity, Developability, and Process Challenges

The popular 11th Annual PROTEIN AGGREGATION AND EMERGING ANALYTICAL TOOLS conference covers latest trends, challenges and solutions in understanding, characterization and mitigation of problems generated by protein aggregation in biopharmaceuticals. This conference will feature in-depth case studies, new and unpublished data and interactive discussions on immunogenicity of aggregates, mechanisms of aggregation, new tools for detection and quantitation of aggregates, and how the data is used in regulatory filings, developability assessment, fill/finish challenges and other critical issues.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

UNDERSTANDING AND PREDICTING PROTEIN AGGREGATION

8:10 Organizer's Welcome Remarks
Nandini Kashyap, Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University

KEYNOTE PRESENTATION

8:20 Understanding and Predicting Self-Association in High Concentration Antibody Solutions – A Colloid Approach

Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University

We address the problem of enhanced self-association in high concentration antibody solutions and the concomitant high viscosities. In order to understand and predict the thermodynamic and flow properties of such formulations, we provide the first quantitative description of mAb self-association and viscosity as a function of concentration by combining experiments (static and dynamic scattering and microrheology), theory and computer simulations using a model based on analogies to patchy colloids.

9:00 Estimating Solution Nonideality from Measured Values
Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire

The concentration-dependent chemical potential of a species results from the sum of its repulsive and attractive interactions with neighboring species. The repulsive and attractive terms can be estimated using measured values of size, charge and association constants from a combination of one- and two-component solution measurements. The underlying concepts will be explained and the need for measured values will be highlighted.

9:30 Detection and Characterization is the First Step to Eliminating Aggregation *Sponsored by* WYATT TECHNOLOGY
Kevin McCowen, Southwest Regional Manager, Wyatt Technology

Size exclusion chromatography (SEC) with UV detection gives limited information on the nature of aggregates. In this presentation, we discuss how multi-angle light scattering in conjunction with SEC as well field flow fractionation and dynamic light scattering allow the researcher to rapidly assess formulation stability to aid in the elimination of aggregates in the early development phase, detect the presence of large aggregates, and probe aggregate characteristics such as absolute molecular weight and conformation.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

IN VIVO AGGREGATION AND IMMUNOGENICITY

11:00 Application of an *in vitro* Skin Model System to Assess Potential Risk of *in vivo* Aggregation and Immune Activation of Biotherapeutic Attributes
Josh Tokuda, PhD, Postdoctoral Fellow, Biological Relevance and Characterization, Amgen, Inc.

In this presentation, a new human *in vitro* skin model system will be presented that can be used to assess the potential of biotherapeutics to aggregate and cause immune activation *in vivo*.

11:30 PANEL DISCUSSION: Prediction and Control of *in vivo* Aggregation and Immunogenicity

Discussion Points:
- Current Challenges
- New Predictive Tools
- Data Analysis and Management
- Use of Artifical Intelligence in Better Prediction and Control

Moderator:
Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire
Panelists:
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University
Josh Tokuda, PhD, Postdoctoral Fellow, Biological Relevance and Characterization, Amgen, Inc.
John J. Correia, PhD, Professor, Department of Biochemistry, University of Mississippi Medical Center
Reza Esfandiary, Associate Director, Early Stage Formulation Sciences, BioPharmaceutical Development, AstraZeneca

12:00 pm Shear Rate Dependent Viscosity as an Indicator of Protein-Protein Interactions and Cluster Formation *Sponsored by* RheoSense
Stacey Elliot, Principal Scientist, R&D, RheoSense, Inc

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Everything You Wanted to Know About Protein Aggregation but Were Too Afraid To Ask *Sponsored by* UNCHAINED LABS
Kevin Lance, PhD, Product Manager, Marketing, Unchained Labs

Detecting and understanding aggregation is both complex and critical to the successful development of biologics. Thankfully Uncle delivers six powerful tools to ensure there is no shortage of insights on stability, aggregation, and non-specific interactions. Fluorescence, and static and dynamic light scattering work for your protein, antibody, or viral capsid to understand their willingness to stay folded and solitary, and if you've got the right formulation to keep them that way.

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

IN SILICO MODELING, TOOLS, AND ASSAY

2:15 Chairperson's Remarks
Christoph Brandenbusch, PhD, Group Leader, Biochemical and Chemical Engineering, TU Dortmund

2:20 FDS-AUC Analysis of mAb Nonideality and Self-Association in Serum and Formulation Solutions
John J. Correia, PhD, Professor, Department of Biochemistry, University of Mississippi Medical Center

The Aviv Fluorescence Detection System (Aviv-FDS) has allowed the performance of sedimentation velocity experiments on therapeutic antibodies in highly concentrated environments, like serum and formulation buffers. Methods have been implemented in the software package SEDANAL for the analysis of nonideal, weakly associating AUC data acquired on therapeutic antibodies and proteins using absorbance or FDS optics. This involves determining

both hydrodynamic nonideality Ks and thermodynamic nonideality BM1 plus association constants.

2:50 Mitigation of Reversible Self-Association and Viscosity of Monoclonal Antibodies via Structure-Guided Protein Engineering: Complementing Analytical and *in silico* Tools
Reza Esfandiary, Associate Director, Early Stage Formulation Sciences, BioPharmaceutical Development, AstraZeneca
High protein concentrations can introduce additional development challenges due to issues such as reversible self-association or high viscosity. Protein engineering can provide a complementary mitigation approach to formulation optimization in improving high concentration developability properties. Here, case studies utilizing complementary analytical and *in silico* methods are presented where molecular hotspots in monoclonal antibodies, responsible for high concentration issues, are systematically identified and engineered to generate variants with improved developability profiles.

3:20 Networking Refreshment Break

3:45 Thermodynamics-Based Approach for Predicting Aggregation Propensity and Beneficial Solution Conditions in Antibody Formulations
Christoph Brandenbusch, PhD, Group Leader, Biochemical and Chemical Engineering, TU Dortmund
Protein aggregation is caused by the molecular interactions of all components in solution. We developed a thermodynamics-based approach to predict beneficial solution conditions taking the competition for water by a specific excipient, as well as the molecular interactions of the proteins in the presence of excipients into account. This allows predicting a first estimate on aggregation propensity induced by the respective excipients and thus enables a first choice of preferential excipients with a minimum of experimental effort.

4:15 Discerning the Synergistic Effect of Hydrodynamic Flow and Interfaces on Protein Aggregation
Paolo Arosio, PhD, Professor, Biochemical Engineering, Department of Chemistry and Applied Biosciences, ETH Zurich
Despite being an area of extensive investigation, the effect of hydrodynamic flow and shear on protein aggregation is still controversial. Here, we demonstrate the presence of a synergistic effect of interfaces and hydrodynamic flow in flow-induced protein aggregation. We propose that hydrodynamic flow and shear stress should be considered in close association with interfaces when discussing sources of protein aggregation.

4:45 Computer Simulations of Aggregation of Proteins and Peptides
Andrzej Kloczkowski, PhD, Professor, Pediatrics, Nationwide Children's Hospital and The Ohio State University
Aggregation of proteins and peptides is an important biological phenomenon often related to protein misfolding and correlated with various diseases, such as Alzheimer's or Parkinson's; recently it has been shown that preeclampsia has similar molecular mechanism as Alzheimer's. Computer simulations are excellent tools to study the molecular mechanism, structural features and dynamics of protein aggregation, and formation of amyloid filaments and fibrils. Results of our recent computational simulations studies focused on specific diseases such as Alzheimer's, and preeclampsia will be revealed.

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

CHARACTERIZATION, DEVELOPABILITY ASSESSMENT, AND FILL/FINISH

9:00 Chairperson's Remarks
Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen

9:05 Qualifying a New Method for Submicron Particle Counting and Why It Matters
Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen
We have tested and critically evaluated TRPS (Tunable Resistive Pulse Sensing) by using a rather affordable analytical equipment (IZON) and providing information on how to collect data, how to analyze and how to critically assess them. Comparisons with other techniques like RMM and NTA are made, and examples from very different primary packaging materials on what to expect from submicron particle counting and how to reduce particle burden are provided.

9:35 Challenges in Characterization and Developability Assessments of Multispecific Antibodies
Christian Lange, PhD, R&D Biologics Research, Assays and Analytics, Protein Therapeutics, Sanofi-Aventis Deutschland GmbH
The complexity of multispecific antibodies requires a comprehensive set of analytical techniques to guide lead discovery and optimization. An overview of these techniques will be presented with a focus on mispairing analysis and functional characterization of multispecific drug candidates. Furthermore, the integrated developability concept at Sanofi Biologics will be presented along with showcases highlighting potential challenges in characterization and developability of multispecifics.

10:05 Controlling Aggregation of a Range of Novel Biopharmaceutical Product Modalities
Jan Jezek, PhD, CSO, Arecor Ltd.
Whilst controlling aggregation of monoclonal antibodies has become a routine task through smart candidate screening and platform formulations, there are numerous novel modalities, such as multi-specific antibodies, ADCs, or gene therapy products, where aggregation remains a key problem. This talk will present case studies showing novel formulation approaches to reduce aggregation in these products and enable user-friendly formats.

10:35 Networking Coffee Break

11:00 Fill/Finish Strategies to Prevent and Overcome Aggregation Challenges
Marcel Tigges, PhD, Associate Director, The Janssen Pharmaceutical Companies of Johnson & Johnson
Fill & Finish processes for large molecule parenterals require a quality control toolbox that allows for efficient monitoring of stress factors potentially impacting drug product quality. New technologies and PAT (Process Analytical Technology) tools allow for real-time monitoring of protein concentration (FlowVPE) and low volume protein stability analysis (nanoDSF). Identification of critical process parameters (CPPs) and process steps that potentially cause protein aggregation guides the design of robust processes towards optimal mixing, filtration and filling conditions for highest drug product quality and stability standards.

11:30 Towards a Better Development of Robust High Concentration Protein Formulations
Vishal Toprani, PhD, Development Scientist-I, Pharmaceutical Development, Alexion Pharmaceuticals
The development of high concentration protein formulations presents a number of analytical, formulation, process and delivery challenges. This talk will focus on key aspects of successfully developing high concentration protein formulations by better understanding the physicochemical properties and degradation pathways of a molecule along with integrated efforts between various CMC groups.

12:00 pm Conference Wrap-Up
Jan Jezek, PhD, CSO, Arecor Ltd.

12:30 Close of Conference

ANALYTICS & IMPURITIES

Traditional biologics, new biotherapeutics modalities and biosimilars are flooding discovery and development pipelines. Thus, analytical function is rapidly evolving, demanding high-throughput and high-resolution tools, focused biomolecular and biophysical assays, and rapid analytical and impurity profiling strategies. The Analytics & Impurities pipeline features in-depth perspectives on the latest developments and most critical steps in characterization of biologics, stability issues arising from particles, impurities, immunogenicity, protein aggregates and their impact on stability and safety of biopharmaceuticals.

January 20-21

AGENDA Characterization of Biotherapeutics

January 21-22

AGENDA Detection and Characterization of Particulates and Impurities

January 23-24

AGENDA Protein Aggregation and Emerging Analytical Tools

Also part of **FORMULATION & STABILITY**

CHARACTERIZATION OF BIOTHERAPEUTICS

Improving Prediction, Screening, and Characterization of New Biologics

The popular 6th Annual CHARACTERIZATION OF BIOTHERAPEUTICS conference will bring together leading scientists from the biopharmaceutical industry, academia, and government to discuss case studies, new technologies, assay on analytical development, and characterization of mAbs, ADCs, bispecifics, novel protein formats, and biosimilars. Some of the hot topics for discussion this year will include regulatory expectations and developability of new product formats, cell and gene therapy products, high-throughput analytics, multi-attribute methods, glycosylation/post-translational modifications, biophysical assays, and more.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

CHALLENGES, DEVELOPABILITY, RISK ASSESSMENT, AND STRATEGIES

9:00 Organizer's Welcome Remarks
Nandini Kashyap, Conference Director, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Suzanne D'Addio, PhD, Principal Scientist - Discovery Pharmaceutical Sciences, Merck & Co., Inc.

FEATURED PRESENTATION

9:10 Developability Assessment to Select Candidates for Clinical Development
Anup Arumughan, PhD, Principal Scientist, Antibody Analytics, Roche
We have developed a highly versatile next-generation biologics platform with a number of candidates in clinical development. During lead identification and optimization of candidates we typically rank molecules based on their potential for successful future development. Such developability assessments provide important information about potential liabilities, e.g., chemical degradation of amino acids or unfavorable CMC properties. We have recently expanded our developability concept to systematically combine *in silico* analysis including pharmacokinetics analysis with biophysical and functional testing. In summary, this concept provides a more holistic picture of a candidate's fitness for future development.

9:50 Analytics in the Development of Biosimilars and Beyond
Robert Mayer, PhD, Senior Fellow, Novartis - Global Drug Development, Technical Research & Development, Sandoz GmbH
Analytical characterization is one of the key pillars for biosimilars development. With the help of case studies, we will demonstrate the powerfulness of analytical methods. In one case study, the elucidation of structure-function relationship will be addressed. In another case study, an innovative approach for the glycan analysis in PK studies will be shown to evaluate the (possible) impact of individual N-glycan species onto clearance. Furthermore, analytical challenges and requirements for the development of "fit-for-purpose" analytical methods will be briefly addressed.

10:20 Networking Coffee Break

10:45 Antimicrobial Excipient-Induced Reversible Association of Therapeutic Peptides in Parenteral Formulations
Suzanne D'Addio, PhD, Principal Scientist - Discovery Pharmaceutical Sciences, Merck & Co., Inc.
The high potencies and longer half-lives of therapeutic peptides have given rise to multiuse injectable dosage forms that enable less frequent dosing and patient self-administration, but required antimicrobial preservatives can impact other attributes of protein and peptide formulations. To understand molecular mechanisms of peptide-preservative interactions influencing solution-phase self-association, we investigated the interactions of commonly used antimicrobial preservatives with an acylated peptide. We have demonstrated a reversible association phenomenon granting new insights into mechanisms by which peptides can interact with excipients. These findings have practical implications for drug product formulation development.

11:15 Predicting Antibody Affinity Changes upon Mutations by Combining Multiple Predictors
Yoichi Kurumida, PhD, Postdoctoral Fellow, National Institute of Advanced Industrial Science and Technology(AIST).
The prediction of antibody affinity changes upon mutations is important for antibody engineering. Numerous computational methods have been proposed based on different approaches including molecular mechanics and machine learning. However, the prediction accuracy obtained by each of individual predictors has been limited. In this study, we develop a new prediction method by combining multiple predictors based on machine learning. The method was tested on the SiPMAB database and achieved higher accuracy than other methods.

11:45 Comparative Evaluation of Chelating Agents to Prevent Polysorbates and API Degradation in Biologic Formulations
Sanket Patke, PhD, Senior Scientist, Biologics Drug Product Development, Sanofi
EDTA and other chelators are used in several products, few of which are biologics.Their need, pros, and cons as excipients are, however, still poorly understood. In this case study, a head-to-head comparison of EDTA with other chelating agents is presented, including recommendations for their correct use in the formulation of protein-based therapeutics.

12:15 pm Development of Standards for Cation exchange chromatography Column Qualification
Jie (Amy) Liu, Scientist IV, Biologics & Biotechnology Laboratory Global Biologics

12:45 Session Break

Sponsored by SCIEX

12:55 LUNCHEON PRESENTATION I: High-Resolution Charge Variant Analysis for a Variety of Therapeutic Proteins in as Little as 5 Minutes
Peter Holper, Applications Scientist, CE & BioPharma, SCIEX
In this study, we present a native state charge variant analysis that delivers high resolution results in as little as 5 minutes. Using a technique that requires little to no method development, a simple sample preparation and a higher analytical throughput and wider sample concentration range than icIEF, this platform method can easily be applied to a wide array of therapeutic proteins such as: antibody drug conjugates (ADCs), mono- and multi-specific antibodies, and fusion proteins.

1:25 Luncheon Presentation II *(Sponsorship Opportuinty Available)* **or Enjoy Lunch on Your Own**

MASS SPECTROMETRY ANALYSIS

2:00 Chairperson's Remarks
Elizabeth M. Topp, PhD, Dane O. Kildsig Chair and Department Head, Department of Industrial and Physical Pharmacy, Purdue University

2:05 Diverse Samples, Fast Turnaround: Providing Meaningful Data in Biotherapeutic Early Discovery
Alayna George Thompson, PhD, Senior Scientist I, Drug Discovery Science & Technology, AbbVie
Characterizing early discovery biologics presents challenges related to the diversity of molecules and formats coupled with the need for quick data turnaround. To address these challenges, we expanded a walk-up mass spectrometry analysis workflow for purified proteins to include characterization (protein identification, post translation modifications, and proteolysis) of proteins during transient cell expression. These analyses provide business impact by empowering data-driven decisions for biologics production.

KEYNOTE PRESENTATION

2:35 Solid-State Hydrogen Deuterium Exchange (ssHDX-MS): High-Resolution Characterization of Lyophilized Biotherapeutics

Elizabeth M. Topp, PhD, Dane O. Kildsig Chair and Department Head, Department of Industrial and Physical Pharmacy, Purdue University

More than 40% of biologics approved in the last ten years are marketed in lyophilized form, but the factors controlling stability in these amorphous powders are poorly understood. ssHDX-MS is a novel analytical method that characterizes protein structure and matrix interactions in the solid state with peptide level resolution. Results of ssHDX-MS analysis have been shown to be highly correlated with protein stability on long-term storage. This presentation reviews the ssHDX-MS method and presents new results from ongoing studies of exchange kinetics and mechanisms.

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.

Click here for details.

4:30 Characterization of Glycan Heterogeneity for mAb based molecules using High Resolution and Single Ion Monitoring Mass Spectrometry Techniques.
Sheila Mugabe, MSc, Scientist, MacroGenics, Inc.
Monoclonal antibodies and novel bispecific DART® molecules are being developed for a variety of indications including immune-oncology. This presentation discusses analysis of glycan heterogeneity profiles for such molecules using High Resolution and Single Ion monitoring mass spectrometry techniques. High throughput characterization approach during process development will be discussed.

PROCESS CHARACTERIZATION AND CONTROL

5:00 Computational Methods for Cell Culture Media Optimization and Product Quality Control
Gaurav Chauhan, MS, Associate Principal Scientist, Biologics Process Research and Development, Merck & Co., Inc.
Biologics development leading to approval can take decades. Acceleration is desired to bring safe and efficacious drugs to patients as early as possible. One research focus is to reduce development time for cell culture process development and optimization. Strategies will be shared that cover optimizing cell culture media using Orthogonal-Partial Least Squares (OPLS) regression and modulating glycosylation by altering small molecule compound concentrations based on the Concentration Impact Factor.

5:30 Risk Assessment of Formulation Attributes and Feasibility for Alternative Routes of Administration of Biologics during the Developability Stage
Yingkai Liang, PhD, Senior Scientist, Discovery Pharmaceutical Sciences, Merck & Co., Inc.
While intravenous administration is a generally well-accepted route of administration for biologicals, increasing market competition and desire for local therapy have renewed interest in the delivery of proteins by alternative routes of administration. This presentation will cover the assessment of formulation parameters in the context of optimizing developability properties of proteins intended for administration by alternate routes of delivery.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

HIGH-THROUGHPUT SCREENING, ASSAYS, AND OTHER ANALYTICAL CONSIDERATIONS

8:45 Chairperson's Remarks
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University

8:50 Size and Weight Are Two Related but Different Fundamental Measurables
David Hayes, PhD, Biophysics Consultant, International Solidarity of Scientists
Analytical methods and assays seldom measure product quality attributes directly, but they quantitate attribute levels through a related signal. Speaking of the various methods that quantitate aggregation, the terms such as size, weight, and molecular weight are conflated to mean the same thing. Understanding the strengths and weaknesses of aggregation assays requires more rigorous mathematical definition of measurables.

9:20 Biopharm Critical Quality Attributes (CQAs): It is When Product Analytics, Process, and Clinical Outcomes Connect
Wasfi AlAzzam, PhD, Chief Scientific Officer, TechnoPharmaSphere LLC
Analytical methods have been playing a major role in creating *in vitro* and *in vivo* biopharm product characterization packages. Compiling both sets of data helps in-depth understanding of product's quality attributes (QA) and filters some to figure the product's CQAs. It is proven that some CQAs have impact on the product's biological and clinical profiles. Biopharm industry is now revising their CMC strategy to accelerate product development. This talk will connect analytical, CQAs, and clinical outcomes.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 High-Throughput Biophysical Characterization of New Classes of Antibodies
Mitra Mosharraf, PhD, HTD Biosystems, Inc.
In this talk, characterization of various biomolecules such as mAb, fusion proteins, Fab and bispecifc antibodies will be discussed. We will showcase use of high-throughput technologies such as nDSF, MST, DLS, and protein chip bioanalyzer in characterization of the conformational and colloidal stability of these molecular entities alone and in combination.

11:30 Characterizing Protein Interactions and Solution Viscosities Using Advanced Scattering Tools
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University
Measuring and predicting solution viscosity is essential in formulating biopharmaceuticals. We show how we can use a combination of advanced characterization techniques, such as small-angle neutron (SANS) and X-ray scattering (SAXS) to characterize protein interactions and microrheology experiments to assess and predict solution viscosity in concentrated solutions of biopharmaceuticals. We will discuss recent advances in protein microrheology using either optical or microfluidics approaches.

Sponsored by biotechne

12:00 pm Influences of Sample Preparation and Data Evaluation on CE-SDS and SDS-PAGE
Rebeca Wiesner, PhD, Scientist, Technische Universität Braunschweig, Institute of Medicinal and Pharmaceutical Chemistry
Gel electrophoresis (SDS-PAGE) is the most common approach for molecular mass determination (MW) of proteins. Results are compared to CE-SDS (Maurice, ProteinSimple) and Simple Western (WES, ProteinSimple) concerning precision and accuracy of MW using nine typical model proteins (7-180 kDa) and Matuzumab (IgG antibody). Various conditions of sample preparation e.g. different temperature conditions and reducing agents and the influence of data evaluation by comparison of different molecular weight markers were investigated.

12:30 Session Break

Sponsored by NANOTEMPER

12:40 LUNCHEON PRESENTATION: Improve the Characterization of New Biologics by Knowing Protein Stability First with Prometheus
Peter Fung, PhD, Senior Product Marketing Manager, Nanotemper Technologies

1:10 Close of Characterization of Biotherapeutics Conference

DETECTION AND CHARACTERIZATION OF PARTICULATES AND IMPURITIES

Hot Topics, Emerging Contaminants and Impurities, Case Studies, and New Technologies

Cambridge Healthtech Institute's 6th Annual DETECTION AND CHARACTERIZATION OF PARTICULATES AND IMPURITIES conference will bring together leading researchers to discuss hot topics, emerging contaminants and impurities and new characterization tools for impurities that may come from various sources and stages of product development. Through new presentations, high-level poster presentations, and interactive discussions, top scientists will share new insights into characterization and control of various impurities. Some of the hot topics for this year will be new and novel technologies for aggregates and impurities in gene therapies, AAVs, virus and pathogen detection, host cell proteins, lipases and enzymatic degradation, other particles and aggregations, and chemistry and manufacturing controls (CMC).

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

PARTICLES, AGGREGATES, AND STABILITY

2:00 Chairperson's Opening Remarks
Boxu Yan, PhD, Senior Director, Analytical Development and Quality Control, Acceleron Pharma

KEYNOTE PRESENTATION

2:05 Microfluidic Approaches for the Characterization of Biopharmaceuticals

Paolo Arosio, PhD, Professor, Biochemical Engineering, Department of Chemistry and Applied Biosciences, ETH Zurich

We highlight the emerging possibilities offered by advances in microfluidic technology for the analysis of therapeutic proteins during manufacturing and formulation. We discuss a diffusion microfluidic platform for the characterization of: a) polydisperse size distributions in the sub-micron range; b) sizes and interactions in solutions at high protein concentration; and c) specific interactions in complex mixtures.

2:45 Cell-Based FcgR Binding Assay for Sensitive Detection of Biologics Aggregates
Joel F. Cohen-Solal, PhD, Senior Scientist, Global Protein Sciences, AbbVie Bioresearch Center, Inc.

Low-affinity Fc gamma receptors of different species have the ability to specifically bind to immune complexes or IgG aggregates, thus acting as either physiological sensors or uptake receptors. We will review the literature and internal data showing that a cell-based FcgR binding assay is, therefore, the relevant assay to monitor the presence of physiologically active aggregates in biologics solution or in serum.

Sponsored by halo labs

3:15 Fast, Low Volume Subvisible Particle Analysis with HORIZON
Renee Tobias, Director, Marketing, HALO LABS

The HORIZON is the industry's first analytical system to address the need for rapid, comprehensive subvisible particle analysis even when limited sample material is available. Based on the USP <788> method of Membrane Microscopy, image analysis on HORIZON is fully automated, uses a simple 96-well plate based approach, and requires only 25µL per sample. HORIZON enables incorporation of subvisible particle analysis into biologics workflows as early as developability assessment through late stage formulation and QC.

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

4:30 Moving towards Harmonization in Subvisible Particle Measurements: Advanced Data Analytics and New Reference Standards
Richard Cavicchi, PhD, Research Physicist, Biomolecular Measurement Division, Material Measurement Laboratory, National Institute of Standards and Technology

Improved quantitative measurements of subvisible particles will require advanced analytic methods to relate measured quantities to particle attributes (e.g., an equivalent diameter). New NIST reference materials can help with calibration and validation of these measurements.

5:00 Insight into Process Development of Oligonucleotide/ Polymeric Carrier Formulation
Rui Fang, PhD, Senior Scientist, Sterile Formulation Sciences, Merck & Co., Inc.

This presentation highlights investigations into formulation and process variables to understand the root cause of particle formation in an oligonucleotide/polymeric carrier formulation during manufacturing. Process variables that potentially lead to the failure were identified. Innovative approaches were applied to study pump pulsation. Predictive tools including CFD modeling and the 4th Bourne reaction were used to study mixing efficiency of the mixing chamber that potentially influences formulation composition and stability.

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*
Click here for details.
**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

SURFACTANT-RELATED AND PRODUCT IMPURITIES

8:15 Chairperson's Remarks
Paolo Arosio, PhD, Professor, Biochemical Engineering, Department of Chemistry and Applied Biosciences, ETH Zurich

FEATURED PRESENTATION

8:20 Human IgG1 Hinge Fragmentation as the Result of Radical Mediated Cleavage
Boxu Yan, PhD, Senior Director, Analytical Development and Quality Control, Acceleron Pharma

Hinge cleavage of a recombinant human IgG1 antibody is commonly observed from purified drug substance and in stability samples. The hinge cleavage was found initiated by radical-induced breakage of the disulfide bond between the two hinge cysteines. As hydroxyl radicals exist in healthy cells' tissues and most buffer solutions, they could therefore be the source for the radical-induced fragmentation of human IgG1 antibodies *in vivo*.

8:50 Impact of Buffer Species and Stainless-Steel Contact on Polysorbate and Protein Stability
Hieu (Vinnie) La, Associate Scientist, Formulation and Process Development, Pharmaceutical R&D, Bio-Therapeutics Pharmaceutical Sciences, Pfizer, Inc.
We explore the impact of buffer species, Fe spike and stainless-steel contact on polysorbate 80 (PS80) stability to enable a better understanding of histidine/EDTA-based formulations. We monitored PS80 degradation and protein methionine oxidation (MetOx) in formulations of a monoclonal antibody (mAb) containing several different buffers. It was found that polysorbate stability was sensitive to buffer species and that formulations containing histidine had much faster PS80 and MetOx rates. The metal exposure study suggested that PS80 was extremely sensitive to metal leachables. Stainless steel exposure in histidine buffer resulted in more rapid degradation of PS80 compared to what was ob-served for the other buffering systems examined. Addition of EDTA, however, was able to inhibit both PS80 and methionine oxidation in histidine-containing formulation.

9:20 Sponsored Presentation *(Opportunity Available)*

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

10:35 Case Study: Formulation Strategies to Eliminate Polysorbate Degradation-Related Particle Formation
Sandy Wang, MSc, Engineer II, Pharmaceutical Development, Genentech
Polysorbate 20 degradation resulting in the formation of free fatty acids can lead to particles in mAb formulations. This presentation will discuss a case study where different approaches were taken to identify a particle-free formulation.

11:05 Opportunities and Pitfalls in the Characterization of Submicron Particles during Biologics Product Development
Danny K. Chou, PharmD, PhD, President, Biopharmaceutical Characterization and Formulation Development, Compassion BioSolution, LLC
The presentation will focus on how one can take advantage of the newly available technologies for submicron and microsized particles while avoiding potential pitfalls.

11:35 Monitoring Clearance of Lipase Host Cell Proteins during Biotherapeutics Process Development Using a LC-MRM Quantitation Method
Rachel Chen, Scientist II, Analytical Development, Biogen
Successful removal of host cell proteins (HCPs) is very important for biopharmaceutical product development to ensure product quality and safety. Recently, it has been demonstrated that certain lipases may be the cause for enzymatic degradation of polysorbate 20 and 80, which are common surfactants used in protein formulations. An LC-MS/MS method was developed to achieve a sub ppm quantitation level of three lipases. The method has been applied to monitor the clearance of lipases for various mAbs and fusion proteins under different downstream processes.

12:05 pm Session Break

12:15 LUNCHEON PRESENTATION: Dig Deep into Particle Identification With Hound
Sponsored by UNCHAINED LABS
Robin Sweeney, PhD, Product Manager, Marketing, Unchained Labs
Particles muck up drug quality, cause headaches throughout development, and can shut down production. Hound pairs Raman 785 nm, Raman 532 nm, and laser induced breakdown spectroscopy (LIBS) with automated microscopy to count and ID particles.Hound is equipped to identify organic, inorganic, and elemental particles through built-in and customizable reference databases to track down the source of any contaminant.
We'll discuss Hound applications that highlight its role as an indispensable particle identification tool.

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

AGGREGATES AND IMPURITIES IN GENE THERAPY PRODUCTS

4:00 Chairperson's Remarks
Lisa Lundberg, Bioassay & Cell Culture Lead, Spark Therapeutics, Inc

4:05 Monitoring and Control of Aggregates and Impurities in Large Scale AAV Production
Lisa Lundberg, Bioassay & Cell Culture Lead, Spark Therapeutics, Inc
Monitoring and control of aggregates and impurities are important for successful large-scale production of gene therapies. In this presentation, we will discuss various aggregates and different types of impurities that can be encountered in a large scale AAV production, what tools and techniques can be used to monitor and characterize them, consideration for setting specification, etc.

4:35 Characterization and Quantification of Empty and Full AAV Capsids
Qin Zou, PhD, Associate Research Fellow and Group Leader, Analytical Research and Development, Pfizer, Inc.
This presentation can highlight various analytical methods for AAV empty and full capsids and emphasize the proper use of analytical ultracentrifugation for this purpose. AAV empty and full capsids is a product-related impurity and a critical quality attribute. Careful consideration of using appropriate analytical techniques to control that is important for a successful product.

5:05 Analytical Solutions for AAV Manufacturing
Tristan Thwaites, PhD, Lead Technical Scientist, Industrialization, Cell and Gene Therapy Catapult
With a push towards more sophisticated pipelines, we need to develop systems that can help us understand the interaction between the complex bioproduct and the process tools so that we can scale and control the manufacturing process. In this presentation, we will discuss different analytical solutions for AAV manufacturing.

5:35 Predicting Viral Clearance: DOE, HTS and AAV Case Studies Utilizing a Non-Infectious MVM Surrogate during Downstream Development
David Cetlin, Founder & CEO, MockV Solutions LLC
Viral clearance studies are expensive and logistically challenging. This presentation will highlight data from the use of a non-infectious MVM surrogate in a variety of downstream applications and processes.

POSTER PRESENTATION: Detection of AAV Capsid Proteins by CE-SDS as an Alternative to Silver Stain SDS-PAGE
April Blodgett, MS, LAT, Biotherapeutics Senior Sales Specialist, PerkinElmer, Inc.
SDS-PAGE followed by silver staining has typically been used to visualize the VP1, VP2, VP3 ratio. This approach is labor and time-intensive but yields only qualitative data with poor reproducibility. Here, we describe the use of microfluidic CE-SDS for the characterization of capsid proteins from AAV serotype 8 as the rapid, quantitative, reproducible alternative to SDS-PAGE with silver stain.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Detection and Characterization of Particulates and Impurities Conference

PROTEIN AGGREGATION AND EMERGING ANALYTICAL TOOLS

Mechanism, Prediction, Ummunogenicity, Developability, and Process Challenges

The popular 11th Annual PROTEIN AGGREGATION AND EMERGING ANALYTICAL TOOLS conference covers latest trends, challenges and solutions in understanding, characterization and mitigation of problems generated by protein aggregation in biopharmaceuticals. This conference will feature in-depth case studies, new and unpublished data and interactive discussions on immunogenicity of aggregates, mechanisms of aggregation, new tools for detection and quantitation of aggregates, and how the data is used in regulatory filings, developability assessment, fill/finish challenges and other critical issues.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

UNDERSTANDING AND PREDICTING PROTEIN AGGREGATION

8:10 Organizer's Welcome Remarks
Nandini Kashyap, Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University

KEYNOTE PRESENTATION

8:20 Understanding and Predicting Self-Association in High Concentration Antibody Solutions – A Colloid Approach

Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University

We address the problem of enhanced self-association in high concentration antibody solutions and the concomitant high viscosities. In order to understand and predict the thermodynamic and flow properties of such formulations, we provide the first quantitative description of mAb self-association and viscosity as a function of concentration by combining experiments (static and dynamic scattering and microrheology), theory and computer simulations using a model based on analogies to patchy colloids.

9:00 Estimating Solution Nonideality from Measured Values
Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire

The concentration-dependent chemical potential of a species results from the sum of its repulsive and attractive interactions with neighboring species. The repulsive and attractive terms can be estimated using measured values of size, charge and association constants from a combination of one- and two-component solution measurements. The underlying concepts will be explained and the need for measured values will be highlighted.

9:30 Detection and Characterization is the First Step to Eliminating Aggregation *Sponsored by* **Wyatt Technology**

Sponsored by WYATT TECHNOLOGY

Kevin McCowen, Southwest Regional Manager, Wyatt Technology

Size exclusion chromatography (SEC) with UV detection gives limited information on the nature of aggregates. In this presentation, we discuss how multi-angle light scattering in conjunction with SEC as well field flow fractionation and dynamic light scattering allow the researcher to rapidly assess formulation stability to aid in the elimination of aggregates in the early development phase, detect the presence of large aggregates, and probe aggregate characteristics such as absolute molecular weight and conformation.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

IN VIVO AGGREGATION AND IMMUNOGENICITY

11:00 Application of an *in vitro* Skin Model System to Assess Potential Risk of *in vivo* Aggregation and Immune Activation of Biotherapeutic Attributes
Josh Tokuda, PhD, Postdoctoral Fellow, Biological Relevance and Characterization, Amgen, Inc.

In this presentation, a new human *in vitro* skin model system will be presented that can be used to assess the potential of biotherapeutics to aggregate and cause immune activation *in vivo*.

11:30 PANEL DISCUSSION: Prediction and Control of *in vivo* Aggregation and Immunogenicity

Discussion Points:
- Current Challenges
- New Predictive Tools
- Data Analysis and Management
- Use of Artifical Intelligence in Better Prediction and Control

Moderator:
Thomas Laue, PhD, Professor Emeritus, Biochemistry and Molecular Biology; Director, Biomolecular Interaction Technologies Center (BITC), University of New Hampshire
Panelists:
Peter Schurtenberger, PhD, Professor, Department of Chemistry, Lund University
Josh Tokuda, PhD, Postdoctoral Fellow, Biological Relevance and Characterization, Amgen, Inc.
John J. Correia, PhD, Professor, Department of Biochemistry, University of Mississippi Medical Center
Reza Esfandiary, Associate Director, Early Stage Formulation Sciences, BioPharmaceutical Development, AstraZeneca

12:00 pm Shear Rate Dependent Viscosity as an Indicator of Protein-Protein Interactions and Cluster Formation *Sponsored by* RheoSense

Stacey Elliot, Principal Scientist, R&D, RheoSense, Inc.

Protein-protein interactions and the resulting microstructure influence the low shear viscosity and onset of shear thinning, which are both practically relevant to pharmaceutical development. Shear rate dependent viscosity measurements on concentrated proteins are analyzed using concepts from colloidal systems to facilitate interpretation with respect to attraction strength and cluster size.

12:30 Session Break

12:40 LUNCHEON PRESENTATION: Everything You Wanted to Know About Protein Aggregation but Were Too Afraid To Ask *Sponsored by* UNCHAINED LABS

Kevin Lance, PhD, Product Manager, Marketing, Unchained Labs

Detecting and understanding aggregation is both complex and critical to the successful development of biologics. Thankfully Uncle delivers six powerful tools to ensure there is no shortage of insights on stability, aggregation, and non-specific interactions. Fluorescence, and static and dynamic light scattering work for your protein, antibody, or viral capsid to understand their willingness to stay folded and solitary, and if you've got the right formulation to keep them that way.

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

IN SILICO MODELING, TOOLS, AND ASSAY

2:15 Chairperson's Remarks
Christoph Brandenbusch, PhD, Group Leader, Biochemical and Chemical Engineering, TU Dortmund

2:20 FDS-AUC Analysis of mAb Nonideality and Self-Association in Serum and Formulation Solutions
John J. Correia, PhD, Professor, Department of Biochemistry, University of Mississippi Medical Center

The Aviv Fluorescence Detection System (Aviv-FDS) has allowed the

performance of sedimentation velocity experiments on therapeutic antibodies in highly concentrated environments, like serum and formulation buffers. Methods have been implemented in the software package SEDANAL for the analysis of nonideal, weakly associating AUC data acquired on therapeutic antibodies and proteins using absorbance or FDS optics. This involves determining both hydrodynamic nonideality Ks and thermodynamic nonideality BM1 plus association constants.

2:50 Mitigation of Reversible Self-Association and Viscosity of Monoclonal Antibodies via Structure-Guided Protein Engineering: Complementing Analytical and *in silico* Tools
Reza Esfandiary, Associate Director, Early Stage Formulation Sciences, BioPharmaceutical Development, AstraZeneca
High protein concentrations can introduce additional development challenges due to issues such as reversible self-association or high viscosity. Protein engineering can provide a complementary mitigation approach to formulation optimization in improving high concentration developability properties. Here, case studies utilizing complementary analytical and *in silico* methods are presented where molecular hotspots in monoclonal antibodies, responsible for high concentration issues, are systematically identified and engineered to generate variants with improved developability profiles.

3:20 Networking Refreshment Break

3:45 Thermodynamics-Based Approach for Predicting Aggregation Propensity and Beneficial Solution Conditions in Antibody Formulations
Christoph Brandenbusch, PhD, Group Leader, Biochemical and Chemical Engineering, TU Dortmund
Protein aggregation is caused by the molecular interactions of all components in solution. We developed a thermodynamics-based approach to predict beneficial solution conditions taking the competition for water by a specific excipient, as well as the molecular interactions of the proteins in the presence of excipients into account. This allows predicting a first estimate on aggregation propensity induced by the respective excipients and thus enables a first choice of preferential excipients with a minimum of experimental effort.

4:15 Discerning the Synergistic Effect of Hydrodynamic Flow and Interfaces on Protein Aggregation
Paolo Arosio, PhD, Professor, Biochemical Engineering, Department of Chemistry and Applied Biosciences, ETH Zurich
Despite being an area of extensive investigation, the effect of hydrodynamic flow and shear on protein aggregation is still controversial. Here, we demonstrate the presence of a synergistic effect of interfaces and hydrodynamic flow in flow-induced protein aggregation. We propose that hydrodynamic flow and shear stress should be considered in close association with interfaces when discussing sources of protein aggregation.

4:45 Computer Simulations of Aggregation of Proteins and Peptides
Andrzej Kloczkowski, PhD, Professor, Pediatrics, Nationwide Children's Hospital and The Ohio State University
Aggregation of proteins and peptides is an important biological phenomenon often related to protein misfolding and correlated with various diseases, such as Alzheimer's or Parkinson's; recently it has been shown that preeclampsia has similar molecular mechanism as Alzheimer's. Computer simulations are excellent tools to study the molecular mechanism, structural features and dynamics of protein aggregation, and formation of amyloid filaments and fibrils. Results of our recent computational simulations studies focused on specific diseases such as Alzheimer's, and preeclampsia will be revealed.

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

CHARACTERIZATION, DEVELOPABILITY ASSESSMENT, AND FILL/FINISH

9:00 Chairperson's Remarks
Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen

9:05 Qualifying a New Method for Submicron Particle Counting and Why It Matters
Gerhard Winter, PhD, Professor, Chair, Pharmaceutical Technology and Biopharmaceutics, LMU Munchen
We have tested and critically evaluated TRPS (Tunable Resistive Pulse Sensing) by using a rather affordable analytical equipment (IZON) and providing information on how to collect data, how to analyze and how to critically assess them. Comparisons with other techniques like RMM and NTA are made, and examples from very different primary packaging materials on what to expect from submicron particle counting and how to reduce particle burden are provided.

9:35 Challenges in Characterization and Developability Assessments of Multispecific Antibodies
Christian Lange, PhD, R&D Biologics Research, Assays and Analytics, Protein Therapeutics, Sanofi-Aventis Deutschland GmbH
The complexity of multispecific antibodies requires a comprehensive set of analytical techniques to guide lead discovery and optimization. An overview of these techniques will be presented with a focus on mispairing analysis and functional characterization of multispecific drug candidates. Furthermore, the integrated developability concept at Sanofi Biologics will be presented along with showcases highlighting potential challenges in characterization and developability of multispecifics.

10:05 Controlling Aggregation of a Range of Novel Biopharmaceutical Product Modalities
Jan Jezek, PhD, CSO, Arecor Ltd.
Whilst controlling aggregation of monoclonal antibodies has become a routine task through smart candidate screening and platform formulations, there are numerous novel modalities, such as multi-specific antibodies, ADCs, or gene therapy products, where aggregation remains a key problem. This talk will present case studies showing novel formulation approaches to reduce aggregation in these products and enable user-friendly formats.

10:35 Networking Coffee Break

11:00 Fill/Finish Strategies to Prevent and Overcome Aggregation Challenges
Marcel Tigges, PhD, Associate Director, The Janssen Pharmaceutical Companies of Johnson & Johnson
Fill & Finish processes for large molecule parenterals require a quality control toolbox that allows for efficient monitoring of stress factors potentially impacting drug product quality. New technologies and PAT (Process Analytical Technology) tools allow for real-time monitoring of protein concentration (FlowVPE) and low volume protein stability analysis (nanoDSF). Identification of critical process parameters (CPPs) and process steps that potentially cause protein aggregation guides the design of robust processes towards optimal mixing, filtration and filling conditions for highest drug product quality and stability standards.

11:30 Selected Poster Presentation: Detection and Characterization of Antibody Aggregates by Light Scattering and Fluorescence
Cornelia S. Ziegler, PhD, Scientist, Biologics Development-Bioanalytics, Sanofi France
Therapeutic antibodies are prone to aggregation like all proteins. A prime aspect of their development is the monitoring of their aggregation state during their shelf-life studies. Dynamic light scattering (DLS) is widely used to describe the colloidal status of the samples in the submicron size range. Currently, we are developing an orthogonal fluorescence-based technique, which will allow the specific detection and quantification of denatured state and native state protein aggregates.

12:00 pm Conference Wrap-Up
Jan Jezek, PhD, CSO, Arecor Ltd.

12:30 Close of Conference

PROCESS TECHNOLOGIES & PURIFICATION

The Process Technologies & Purification pipeline provides insights into new technologies and advanced strategies for protein processing, including high-throughput, continuous processing, and achieving optimized operations through cutting-edge data analytics and interpretation. Ensuring quality while streamlining process steps will also be addressed as well as developing methods that translate into scale-up. The weeklong pipeline explores practical methods that improve processes, trim costs, and lead to successful results.

January 20-21

AGENDA Bioprocess Data Management and Analysis

January 21-22

AGENDA Protein Purification and Recovery

January 23-24

AGENDA Higher-Throughput Protein Production and Characterization

JANUARY 20-21, 2020 | 4TH ANNUAL

BIOPROCESS DATA MANAGEMENT AND ANALYSIS

Advancing Bioprocessing through Instrumentation, Characterization, Control, and Analytics

The biopharmaceutical industry is meeting increasing demands and costs for biotherapeutics through process optimization. Data from advanced instrumentation through sampling techniques, new sensor technologies, and analyzers have emerged to monitor both upstream and downstream processes. When well-prepared and analyzed, this data leads to process knowledge, process control, and continuous improvement, resulting in greater speed, quality, and economy. Cambridge Healthtech Institute's 4th Annual BIOPROCESS DATA MANAGEMENT AND ANALYSIS conference addresses statistical analysis strategies allowing for optimized and informed control of bioprocessing.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

DATA DEFINES PROCESS DEVELOPMENT

9:00 Organizer's Welcome Remarks
Mary Ann Brown, Executive Director, Conferences & Team Lead, PepTalk, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Anne Richelle, PhD, Senior Specialist - Metabolic Modeling, Global Vaccines, Technical R&D, GlaxoSmithKline Vaccines

KEYNOTE PRESENTATION

9:10 Intelligent Data Management and Analytics towards Advanced Biopharmaceutical Process Development and Manufacturing

Cenk Undey, PhD, Executive Director, Process Development, Amgen

We generate a significant amount of data during development and manufacturing of biopharmaceutical therapeutic proteins. Managing data right from the start and throughout the product development lifecycle into manufacturing is critical for data flow, as well as optimizing and accelerating the development activities. We will review how we have been advancing the intelligent capture, management and leveraging of development data to optimize manufacturing using machine learning and other advanced data analytical methods.

9:50 Digital Twins as Product Life Cycle Companions
Thomas Zahel, PhD, Head of Innovation, Exputec GmbH

Digital Twins are *in silico* representations of entire manufacturing processes. Due to the linkage of models of multiple unit operations, it is possible to predict the impact of any process parameter or material attribute onto final product quality. Thereby, multiple benefits for manufacturers can be achieved such as setting feasible acceptance limits as well as a model-based control strategy, both leading to lowered number of failed batches and increased patient safety.

10:20 Networking Coffee Break

10:45 Importance of Upstream Analytical Assays and DOE Studies to Guide Early Process Development
Jonathan Mott, MS, Scientist, Upstream Process Sciences, Nektar Therapeutics

For some fast-paced programs, there is a temptation to rush the upstream process development and move forward with a functional but poorly characterized process. Here I present two case studies demonstrating how upstream analytical assays and DOE studies early in upstream process development are crucial to successful scale-up and commercialization.

11:15 Digital Bioprocessing: The Impact of Instrument and Software Integration
Spin Wang, MS, Co-Founder and CEO, TetraScience

Scientists and informatics teams place a heavy reliance on the manual collection, transfer, manipulation, storage, and reporting of their instrument data. This lack of automation slows processes, inhibits scalability, and can jeopardize data integrity. We have designed and developed a new approach to collect and manage data from a bioprocess workflow. Our hope is for this to serve as a blueprint to those pursuing a digital bioprocessing strategy.

11:45 How Can Systems Biology Tools Facilitate a Cost-Effective Upstream Process Development in the Biopharmaceutical Industry?
Anne Richelle, PhD, Senior Specialist - Metabolic Modeling, Global Vaccines, Technical R&D, GlaxoSmithKline Vaccines

In biotechnology, the emergence of high-throughput technologies challenges the interpretation of large datasets. One way to identify meaningful outcomes impacting process and product attributes from large datasets is using systems biology tools. While pharmaceutical companies are already investing substantially in computational approaches to guide drug discovery and cell design, model-based methods can also be applied for upstream process development to improve process understanding, lower the experimental effort and increase the process robustness.

Sponsored by GE Healthcare

12:15 pm Digitalization of Process Development – Current State and Future Outlook
Harlan Knapp, Business Development, Enterprise Solutions, Enterprise, GE Healthcare Life Sciences

Digitalization is a global trend across industries. Although the pharma industry is a late adopter, a shift is on the horizon. In this presentation we will highlight process development and the critical role of control strategy for implementing Industry 4.0 in pharma. We will assess the current state of our industry and provide a vision of the desired future state. Then, we will discuss key challenges and technological breakthroughs to address them.

12:45 Session Break

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

BIOREACTORS AND CONTINUOUS PROCESSING

2:00 Chairperson's Remarks
Bryan E. Jones, PhD, Research Fellow, BioTechnology Discovery Research, Eli Lilly and Company

2:05 Separation of Recombinant Protein in Perfusion Bioreactor Bleed Material Using Acoustic Wave Separator
Jin Sung Hong, PhD, ORISE Research Fellow, Center for Drug Evaluation and Research, FDA
In this study, we assessed separation of recombinant protein from a perfusion WAVE bioreactor bleed material using acoustic wave separator (AWS) for continuous upstream bioprocessing approach. We integrated a perfusion WAVE 25 bioreactor for perfusion cell culture to a Cadence AWS, thus providing continuous cell clarification of bleed material. Our data indicate AWS can provide effective cell clarification/filtration, and product recovery and quality.

2:35 Presentation to be Announced

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.

Click here for details.

HIGH-THROUGHPUT PLATFORMS: DATA MANAGEMENT AND MODELING

4:30 E2E Biologics Platform – From Discovery to Development
Yuan Lin, MSc, Senior Manager, Biologics Solution Lead, Pfizer
For the past 5 years, Pfizer has developed an E2E Biologics informatics Platform. The platform is a cohesive and authoritative data repository for Pfizer Biologics-oriented therapeutic projects across R&D. It streamlines sample registration, workflow and inventory management, assay data capture, and biomolecule analysis. In addition, it provides comprehensive data search, navigation, and report functionalities, and enables machine learning for better designing and developing biologics products.

5:00 Development of Higher-Throughput Assays for Antibody Discovery that Are Predictive of Developability Properties
Bryan E. Jones, PhD, Research Fellow, BioTechnology Discovery Research, Eli Lilly and Company
Therapeutic antibodies must possess suitable biophysical & developability properties to allow for their manufacture and ultimate delivery to the patient. Unfortunately, many of the common difficulties that arise during development of antibodies often only manifest under specific conditions (e.g., high concentration) that are impossible to "screen" for during antibody discovery. Therefore, we have focused on developing assays that exhibit predictability of downstream behavior (e.g., solubility), that are useful earlier in antibody discovery.

5:30 Platformization of Multi-Specific Protein Engineering: Learning from High-Throughput Screening Data
Norbert Furtmann, PhD, Head of Data Lab, High Throughput Biologics, Sanofi-Aventis Deutschland GmbH
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). Here we report on our visualization and data analysis workflows to improve the understanding of our complex molecules and guide the engineering process.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

CHO CELL BIOANALYTICAL AND BIOLOGICAL PROCESS DEVELOPMENT

8:45 Chairperson's Remarks
Nathan E. Lewis, PhD, Associate Professor, Department of Pediatrics, University of California, San Diego

8:50 Modeling Chinese Hamster Ovary Cell Metabolism: A Systematic Look at Model Parameters and Risk of Overfitting
Matthew Schinn, PhD, Postdoctoral Researcher, Department of Pediatrics, University of California, San Diego
Metabolic network models provide mechanistic understandings of cell metabolism, and therefore could guide the rational design of cell lines and culture processes. However, such models are liable to overfit due to their high degrees of freedom. Here we systematically evaluate a wide range of model parameters important to describing CHO fedbatch culture performance.

9:20 Model-Driven Process Development for Enhanced Bioprocessing
*Meiyappan Lakshmanan, PhD, Research Scientist & Group Leader, Systems Biology, Bioprocessing Technology Institute, A*STAR*
Chinese hamster ovary (CHO) cells are the preferred choice for biotherapeutic protein production. However, ensuring consistent high product quality remains a major challenge. The availability of the CHO genome sequence has enabled the development of genome-scale models (GEMs) to examine the metabolic signatures of CHO cells upon varying bioprocess conditions. This talk will show how the genome-scale models can help process development by characterizing key bottlenecks in media formulations and propose targets for media/feed optimization.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 Chairperson's Remarks
Khandaker Siddiquee, PhD, Principal Scientist, Abbott Diagnostic Division, Abbott Laboratories

11:00 Use of Statistics in Early Phase Bioprocess Development
Ruojia Li, PhD, Principal Scientist, Statistics Team Lead, Biologics Development, Bristol-Myers Squibb
Statistical analyses play a critical role in bioprocess development. Typical applications include power and sample size calculations, determination of proper threshold for comparison, design of experiments (DOE), and predictive modeling for process optimization. This talk will provide an overview and some case studies on how statistical analyses can be applied to advance early phase biologic process development.

11:30 Quality by Design Revealed that Oxidation of a Recombinant Fab Is Driven by CHO Cell Growth Conditions, Physiology, and Overexpression of Oxidative Stress Genes
Khandaker Siddiquee, PhD, Principal Scientist, Abbott Diagnostic Division, Abbott Laboratories
Quality by Design (QbD) and Design of Experiment (DOE) tools were utilized to optimize a bioprocess for production of a CHO recombinant antigen binding fragment (rFab) in small-scale bioreactors. The study also revealed the mechanism and pathway for oxidation of the rFab molecule during cell culture bioprocess optimization. The study further demonstrated the importance of integrating cell culture, analytical chemistry, and gene expression data to optimize the cell culture bioprocess prior to scaling up into the large-scale production bioreactor.

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

12:30 Session Break

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

1:10 Close of Bioprocess Data Management and Analysis Conference

JANUARY 21-22, 2020 | 12TH ANNUAL

PROTEIN PURIFICATION AND RECOVERY

Streamlining & Innovating Processes

Protein-based biologics depend on the expression and purification of viable proteins that can be scaled up and transported for human use. But, purifying protein remains a constant bottleneck that often involves time-consuming steps and techniques. However, today breakthrough technologies and tools are being employed to improve processes leading to properly folded proteins. Cambridge Healthtech Institute's PROTEIN PURIFICATION AND RECOVERY conference examines the strategies that efficiently lead to pure protein. This leading conference illustrates how 'traditional' strategies (protein A, chromatography, affinity tags) are being innovated and enhanced, while also demonstrating new tools that are being introduced and integrated to help streamline purification and ensure quality. This conference will also explore the finesse required when purifying complex molecules, such as membrane proteins, in the ever-present quest for purity.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

CONTINUOUS PURIFICATION PROCESSING

2:00 Chairperson's Opening Remarks
David Wood, PhD, Professor, Chemical and Biomolecular Engineering, Microbiology, Chemistry & Biochemistry, Ohio State University

KEYNOTE PRESENTATION

2:05 Continuous Purification of Antibody with Precipitation, a Process with Non-Interrupted Mass Flow of the Product

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

We developed a new continuous precipitation process where the mass flow of the product is not interrupted. This process is robust, because fluctuations in the feed stream can be readily handled and can be easily realized as a disposable unit, because the necessary equipment, such as tubing, fittings, static mixers, and hollow fiber modules, are commercially available and do not require surge tanks. This process is truly continuous compared to other, quasi/semi-continuous chromatography processes, which require cyclic operation.

2:45 Rapid Protein Production and Purification by Continuous Flow
Gregory Weiss, PhD, Professor, Chemistry, Pharmaceutical Sciences, Molecular Biology & Biochemistry, University of California, Irvine

The vortex fluid device invented by collaborator Professor Colin Raston (Flinders University, Australia) and the speaker, Professor Weiss, accelerates protein folding and purification using micrometer-scale thin fluidics to input mechanical energy, micromixing, and centrifugal force. The approach allows 10-minute purification from cell lysate to single band on SDS-PAGE and avoids centrifugation. Applying thin chromatographic layers avoids the clogging inherent to conventional chromatography and simplifies the protein purification process.

3:15 SymphonX™: Disruptive Multi-functional Downstream Bioprocessing for Batch and Continuous Operations

Sponsored by FUJIFILM Diosynth Biotechnologies

Jonathan Haigh, PhD, MBA, Senior Director Bioprocess Strategy & Development, FUJIFILM Diosynth Biotechnologies

SymphonX™ is a multi-functional bioprocess system capable of a range of downstream process unit operations. Advanced automation enables SymphonX™ to be deployed in both traditional (batch) and future (continuous) modes of biomanufacturing. This presentation introduces the technology and examples capability through a proof-of-concept continuous biomanufacturing facility. Apollo™-X mammalian cell system, operated in a 500L perfusion bioreactor, connected to seven SymphonX™ units, will aim to generate ~15kg purified monoclonal antibody over a 30 day process.

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

AFFINITY TAG TECHNOLOGIES

4:30 A Self-Cleaving Tag with Case Studies: Biosimilar Targets Expressed in *E. coli* and Mammalian Cells
David Wood, PhD, Professor, Chemical and Biomolecular Engineering, Microbiology, Chemistry & Biochemistry, Ohio State University

We have developed a functional prototype capture resin based on a self-cleaving intein tag and used the system to successfully purify several affinity-tagged target proteins. The proteins were expressed in *E. coli* or mammalian cells and purified using a single-column format, where the tag is automatically removed during the purification process. We will present data on the resulting purity and yield for several protein targets, including established therapeutic glycoproteins.

5:00 TAG TECHNOLOGIES PANEL DISCUSSION
Moderator:
Richard Altman, MS, Staff Scientist, Life Science Solutions, Thermo Fisher Scientific
Panelists:
Dennis Karthaus, MSc, Group Leader Cell Culture Sciences, IBA Lifesciences
Alexei Yeliseev, PhD, Staff Scientist and Leader, Protein Expression Group, NIH
David Wood, PhD, Professor, Chemical and Biomolecular Engineering, Microbiology, Chemistry & Biochemistry, Ohio State University

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*

Click here for details.

**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

EMERGING STRATEGIES FOR DEVELOPING VACCINES, BIOMATERIALS, AND ANTIBODIES

8:15 Chairperson's Remarks
Timothy M. Pabst, PhD, Principal Scientist, Protein Purification & Downstream Process Development, AstraZeneca

FEATURED PRESENTATION

8:20 Challenges and Advances in Vaccine Purification Development and Manufacture
Yan-ping Yang, PhD, Associate Vice President and Head, Bioprocess R&D, North America, Sanofi Pasteur

Over the last three decades, there has been significant evolution in downstream purification technologies to support vaccine development. The advances in this field have greatly benefited the vaccine industry to achieve consistent product purity and quality in a timely and cost-effective manner. In recent years, the vaccine field has attracted significant interest due to a rapid growth of the global market. However, it remains a challenging and complex industry. This presentation reviews the constraints and complexities in vaccine purification development and manufacture and describes the evolution of purification technology innovation to overcome these challenges, with an outlook into the future.

8:50 Spy and Snoop Peptide Superglues to Empower Vaccines, Biomaterials, and Antibodies
Mark Howarth, PhD, Professor, Biochemistry, University of Oxford

SpyTag peptide forms a spontaneous amide bond to the protein, SpyCatcher. Reaction is genetically-encodable and specific in diverse environments. Latest advances include accelerated reactivity, a toolbox for oligomerization, and Spy&Go purification. SpyTag and related SnoopTag allow programmable synthesis of polyproteams or biomaterials, modulating cancer cell signaling. Spy-VLP assembly has the potential to enhance vaccines against diverse existing and emerging diseases. SpyTag empowers antibodies, extending function with fluorophores, enzymes, toxins, or bispecifics.

9:20 Scalable Protein A-Based Fiber Chromatography for mAb Purification with Rapid Cycling *Sponsored by*

Linnea Troeng, Product Manager, Protein Purification, Product Manager, GE Healthcare

The protein A fiber matrix of Fibro technology has an open pore structure with mass transfer governed by convective flow. In this presentation we will show examples where automation and a combination of capture and desalting steps increase throughput in upstream process development. Further, we will discuss how Fibro can help to optimize wash and elution buffers in downstream process development. We will also show how this scalable technology enhances productivity at process scale.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

PURIFYING ANTIBODIES

10:35 Understanding and Exploiting the Nuances of Ion-Exchange Purification of mAbs

Abraham M. Lenhoff, PhD, Allan P. Colburn Professor, Chemical and Biomolecular Engineering, University of Delaware

Although the general principles of ion-exchange purification of proteins are well-known, observed column behavior can be appreciably influenced by effects at the particle and the column level that have received less attention. This presentation will discuss such effects as seen in both modeling studies and experimental observations; and will point out how such behavior can be exploited to improve separations performance.

11:05 Design and Application of Fc-Containing Bispecific Antibody Platform for Immunotherapy

Rumana Rashid, PhD, Lead Scientist, Protein Sciences, Xencor, Inc.

Xencor's heterodimeric Fc domain is a robust platform that enables us to develop bispecific antibodies and Fc fusion proteins efficiently. Its straightforward purification of the heterodimeric species is achieved through engineering isoelectric point differences in the Fc region, followed by a novel set of Fc substitutions. This can successfully produce heterodimer yields over 95% with little change in thermostability. We have exploited this platform to develop anti-cancer drugs of different classes. Finally, we present manufacturing data reinforcing the robustness of the heterodimeric Fc platform at GMP scale.

11:35 Using a Design of Experiment (DoE) Approach to Develop a Cost-Effective Antibody Fragment Purification Process

Wan-Ching Lai, PhD, Principal Scientist, Diagnostics, Abbott Laboratories

With the constant improvements to genetic engineering, the production of recombinant Fabs has become a viable alternative to antibodies. Here, we demonstrate the development of robust, cost-effective CH1-XL affinity chromatography process using a Design of Experiment approach. Further improvements include the implementation of a cycling purification approach to increase overall yield without increasing the amount of resin required. The optimized process resulted in near 15-fold increase in yield per ml/resin.

12:05 pm Session Break

12:15 LUNCHEON PRESENTATION I: Alleviate the Purification Bottleneck in Late Stage Discovery and Process Development *Sponsored by*

William Barrett, PhD, Product Specialist, Chromatography, Gore & Associates, Inc.

Traditionally, affinity chromatography using membrane technology has had limited scalability for process development and manufacturing. The new GORE Protein Capture Device offers a Protein A membrane solution to alleviate the purification bottleneck in late stage discovery and process development. The GORE Device combines high binding capacity and short residence times to aid higher productivity. Results will highlight two studies across two titers and present initial data for next generation larger devices.

12:45 LUNCHEON PRESENTATION II: Small scale (10-40ml) Automated HTP- Paramagnetic Bead Antibody Purification Technology *Sponsored by*

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

Amgen presents one of its latest innovations for antibody screening and drug discovery using an automated parallel HTP paramagnetic bead purification platform. The technology eliminates the need for centrifugation and filtration. Beads are added directly to whole cell cultures during expression. After binding, the beads are magnetically separated from the cell cultures, washed and the target is eluted for analysis. Some of Amgen's technology has been deployed and licensed to GenScript for commercialization.

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL

Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

EMERGING TOOLS & TECHNOLOGIES

4:00 Chairperson's Remarks

Gregory Weiss, PhD, Professor, Chemistry, Pharmaceutical Sciences, Molecular Biology & Biochemistry, University of California, Irvine

4:05 Production of Complex Target Proteins to Enable Antibody Generation

Corey Smith, PhD, Senior Scientist, Abbvie Bioresearch Center

Obtaining stable recombinant proteins that resemble the native target structure and function is essential for the advancement of pipeline projects. The complexity of many targets like membrane proteins poses a challenge, and I will present methods that we have developed to purify and stabilize such complex proteins. Case studies will be presented for the preparation of co-receptor complexes and of multi-span transmembrane proteins that enabled the generation of agonist and IHC antibodies, respectively.

4:35 Tools to Evaluate Protein A Chromatographic Stationary Phases

Timothy M. Pabst, PhD, Principal Scientist, Protein Purification & Downstream Process Development, AstraZeneca

As therapeutic use of monoclonal antibodies and related molecules continues to grow, Protein A chromatography remains the primary mode of purification due to high specificity, platformability, and strong regulatory track record. But as the biopharmaceutical industry faces pressures for lower costs, process developers continue to look for opportunities to improve productivity and lower cost of goods. In this presentation, we provide the tools that can be used to evaluate Protein A stationary phases, many of which offer high binding capacities coupled with excellent impurity clearance.

5:05 Enhancing Virus Filter Throughput for Hydrophobic Proteins Using a High-Throughput Screening Tool

Lu Wang, PhD, Associate Director, CMC Process Development, Teva Pharmaceuticals USA, Inc.

Virus reduction filtration (VRF) is considered as one of the most robust and effective virus clearance steps used in the manufacture of biologics. However, for hydrophobic proteins, VRF process development can be challenging due to filter fouling, which results in low throughput. This presentation is a case study that compares the VRF performance based on protein hydrophobicity and demonstrates a strategy to improve the viral filter throughput to enable GMP manufacturing facility fit.

5:35 Will the Real KRAS Please Stand Up?

Simon Messing, PhD, Scientist II, Protein Expression Laboratory, Leidos Biomedical/Frederick National Laboratory for Cancer Research

Human KRAS GTPase is one major hub involved in processing growth-related cellular signals. Hence, mutations in KRAS drive or contribute to roughly 30% of all cancers and make for a desirable target for therapeutic intervention. A large part of this work is done on recombinant KRAS with a non-native N-terminus. Here we have produced KRAS with proper post-translational modifications on both N- and C-termini from mammalian and insect expression systems.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Protein Purification and Recovery Conference

HIGHER-THROUGHPUT PROTEIN PRODUCTION AND CHARACTERIZATION

Analyzing & Improving Processes

In Cambridge Healthtech Institute's HIGHER-THROUGHPUT PROTEIN PRODUCTION AND CHARACTERIZATION conference, HTP is explored in the quest to develop methods that ensure quality and translate to large scale much more quickly and efficiently than in the past. Automation, robotics, and liquid handlers will be discussed, along with developing small-scale models and multi-scale models that shed light on bioproduction, particularly for continuous processing. Case studies will be presented that illustrate how leaders in the field are integrating HTP approaches to reduce the time and effort needed to successfully analyze proteins, fine tune processes, and develop new classes of biological products.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

GENERATING PROTEIN LIBRARIES AND LARGE DATASETS WITH HTP

8:10 Organizer's Welcome Remarks
Mary Ruberry, MA, Senior Conference Director, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Christopher Bahl, PhD, Head, Protein Design, Protein Design Laboratory, Institute for Protein Innovation

KEYNOTE PRESENTATION

8:20 High-Throughput Generation of Protein Libraries for Early-Stage Development of Novel Therapeutics

Renaud Vincentelli, PhD, Head, High-Throughput Protein Production, Structural Biology Core, Architecture et Fonction des Macromolécules Biologiques (AFMB), UMR, CNRS – Aix-Marseille University

This presentation details the high-throughput *E. coli* protein production pipeline at the AFMB and its streamlining to generate exhaustive libraries of various protein families, including animal toxins and PDZ domains. The pipeline facilitates rapid expression screening, protein production, and sample quality control; thereby harnessing the potential of these large protein families for the development of novel therapeutics.

9:00 Platformization of Multi-Specific Protein Engineering III: Generating Large, Multiparametric Data Sets for Data Mining through End-to-End Automated High-Throughput Engineering Workflows
Jörg Birkenfeld, PhD, Section Head, High-Throughput Biologics, R&D Biologics Research/Protein Therapeutics, Sanofi-Aventis Deutschland GmbH

We recently established a novel, end-to-end automated process for the fast generation and characterization of very large panels of multi-specific variants (up to 10.000). Here we report on how we apply this high-throughput engineering platform for multiparametric optimization of next-generation protein therapeutics.

Sponsored by PerkinElmer

9:30 Extended Horizons of LabChip™ Microfluidic Characterization Platform for Biotherapeutic Screening and Quality Control
Guangnan Meng, Product Manager, Microfluidics, PerkinElmer

The LabChip™ GXII Touch protein characterization system from PerkinElmer is a smart microfluidic platform for high throughput quantification and quality screening of protein molecules. With simple sample preparation setup, minimal sample volume consummation, and accurate and reliable measurements, it has been widely adopted into modern biotherapeutic screening and quality control processes. We will present our latest development of protein characterization assays, and discuss the new range and capabilities of the LabChip™ GXII Touch platform.

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

HIGH-THROUGHPUT PROTEIN PRODUCTION

FEATURED PRESENTATION

11:00 PEPP: An Automated High-Throughput Protein Production Platform
Sarah Rue, PhD, Associate Director, Advanced Automation Technologies, Genomics Institute of the Novartis Research Foundation (GNF)

Recombinant protein expression and purification is critical to support biomedical research. Chinese hamster ovary (CHO) cells and Human Embryonic Kidney (HEK) cells are workhorse cell lines for protein production from mammalian cells. GNF has developed a suite of automation and custom software to support transient protein production in CHO or HEK cells, stable pool establishment in CHO cells, the archive of cell banks, and protein purification. Cells are handled in AutoFlasks™ on the system, and cell growth is monitored in a non-invasive manner daily using a custom Flask Density Reader. An innovative new software Dashboard to help the operator manage projects and execute processes will be described, as will new hardware to enable a magnetic bead-based purification workflow. This platform enables cost-effective, facile production of proteins at quantities and of quality useful for early stage drug discovery tasks such as screening and even *in vivo* studies.

11:30 High-Throughput Production of Human Proteins for Structure/Function Analyses
Nicola Burgess-Brown, PhD, Principal Investigator, Nuffield Department of Medicine, SGC, University of Oxford

The SGC promotes research advancement through our open access policy. Globally, we have solved more than 2000 human protein structures and 12 novel integral membrane proteins (IMPs). Our well-established high-throughput processes for production and validation of intracellular and membrane proteins will be presented with their success rates. In addition, optimization strategies employed over the past 15 years to tackle the most recalcitrant proteins; including mutagenesis, mammalian (BacMam) expression, FSEC, and twin-step purification will be discussed.

12:00 pm Rapid Development of Soluble, Highly Productive, Scalable Biomanufacturing Solutions for Complex Biologics in *E. coli* SoluPro®
Matthew Weinstock, PhD, Group Leader, Molecular Sciences

Sponsored by AbSci

12:30 Session Break

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

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

HIGH-THROUGHPUT SCREENING

2:15 Chairperson's Remarks
Sarah Rue, PhD, Associate Director, Advanced Automation Technologies, Genomics Institute of the Novartis Research Foundation (GNF)

2:20 DNA-Encoded Glycan Libraries as a Next-Generation Tool for Screening and Measuring Sugar Binding
Peng George Wang, PhD, Professor, Pharmacology and Chemical Biology, Baylor College of Medicine
Screening, detecting, and measuring carbohydrate-protein or carbohydrate-cell interaction/recognition is crucial to the understanding of glycan involving physiological and pathogenic processes, intervention, and regulation. Adopting DNA next-gene sequencing, we used DNA-encoded glycan library (DEGL) for high-content, high-throughput study of glycan-protein interaction. Here we will discuss novel methods designed specifically for the high-content synthesis of DNA-encoded glycans, encoding and decoding principles, selection, and sequencing approaches for the easy and universal application of DEGL for screening and measuring sugar binding.

2:50 A High-Throughput Approach for Screening Protein-Protein Interactions in Complex Biofluids Using Protein Engineering
Liviu Movileanu, PhD, Professor, Physics, Biomedical and Chemical Engineering, Syracuse University
Protein-protein interactions (PPIs) are at the heart of cell signaling. Yet, we have very limited ways to quantitate them, especially in a heterogeneous solution, such as blood serum. We have manufactured a single-polypeptide chain protein sensor capable of detecting transient PPIs, one interaction at a time. In this talk, I will show how a parallel electrical recording technology can be used for assessing this protein sensor in a scalable fashion.

3:20 Networking Refreshment Break

HIGH-THROUGHPUT ANTIBODY PROCESSES

3:45 Application of a High-Throughput Antibody Optimization Platform: From NGS-Supported Library Generation to High-Throughput Antibody Expression and Multi-Parameter Characterization of Large Variant Libraries
Ernst Weber, PhD, Laboratory Head, Biologics Lead Optimization and Project Leader, Ophthalmology, Bayer Healthcare AG
The presentation will focus on the set-up of an HT antibody optimization platform capable of improving multiple parameters in parallel. It will cover the NGS-supported generation of 1-10k variants, their HT expression and testing in parallel for multiple parameters, including stability, x-reactivity, affinity, potency, immunogenicity potential, etc., and will also include the IT infrastructure assembling and compiling the data. Case studies showing the capabilities and flexibility of such platform success, including the optimization of antibodies targeting GPCRs, will be presented.

4:15 Characterization of Novel and Complex Antibody Formats
Markus Haberger, Group Leader, Development Characterization Analytics, Roche Diagnostics GmbH
The number of novel biotherapeutic antibody-based formats in drug development is continuously increasing. Characterization of these formats is challenging. Since established physiochemical and mass spectrometric methods show limited capabilities for characterization of product-related impurities, new analytical strategies have to be developed. Here, we present a native MS-based HT analytical approach which successfully assisted in the elucidation of size and charge variants of complex antibody formats, such as bispecific antibodies or antibody fusion proteins.

4:45 High-Throughput Production of Antibodies Using Yeast and Mammalian Cells
Jürgen Nett, PhD, Director, High-Throughput Expression, Adimab, LLC
High-throughput, small-scale protein production is an essential part of the antibody discovery workflow. After isolation from a large yeast-based antibody library, we directly express large panels of full-length IgGs in 96-well and 24-well formats. Protein purification is accomplished in a plate-based format using liquid handling platforms. The same semi-automated process is also compatible with IgGs expressed in mammalian hosts. Process setup, attributes, and output will be reviewed.

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

IMPROVING PROCESSES USING HTP

9:00 Chairperson's Remarks
Nicola Burgess-Brown, PhD, Principal Investigator, Nuffield Department of Medicine, SGC, University of Oxford

9:05 From DNA to Protein in Under 24 Hours; A Rapid and High-Throughput Method to Produce Native Protein
Christopher Bahl, PhD, Head, Protein Design, Protein Design Laboratory, Institute for Protein Innovation
We have optimized a protein production pipeline that enables the automatic expression and purification of proteins in 96-well plate format. Starting from plasmid DNA, the process can be performed in under 24 hours. Our method leverages transformation and expression in *Escherichia coli*, autoinduction media, affinity purification using paramagnetic beads, on-bead post-translational modification and elution; and it enables proteins to be produced in user-defined buffers.

9:35 Automated Formulation Development Using a High-Throughput Approach
Sabine Eichling, PhD, Head, Advanced Formulation Development, NBE Formulation Sciences, AbbVie Deutschland GmbH & Co KG

10:05 High-Throughput Cloning and IVTT Expression for Biomarker Discovery and Functional Genomics
Vel Murugan, PhD, MBA, Research Scientist, Virginia G. Piper Center for Personalized Diagnostics, The Biodesign Institute, Arizona State University
DNASU is a central repository for plasmid clones and collections. Currently, we store and distribute over 300,000 plasmids, including 75,000 human and mouse plasmids, full genome collections, the protein expression plasmids from the Protein Structure Initiative as the PSI: Biology Material Repository, and both small and large collections from individual researchers. We currently possess the largest collection of human full-length clones in multiple expression-ready plasmids. I will discuss HT cloning methods that we employ for generating expression clones.

10:35 Networking Coffee Break

HIGH-THROUGHPUT ANALYTICS

11:00 Implementing High-Throughput Purification and Analytics Processes to Accelerate Identification of Promising Biologics Therapeutics
Daniel Yoo, Scientist, Therapeutic Discovery, Biologics Optimization, Amgen, Inc.
As new and emerging biologic therapeutics rapidly increase in complexity, there is a significant need for high throughput (HT) purification and analytics processes. Here, I present

our implementation of rapid processes for screening panels, advancements to our higher-throughput platforms to enable automated complex chromatography, and tools for robust, rapid protein characterization. These enhancements enable more comprehensive screening and informed lead selection decisions.

11:30 Antibody Specificity Measurement and Scoring for Targeting Protein Post-Translational Modification Sites
Yongku Cho, PhD, Assistant Professor, Chemical and Biomolecular Engineering, University of Connecticut
Antibodies targeting site-specific protein post-translational modification (PTM) is an emerging category of biotherapeutics. Many antibodies claim PTM-specificity, but users have no means of comparing their specificity. Here we report a robust flow cytometry assay that enables the determination of a specificity parameter termed Φ, which measures the fraction of non-specific signal in antibody binding.

12:00 pm Conference Wrap-Up
Renaud Vincentelli, PhD, Head, High-Throughput Protein Production, Structural Biology Core, Architecture et Fonction des Macromolécules Biologiques (AFMB), UMR, CNRS – Aix-Marseille University

12:30 Close of Conference

BIOTHERAPEUTIC EXPRESSION & PRODUCTION

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 biotherapeutic research and manufacturing pipelines. Throughout the week, the Biotherapeutic Expression & Production pipeline explores the newest data, innovations and strategies to make the expression of therapeutic proteins more efficient, effective and trouble-free.

January 20-21

AGENDA Engineering Genes, Vectors, Constructs, and Clones

January 21-22

AGENDA Recombinant Protein Expression and Production

January 23-24

AGENDA Optimizing Expression Platforms

JANUARY 20-21, 2020 | 12TH ANNUAL

ENGINEERING GENES, VECTORS, CONSTRUCTS, AND CLONES

Exploring Tools and Developing Strategies to Expand the Protein Expression Toolbox

The demand for high-quality biotherapeutic proteins has never been greater. Many variables still must be considered during the cell-line development process, including verification and sequence analysis of the gene or protein of interest, codon optimization, vector construction, and clone/host selection – a time-consuming and expensive process. Additionally, protein expression scientists are now exploring new engineering tools, such as synthetic biology and systems engineering. Ultimately, these tools must be weighed against traditional expression and production strategies to achieve the desired quantity and quality. Cambridge Healthtech Institute's 12th Annual ENGINEERING GENES, VECTORS, CONSTRUCTS, AND CLONES conference continues the tradition of applying effective engineering strategies for protein expression and production research leading to functional biotherapeutic products.

SUNDAY, JANUARY 19

4:00 - 6:00 pm Pre-Conference Registration

MONDAY, JANUARY 20

7:00 am Registration and Morning Coffee

EXPLORING EXPRESSION TOOLS

9:00 Organizer's Welcome Remarks
Mary Ann Brown, Executive Director, Conferences & Team Lead, PepTalk, Cambridge Healthtech Institute

9:05 Chairperson's Opening Remarks
Harun Rashid, PhD, Senior Principal Scientist, Molecular Technology, Ambrx, Inc.

KEYNOTE PRESENTATION

9:10 High-Throughput Expression of Functional Proteins in a Microarray Format

Josh LaBaer, MD, PhD, Executive Director, Biodesign Institute, Arizona State University

The Nucleic Acid Programmable Protein Array uses printed cDNAs as templates to produce full-length proteins *in situ*, enabling high-throughput biochemical testing of thousands of well-folded proteins simultaneously. The recombination-based vector system allows users to routinely execute the automated transfer of thousands of genes into useful protein expression vectors overnight. These methods are now extended to include decorating the proteins with post-translational modifications, including glycosylation, acetylation, citrullination and others.

FEATURED PRESENTATION

9:50 Codon and Codon-Pair Usage Tables (CoCoPUTs): Facilitating Genetic Variation Analyses and Recombinant Gene Design
Chava Kimchi-Sarfaty, PhD, Deputy Associate Director for Research, Office of Tissues and Advanced Therapies, CBER, FDA

We have created for codon and codon-pair usage tables (CoCoPUTs), genome and tissue specific, a new and regularly updated website that encompasses the previously generated High-Performance Integrated Virtual Environment codon usage tables (HIVE-CUTs) that has also been expanded to include codon-pair usage and dinucleotide statistics. The use of this tool will be discussed specifically for therapeutics' design.

10:20 Networking Coffee Break

10:45 Cell-Free Protein Synthesis from Genomically Recoded Bacteria Enables Multisite Incorporation of Non-canonical Amino Acids
Antje Krüger, PhD, Postdoctoral Fellow, Michael Jewett Laboratory, Department of Chemical and Biological Engineering, Northwestern University

Cell-free protein synthesis has emerged as a powerful approach for expanding the range of genetically encoded chemistry into proteins. We recently established a bacterial cell-free protein synthesis platform based on genomically recoded *Escherichia coli* lacking release factor 1 that enables both high-yield protein synthesis and incorporation of multiple, identical non-canonical amino acids. In this talk, we will discuss the development of this platform and its use in engineering the translation machinery.

11:15 Expression Optimization of an Antibody Fab Fragment in *Escherichia coli* with Non-Native Amino Acid (NNAA) Incorporated
Harun Rashid, PhD, Senior Principal Scientist, Molecular Technology, Ambrx, Inc.

In this study, expression of a "difficult-to-express" antibody Fab fragment with a non-native amino acid (NNAA) inserted was systematically optimized by expression vector engineering. After the various genetic elements on expression vector were tested individually, the beneficial ones were then combined into a single expression vector, which resulted in significant improvement of Fab titer over the starting strain.

11:45 Optimizing Gene Sequences for Improved Protein Expression in Industrial Microorganisms
Tomoshi Kameda, PhD, Senior Research Scientist, National Institute of Advanced Industrial Science and Technology

Codon optimization by synonymous substitution is widely used for recombinant protein expression. Recent studies have investigated sequence features for codon optimization based on large-scale expression analyses. However, these studies have been limited to common host organisms such as *Escherichia coli*. Here, we develop a codon optimization method for Rhodococcus erythropolis, a gram-positive GC-rich actinobacterium attracting attention as an alternative host organism. We optimize the coding sequences of 12 genes and confirm that 9 of them (75%) achieve increased expression levels compared with wild-type sequences. And, we also confirm our method is effective in other bacteria for industrial use.

12:15 pm Sponsored Presentation *(Opportunity Available)*

12:45 Session Break

Sponsored by ATUM

12:55 LUNCHEON PRESENTATION I: Machine Learning for Predictive Antibody Design and Humanization
Claes Gustafsson, PhD, Co-Founder, CEO, ATUM

Engineering of better antibodies, improved cell lines and higher production yields requires efficient tools to navigate biological high dimensional sequence-function space. We describe how traditional humanization approaches that incorporate homology modeling and CDR grafting can be drastically improved by applying DoE and machine learning methodologies to generate a small number of humanized molecules with improved develop-ability profiles. The results from humanization experiments from 12 different antibodies impart predictive design strategies for future antibody humanizations.

1:25 Luncheon Presentation II *(Sponsorship Opportunity Available)*

GENE EDITING

2:00 Chairperson's Remarks
Jeffrey Barrick, PhD, Associate Professor, Molecular Biosciences, The University of Texas at Austin

2:05 Transposon-Encoded CRISPR–Cas Systems Direct RNA-Guided DNA Integration
Samuel H. Sternberg, PhD, Assistant Professor, Department of Biochemistry and Molecular Biophysics, Columbia University
Conventional CRISPR–Cas systems maintain genomic integrity by leveraging guide RNAs for the nuclease-dependent degradation of mobile genetic elements. We uncovered a remarkable inversion of this paradigm, in which bacterial transposons co-opt nuclease-deficient CRISPR–Cas systems to catalyze RNA-guided integration of mobile genetic elements into the genome. This discovery of a fully programmable, RNA-guided integrase lays the foundation for genomic manipulations that obviate the requirements for double-strand breaks and homology-directed repair.

2:35 Defending Engineered Bacteria against Evolutionary Failure
Jeffrey Barrick, PhD, Associate Professor, Molecular Biosciences, The University of Texas at Austin
Mutations in engineered DNA sequences can occur rapidly and infiltrate processes with 'broken' cells. Selfish genetic parasites–such as transposons and prophages–are a major source of inactivating mutations in bacterial genomes. In this talk, I will describe the broad-host-range CRISPRi-ME system that can be added to a bacterial cell to repress these mobile elements and other strategies for creating chassis cells with lower-than-natural mutation rates to stabilize their functions.

3:05 Find Your Table and Meet Your BuzZ Session Moderator

3:15 BuzZ Sessions with Refreshments
Join your peers and colleagues for interactive roundtable discussions.
Click here for details.

VECTOR DESIGN AND CELL ENGINEERING

4:30 Generation of Improved Host Cell Lines for Biomanufacturing Using Vector and Cell Line Engineering Technologies
Dennis Pfaff, PhD, Investigator III, CLSD, NIBR Biologics Center, Novartis Pharma AG
A toolbox of vector elements and novel engineered CHO cell lines were developed, which resulted in an increase of titer and improved product quality. By integrating these vector and cell line engineering technologies, we are aiming to further reduce timelines during cell line development.

5:00 Sequential Mechanism-Derived Heterogeneity in a Therapeutic Monoclonal Antibody
Matthew Schenauer, PhD, Senior Research Scientist II, Biologics Analytical Operations, Gilead Sciences
The observation, identification, and mechanistic basis for a unique product-related variant in a purified monoclonal antibody (mAb) therapeutic is described. It will be demonstrated that unlike typical mAb heterogeneity, the variant arose by via distinct and sequential biochemical and molecular biological processes.

5:30 The Cellular Impact of Glycoengineering
Nathan Lewis, PhD, Associate Professor, Department of Pediatrics, University of California, San Diego
Many therapeutic proteins are glycosylated, and the glycans often significantly impact drug safety and efficacy. Thus, there has been an increased interest in engineering the host cell to provide tailored glycosylation. Here I will present our work wherein we have deeply studied the impact of cell engineering on >180 clones, and how the engineering of glycosylation impacts cell phenotypes, their transcriptomes, and glycan patterns in expected and unexpected ways.

6:00 - 7:15 Welcome Reception in the Exhibit Hall with Poster Viewing

7:15 Close of Day

TUESDAY, JANUARY 21

8:15 am Registration and Morning Coffee

CHO CELL LINE ENGINEERING

8:45 Chairperson's Remarks
Nathan E. Lewis, PhD, Associate Professor, Department of Pediatrics, University of California, San Diego

8:50 Modeling Chinese Hamster Ovary Cell Metabolism: A Systematic Look at Model Parameters and Risk of Overfitting
Matthew Schinn, PhD, Postdoctoral Researcher, Department of Pediatrics, University of California, San Diego
Metabolic network models provide mechanistic understandings of cell metabolism, and therefore could guide the rational design of cell lines and culture processes. However, such models are liable to overfit due to their high degrees of freedom. Here we systematically evaluate a wide range of model parameters important to describing CHO fedbatch culture performance.

9:20 Model-Driven Process Development for Enhanced Bioprocessing
*Meiyappan Lakshmanan, PhD, Research Scientist & Group Leader, Systems Biology, Bioprocessing Technology Institute, A*STAR*
Chinese hamster ovary (CHO) cells are the preferred choice for biotherapeutic protein production. However, ensuring consistent high product quality remains a major challenge. The availability of the CHO genome sequence has enabled the development of genome-scale models (GEMs) to examine the metabolic signatures of CHO cells upon varying bioprocess conditions. This talk will show how the genome-scale models can help process development by characterizing key bottlenecks in media formulations and propose targets for media/feed optimization.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

CELL-FREE SYSTEMS

11:00 Democratizing Cell-Free Protein Synthesis: Improving Access for Broad Bioengineering Applications
Javin P. Oza, PhD, Assistant Professor, Chemistry & Biochemistry, California Polytechnic State University, SLO
Cell-free protein synthesis (CFPS) is a platform technology that leverages cell extracts for the on-demand production of proteins. CFPS supports discovery by obviating the barriers presented by the cell, enabling scientists and engineers to rapidly characterize genes, constructs, and clones associated with functional genomics, 'difficult' proteins, and metabolic engineering. I will discuss our efforts to reduce the barriers to implementing CFPS to enable broad applications in bioengineering.

11:30 Using Human Blood Extracts as a Renewable Resource to Produce Recombinant Proteins
David Burgenson, PhD Candidate, Center for Advanced Sensor Technology (CAST), University of Maryland Baltimore County
One of the early *in vitro* translation cell-free protein expression systems used rabbit reticulocytes (immature red blood cells) as a source of cells to produce active cell-free extract. Using this system as a source of inspiration, our group began looking for cells present in human blood that could be used to produce translationally active cell-free extract.

Sponsored by SELEXIS

12:00 pm Engineering of a Viral Free SURE Host Cell Line for Biologic Production
Pierre-Olivier Duroy, PhD, Genome Editing Director, SELEXIS SA
CHO cells have budding type-C endogenous retroviruses (ERVs) embedded in their genome and release viral particles in the culture supernatant. The presence of ERVs has raised safety concerns. We systematically characterized the type-C ERV elements at the genome, transcriptome and viral particle level. Using genome editing methods, we disrupted the expressed ERVs without compromising cell growth, size or recombinant protein production. We will present a novel strategy to mitigate CHO endogenous retroviruses during biopharmaceutical manufacturing.

12:30 Session Break

Sponsored by GLYCOTOPE

12:40 LUNCHEON PRESENTATION: GlycoExpress® - An Alternative Host for Difficult to Express Proteins
Lars Stöckl, PhD, Senior Director, R&D, Glycotope GmbH
The era of classical IgG molecules in bio-pharma development is shifting rapidly to more challenging complex biopharmaceuticals. With CHO being a good production cell line for IgG molecules, they might fail to produce more challenging candidates. The GlycoExpress® (GEX®) system represents an ideal alternative for the production these difficult to express protein molecules and will provide case studies which demonstrate the superiority in productivity and product quality vs CHO cell expression.

1:10 Close of Engineering Genes, Vectors, Constructs, and Clones Conference

RECOMBINANT PROTEIN EXPRESSION AND PRODUCTION

Enhancing Expression, Performance, and Process

Great strides have been made in the expression, production, and purification of biotherapeutics. There is a greater demand for higher-throughput expression and purification, as well as more flexible expression platforms. Unfortunately, there is no "universal" production system which can guarantee high yields of recombinant protein. Cambridge Healthtech Institute's 22nd Annual RECOMBINANT PROTEIN EXPRESSION AND PRODUCTION conference explores the newest data and innovations relating to the best choices in hosts/systems, as well as ways to "rescue" existing systems and make them work more effectively to produce the quality and quantity of the desired biotherapeutic.

TUESDAY, JANUARY 21

1:00 pm Registration

1:30 Refreshment Break in the Exhibit Hall with Poster Viewing

EFFECTIVE EXPRESSION AND PRODUCTION OF UNIQUE BIOPRODUCTS

2:00 Chairperson's Opening Remarks
Henry C. Chiou, PhD, Director, Cell Biology, Life Science Solutions, Thermo Fisher Scientific

KEYNOTE PRESENTATION

2:05 Gene Editing and Robotics Solve Upstream and Downstream Problems in HIV Vaccine Manufacturing in CHO Cells

Phillip Berman, PhD, Distinguished Research Professor, Biomolecular Engineering, University of California, Santa Cruz

The envelope protein, gp120, is a major component of vaccines designed to prevent HIV infection. However, production of gp120 in CHO has been challenging due to low expression, a complex glycosylation structure, and sensitivity to proteolysis. We have used gene editing of the MGAT1 and C1s genes and robotic selection to solve all three problems while at the same time improving the structure of glycan dependent epitopes recognized by monoclonal antibodies.

2:45 A Rapid and High-Yielding Plant-Based Production Platform for Biologics
Albor Dobon-Alonso, PhD, Senior Microbiologist, Leaf Expression Systems Ltd.

Leaf Expression Systems is a CDMO specializing in plant-based production of recombinant proteins for research and biomedical applications using a proprietary, transient expression technology, Hypertrans®. Here we present our eukaryotic expression platform that offers rapid, scalable production of high-quality biologics at lower development costs. We will highlight activity data of biosimilar (bevacizumab) and diagnostic MAbs that we have produced, together with examples from our internal VLP, enzyme and cytokine pipeline.

Sponsored by Sino Biological

3:15 The Optimization of Recombinant Protein Expression
Rob Burgess, Chief Business Officer, Sino Biological Inc

Sino Biological boasts the world's largest selection of recombinant proteins and is a leading provider of CRO services including recombinant protein production. An overview of the company's state-of-the-art technologies for optimizing protein expression will be given addressing production challenges and key influencing factors and will include several example case studies.

Sponsored by WACKER

3:30 Microbial Secretion of Complex Biotherapeutic Proteins by ESETEC® - Case Study with Akari Therapeutics
Arndt Dietrich, PhD, Senior Expert DSP Development, BioProcess Development, Wacker Biotech GmbH

The innovative and highly efficient *E. coli* expression system ESETEC® enables the secretion of native recombinant proteins into the fermentation broth at high titer, thereby greatly simplifying the purification processes. This has recently been demonstrated in collaboration with Akari Therapeutics, a Biotech company focused on development anti-inflammatory Biopharmaceuticals.

3:45 Refreshment Break in the Exhibit Hall with Poster Viewing

4:30 Engineering Cells for Heparin and Heparan Sulfate Production
Charles A. Glass, PhD, President and CSO, TEGA Therapeutics, Inc.

Heparin and heparan sulfate (HS) are polysaccharide chains that serve as cofactors for specific protein binding and therefore have potential therapeutic qualities as drugs or drug targets. Protein binding specificity is determined by sulfate modifications along the polysaccharide backbone, which are cell type specific and which can be engineered through genes in the heparin/HS biosynthetic pathway. Through cell engineering, TEGA is testing a library of heparin/HS compositions for therapeutic applications.

5:00 Scalable Production and Purification of Single-Stranded DNA for Therapeutic Nucleic Acid Delivery
Mark Bathe, PhD, Associate Professor, Biological Engineering, Massachusetts Institute of Technology

Viral-like structured DNA and RNA assemblies, also known as DNA or RNA origami, offer the ability to co-formulate gene-length single-stranded DNA or RNA with CRISPR-RNPs, siRNAs, or ASOs, with integration of active cellular targeting and uptake moieties including sugars and peptides. Scalable bacterial production of custom length and sequence single-stranded DNA will be presented together with co-formulation of siRNA and CRISPR therapeutics with pre-clinical *in vivo* biodistribution and toxicity studies in mouse that offer a platform for next-generation nucleic acid therapeutic delivery.

5:30 Close of Day

5:30 - 5:45 Short Course Registration

5:45 - 8:45 Dinner Short Courses*

Click here for details.

**Separate registration required*

WEDNESDAY, JANUARY 22

7:45 am Registration and Morning Coffee

EFFECTIVE EXPRESSION AND PRODUCTION OF RECOMBINANT PROTEINS

8:15 Chairperson's Remarks
Phillip Berman, PhD, Distinguished Research Professor, Biomolecular Engineering, University of California, Santa Cruz

FEATURED PRESENTATION

8:20 Analysis of the Immunoglobulin G (IgG) Secretion Efficiency in Recombinant Chinese Hamster Ovary (CHO) Cells
Takeshi Omasa, PhD, Professor, Department of Material and Life Science, Graduate School of Engineering, Osaka University
In this study, a CHO cell line producing IgG1, which was genetically fused with fluorescent proteins, was established to directly analyze intracellular secretion. The relationship between the amount of intracellular and secreted IgG was analyzed. An immunofluorescent microscopy study showed that the established clones could be used to analyze the intracellular secretion bottleneck. Also, to improve the production of various therapeutic antibodies, we analyzed the protein secretion process in CHO cells producing the DTE IgG infliximab.

8:50 Novel Prediction Tool to Evaluate Synonymous Changes in Recombinant Therapeutic Proteins
Nobuko Katagiri, PhD, Research Biologist, Division of Plasma Protein Therapeutics, Office of Tissues and Advanced Therapies, CBER, FDA
Accurate prediction of phenotype based on the genotype is a fundamental goal in the medical genetics field. *In silico* tools to predict the effects of single missense variations are available from various sources. On the contrary, prediction of synonymous or multiple mutations remains highly challenging and yet valuable because these sequence changes are often seen in recombinant therapeutics. Our recent efforts towards improvement of such tools will be discussed.

9:20 Boosting VHH Expression Using UNLOCK PICHIA *Sponsored by* VALIDOGEN
Iskandar Dib, Principal Scientist Process Development, Analytics, VALIDOGEN GmbH
VHHs, single-domain antibodies derived from camelid species represent the third generation of antibodies and are currently developed for an increasing number of different applications.
Efficient production of VHHs is enabled by VALIDOGEN's yield-enhancing protein production toolbox known as UNLOCK PICHIA comprising a broad diversity of molecular tools and expression strategies for Pichia. We demonstrate significant enhancement of VHH expression by a set of helper factors acting along the way from transcription to secretion.

9:50 Coffee Break in the Exhibit Hall with Poster Viewing

10:35 Recombinant Protein Production in Research at Novo Nordisk
Brian Vandahl, PhD, Corporate Vice President, Recombinant Technologies, Global Research Technologies, Novo Nordisk A/S
A discussion of challenges and opportunities in recombinant protein production seen from a Novo Nordisk Research perspective.

11:05 Recent Advances in Screening and Production of Recombinant Proteins in Plants and Plant Cells
Johannes Buyel, Dr. rer. nat., Dr-Ing, Head, Bioprocess Engineering, Fraunhofer Institute for Molecular Biology and Applied Ecology IME
High-throughput screening systems in 96-well plate format have been developed for plant-based expression. This can facilitate the production of novel and innovative protein biopharmaceuticals that can otherwise be difficult to express in mammalian or microbial hosts due to toxicity or complexity respectively. We also discuss the translation from screening to production for plant-based systems.

11:35 Antibody Production Using an Inducible CHO Cell Line: Process Development and Intensification
Olivier Henry, PhD, Associate Professor, Chemical Engineering, Polytechnique Montréal
Mammalian-inducible expression systems are increasingly available and offer an attractive platform to produce recombinant proteins. Inducible systems allow to uncouple the growth and the production phases. We have conducted process development for a cumate-inducible GS-CHO cell line expressing rituximab. We have explored the use of fed-batch and continuous perfusion strategies applied during the pre-induction phase to enhance process performance in terms of product yield and quality.

12:05 pm Session Break

12:15 LUNCHEON PRESENTATION I: Optimized Protein and Virus Production in the Expi Expression Systems *Sponsored by* ThermoFisher SCIENTIFIC
Jonathan Zmuda, PhD, Cell Bio R&D, Thermo Fisher

12:45 Luncheon Presentation II *(Sponsorship Opportunity Available)*

1:15 Session Break

1:45 PLENARY KEYNOTE PANEL
Click here for details.

3:05 Refreshment Break in the Exhibit Hall with Poster Viewing

EFFECTIVE EXPRESSION AND PRODUCTION OF DIFFICULT-TO-EXPRESS PROTEINS

4:00 Chairperson's Remarks
Johannes Buyel, Dr. rer. nat., Dr-Ing, Head, Bioprocess Engineering, Fraunhofer Institute for Molecular Biology and Applied Ecology IME

4:05 Statistical Design for Effector Function Engineering of Hexameric Fc Domains
Shirley Peters, PhD, Principal Scientist, UCB
We used antibody engineering and recombinant expression to produce Fc with controlled hexa-valency, "Fc-multimer". Fc-multimer may have clinical potential as a recombinant protein replacement of intravenous immunoglobulin (IVIG) for the treatment of auto-inflammatory immune disorders. Fc-multimer engages with FcgR's on multiple cell types and was engineered to maximize potency whilst minimizing potential safety concerns. We used a statistical design approach ('Design of Experiments') to explore the two effector function extremes defined by IgG1 and IgG4.

4:35 Which Sugar Do You Want: Tailormade Glycosylation of Therapeutic Proteins
Bjørn Voldborg, MSc, Director, CHO Cell Line Development, The Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark

5:05 High-Level Expression of Thermostable Human Cannabinoid Receptor CB2 in Expi293 Cells for Biophysical Studies
Alexei Yeliseev, PhD, Staff Scientist, Group Leader, LMBB, National Institute on Alcohol Abuse and Alcoholism, National Institute of Health
G protein-coupled receptors (GPCR) comprise a large class of integral membrane proteins important for pharmaceutical drug development. We expressed a full-length cannabinoid receptor CB2 in suspension expi293 HEK cells and purified and solubilized it in a Façade-TEG detergent. The receptor was homogenous and did not lose its functional activity even after several hours of exposure to elevated temperature. We propose that post-translational modifications of CB2 are essential for its structural stability.

5:35 Two Cytoplasmic Ubiquitin E3 Ligases and an ER Protease Mediate ER-Associated Degradation of Unfolded Antibody Heavy Chains
Danming Tang, PhD, Technical Development Scientist, Cell Culture, Genentech
Accumulation of unfolded antibody chains in the ER triggers ER stress that may lead to reduced productivity in therapeutic antibody manufacturing processes. We identified UBR4 and UBR5 as ubiquitin E3 ligases involved in HC ER-associated degradation, while an ER protease PDIA3 cleaves ubiquitinated-HC molecules to accelerate HC dislocation. Proteins characterized in this proteolysis/proteasome-dependent pathway of unfolded antibody HC degradation may be novel targets for CHO cell engineering.

6:05 - 7:00 Networking Reception in the Exhibit Hall with Poster Viewing

7:00 Close of Recombinant Protein Expression and Production Conference

JANUARY 23-24, 2020 | 7TH ANNUAL

OPTIMIZING EXPRESSION PLATFORMS

Employment and Development of Cells, Process, and Personnel to Efficiently Produce Biotherapeutics

The utilization of engineered therapeutic proteins for basic research, clinical diagnostics, and therapy continues to expand. Consequently, protein expression laboratory managers and researchers face challenges for efficient expression, production, and purification, even while improving quantity and quality, plus minimizing time and cost. Cambridge Healthtech Institute's 7th Annual OPTIMIZING EXPRESSION PLATFORMS conference convenes protein expression experts to share their day-to-day challenges in high-throughput production and purification labs and provide insights and solutions on meeting these challenges.

THURSDAY, JANUARY 23

7:45 am Registration and Morning Coffee

TRANSIENT PLATFORMS

8:10 Organizer's Welcome Remarks
Mary Ann Brown, Executive Director, Conferences & Team Lead, PepTalk, Cambridge Healthtech Institute

8:15 Chairperson's Opening Remarks
Xiaotian Zhong, PhD, Senior Principal Scientist, Lab Head, BioMedicine Design, Pfizer Worldwide R&D

KEYNOTE PRESENTATION

8:20 Antibody Cascade Continuous Paramagnetic Chromatography

John K. Kawooya, PhD, Director, Biologics Optimization, Discovery Research, Amgen, Inc.
"Cascade Continuous Paramagnetic Chromatography" (CCPC) purifies antibodies from crude cell cultures without centrifugation or filtration. In this process, Protein A paramagnetic beads are added to live cell cultures 18-24 hours prior to harvesting. This maximizes antibody binding, eliminates traditional cell removal and column loading steps. The contents are transferred into a single-use magnetizable tank for bead washing, antibody elution, viral inactivation, pH and ionic strength adjustment prior to SP-CEX polishing.

9:00 Scaling Up and Scaling Out: Pushing the Boundaries of Transient Protein Production
Sponsored by absolute antibody
Ian Wilkinson, CSO, Absolute Antibody
Whilst transient yields have improved drastically in the last decade, scalable systems are time-consuming and costly to implement. Absolute Antibody has developed systems which scale up and scale out protein expression and purification, enabling the rapid and cost effective production of milligram to gram quantities of large panels of proteins.

9:30 Talk Title to be Announced
Sponsored by THOMSON
Sam Ellis, Vice President, Thomson Instrument Company

10:00 Coffee Break in the Exhibit Hall with Poster Viewing

11:00 Making a High Titer Transient System from a Stable CHO Platform
Peter Harms, PhD, Principal Engineer, Cell Culture, Genentech
A high titer (500-1000 mg/L for antibodies) transient system was developed from the host cell and media of an in-house stable CHO platform. Development included screening of subclones and process optimization, but there were also a few surprises along the way. The final system is robust, scalable from 30 mL to 10 L, and provides product quality comparable to the original stable CHO platform.

11:30 Developing a Transient CHO Expression Platform with N-Glycan Compositions Consistent with Stable CHO
Xiaotian Zhong, PhD, Senior Principal Scientist, Lab Head, BioMedicine Design, Pfizer Worldwide R&D
Developing a robust transient expression platform in CHO, the preferred host for many clinical and commercial products, offers a start-to-end quality alignment advantage for therapeutic protein discovery. This talk will present our recent efforts in developing a transient CHO platform to enable efficient sialylation of N-glycans. The talk will also describe new strategies in optimizing transient CHO system with N-glycan compositions consistent with those from stable CHO production.

12:00 pm NEW: A Universal Affinity-tag System: From Protein Purification to Analytic Applications
Sponsored by iba
Sponsored by **IBA**
Dennis Karthaus, Director, Protein Products & Assays, IBA Lifesciences
New expression systems enable high titer production while simultaneously reducing the expression volume and time. Here we show how proteins can be easily and effectively purified from Expi supernatants using Strep-tag technology. Furthermore, Strep-Tactin®XT can be used in combination with BLI sensors for rapid measurement of protein concentrations and kinetics.

12:30 Session Break

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

1:10 Ice Cream Break in the Exhibit Hall with Poster Viewing

CELL LINE DEVELOPMENT

2:15 Chairperson's Remarks
Yves Durocher, PhD, Research Officer, Bioprocess Engineering, National Research Council Canada

2:20 Reducing Recombinant Protein Expression during CHO Pool Selection Enhances Pool Productivity and the Frequency of High-Producing Cells
Yves Durocher, PhD, Research Officer, Bioprocess Engineering, National Research Council Canada
During the generation of stable cell lines, high-level expression of recombinant protein (r-protein) may impose a metabolic burden on the cells and many are not likely to survive the selection process. Using the cumate-inducible expression system, we show that selection in the "off-mode" allows the generation of stable pools with up to 3-fold higher productivity compared to selection in the "on-mode" (mimicking constitutive promoters). Pools selected in the "off-mode" contain a much higher proportion of high-producing cells.

2:50 Integrative Multi-Omics Data and Model-Driven Approaches Guide CHO Cell Line Development for Enhanced Bioprocessing
*Meiyappan Lakshmanan, PhD, Research Scientist & Group Leader, Systems Biology, Bioprocessing Technology Institute, A*STAR*
A systems approach based on high-throughput "-omics" profiling and mathematical modeling of CHO cells offers immense potential to become an indispensable tool in the biopharmaceutical industry for identifying key bottlenecks in the product yield and quality related pathways in a mechanistic manner. The knowledge obtained from such multi-omics data and model-guided systems approaches can further enable the next-generation cell line development.

3:20 Networking Refreshment Break

3:45 Optimization of NGS-Based Sequence Variant Analysis to Facilitate Cell Line Screening
Yizhou Zhou, PhD, Scientist II, Cell Line Development, Biogen
Reliable high-throughput analytic tools are critical for accelerating cell line development to push protein therapeutics into clinical trials. Sequence variants of the transgene can occur at multiple stages during the cell line development. Here we improved the sensitivity and robustness of an amplicon-based NGS assay, which fits into the aggressive timeline of cell line development and allows detection of very low levels of sequence variants for up to 40 clones.

4:15 Establishing a High-Throughput Protein Production Platform for Rapid Antigen Screening
Ying Huang, MD, PhD, Lab Head, Vaccine Design and Characterization, Preclinical R&D, GSK Vaccines
Breakthrough technological innovations in the fields of recombinant protein expression and structural biology have provided new tools to accelerate vaccine design and optimization. Here we describe the establishment of a high-throughput antigen expression and purification platform using the Fluent® Liquid handling robot and the KingFisher™ Flex magnetic beads purification system compatible for antigen production in both bacterial and mammalian cells to rapidly screen hundreds of vaccine candidates from computational design.

4:45 PANEL DISCUSSION: Transient, Stable, or Both?
Speed, limiting risk, and protein quality are often cited as advantages of transient protein production (TPP), while stable transfection – the longer and more complex process – has the advantage of producing long-term expression of the biotherapeutic of interest. The rapidly increasing need for recombinant proteins necessitates further improvements in both technologies.
Moderator:
Yves Durocher, PhD, Research Officer, Bioprocess Engineering, National Research Council Canada
Panelists:
Peter Harms, PhD, Principal Engineer, Cell Culture, Genentech
*Meiyappan Lakshmanan, PhD, Research Scientist & Group Leader, Systems Biology, Bioprocessing Technology Institute, A*STAR*
Xiaotian Zhong, PhD, Senior Principal Scientist, Lab Head, BioMedicine Design, Pfizer Worldwide R&D
Yizhou Zhou, PhD, Scientist II, Cell Line Development, Biogen

5:15 Close of Day

FRIDAY, JANUARY 24

8:00 am Registration

8:00 BuzZ Sessions with Continental Breakfast
Protein therapeutics is a fast-growing global market. As the science improves, so does the complexity of the R&D organization. Ensuring product quality plus speed to market requires insights from stakeholders working across the stages of protein science R&D. Join experts representing this PepTalk pipeline, peers, and colleagues for an interactive roundtable discussion. Topics include highlights from the week's presentations, new technologies and strategies, challenges, and future trends.

HOW TO MAKE THE MOST OF YOUR RESOURCES

9:00 Chairperson's Remarks
Richard Altman, MS, Field Application Scientist, Protein Expression, Biosciences Division, Life Sciences Solutions Group, Thermo Fisher Scientific

9:05 Running a Core Facility: How to Keep Everybody Happy
Bjørn Voldborg, MSc, Director, CHO Cell Line Development, The Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark

9:35 Balancing Platform Delivery, Innovation, and Job Satisfaction in the HT Protein Production Space
Edward Kraft, PhD, Senior Scientific Manager, Biomolecular Resources, Genentech
Working in high-throughput, non-antibody protein production labs represents unique challenges. Producing large batches of protein for diverse protein classes creates continuous challenges. I'll discuss the approaches at Genentech to create a rewarding career experience that blends platform delivery, innovation and job satisfaction.

10:05 Solving Challenges to the Operation of a Protein Production Core Supporting Early Stage Drug Discovery Efforts
Dominic Esposito, PhD, Director, Protein Expression Laboratory, Frederick National Laboratory for Cancer Research

10:35 Networking Coffee Break

11:00 Delivering World-Leading Research Services to Drive Scientific Success
Balaji Somasundaram, PhD, Strategy and Operations Manager, UQ Protein Expression Facility, The University of Queensland
Research service facilities are becoming a vital component of the modern collaborative research environment, where researchers use the technical expertise and experience of the facility to advance their research. This presentation will cover the following key focus areas for a protein research service facility to be integrated as a valued partner in research programs: 1) Enhancing operational excellence; 2) Building strategic partnerships; and 3) Workforce development.

11:30 Balancing Innovation, Efficiency, and Quality in Protein Production
Jessica Williamson, PhD, Protein Production Lead, UCB Biosciences
Running a protein production group in drug discovery requires a lot of organization. We're all engaged in the actual research, but from managing resources and meeting deadlines to maintaining quality and maximizing yield, it's a challenging balancing act. At UCB Biosciences, we have years of experience as a gene-to-structure pipeline and we are applying the lessons we've learned to increase efficiency, embrace innovation, and maintain high quality.

12:00 pm CLOSING PANEL DISCUSSION: Protein Production Lab Challenges: Methodologies, Strategies, and the Art of Managing Multiple Projects
There are many challenges in operating protein production labs. This panel focuses on the following topics: initiating projects, basic expression and purification systems, pros and cons for each system, screening platforms, troubleshooting and how much time should be spent on each system before moving to the next option. In addition to "hands-on" tips, we touch upon strategies on how to manage multiple "top priority" projects.
Moderator:
Richard Altman, MS, Field Application Scientist, Protein Expression, Biosciences Division, Life Sciences Solutions Group, Thermo Fisher Scientific
Panelists:
Dominic Esposito, PhD, Director, Protein Expression Laboratory, Frederick National Laboratory for Cancer Research
Edward Kraft, PhD, Senior Scientific Manager, Biomolecular Resources, Genentech
Balaji Somasundaram, PhD, Strategy and Operations Manager, UQ Protein Expression Facility, The University of Queensland
Bjørn Voldborg, MSc, Director, CHO Cell Line Development, The Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark
Jessica Williamson, PhD, Protein Production Lead, UCB Biosciences

12:30 Close of Conference

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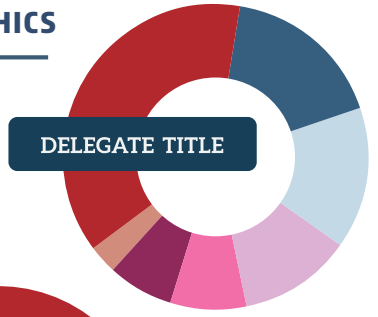

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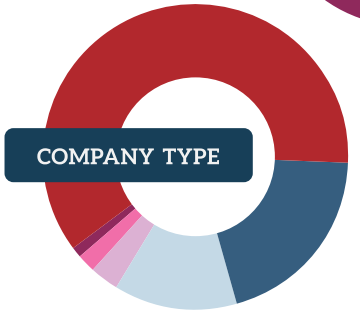

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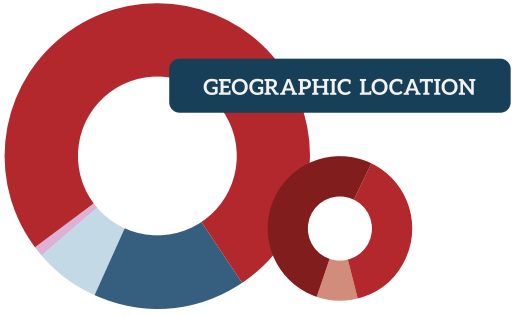

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Registration after November 22	$3,099	$1,499

BASIC PACKAGE *(Includes access to 1 conference and/or Training Seminar. Excludes Short Courses.)*

Early Bird Registration until September 20	$1,599	$829
Early Registration until October 19	$1,799	$929
Advance Registration until November 16	$1,949	$979
Registration after November 16	$2,149	$1,099

PRICING & REGISTRATION INFORMATION

CONFERENCE DISCOUNTS

Poster Submission - Discount ($50 Off): Poster abstracts are due by November 22. Once your registration has been fully processed, we will send an email containing a unique link allowing you to submit your poster abstract. If you do not receive your link within 5 business days, please contact jring@healthtech.com. *CHI reserves the right to publish your poster title and abstract in various marketing materials and products.

REGISTER 3 - 4th IS FREE: Individuals must register for the same conference or conference combination and submit completed registration form together for discount to apply.

Alumni Discount: SAVE 20%: CHI appreciates your participation at our events. As a result of the great loyalty you have shown us, we are pleased to extend to you the exclusive opportunity to save an additional 20% off the registration rate.

Group Discounts: Discounts are available for multiple attendees from the same organization. For more information on group rates contact Frank Doherty at +1-781-972-5489.

**Alumni, Antibody Society, Twitter, LinkedIN, Facebook or any other promotional discounts cannot be combined. Discounts not applicable on event Short Courses.*

If you are unable to attend but would like to purchase the PepTalk CD for $750 (plus shipping), please visit CHI-PepTalk.com. Massachusetts delivery will include sales tax.

How to Register: CHI-PepTalk.com

reg@healthtech.com
P: 781.972.5400 or Toll-free in the U.S. 888.999.6288

Please use keycode **PTK F** when registering!

ADDITIONAL REGISTRATION DETAILS

Each registration includes all conference sessions, posters and exhibits, food functions, and access to the conference proceedings link.

Handicapped Equal Access: In accordance with the ADA, Cambridge Healthtech Institute is pleased to arrange special accommodations for attendees with special needs. All requests for such assistance must be submitted in writing to CHI at least 30 days prior to the start of the meeting.

To view our Substitutions/Cancellations Policy, go to healthtech.com/regdetails

Video and or audio recording of any kind is prohibited onsite at all CHI events.

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