EXPRESSiON STREAM
Conquering Expression Challenges to Optimize Protein Production

APRiL 30 - MAY 4, 2012
The Boston Park Plaza Hotel & Towers | Boston, MA

Difficult to Express Proteins
Optimizing Protein Expression
Purifying Antibodies

KEYNOTE & FEATURED SPEAKERS

William H. Brondyk, Ph.D., Senior Scientific Director, Therapeutic Protein Discovery, Genzyme – A Sanofi Company

Jeff Culp, Ph.D., Associate Research Fellow, Primary Pharmacology Group, Pfizer Worldwide R&D

Sabine Geisse, Ph.D., Director, NLS, Novartis Pharma AG

David J. Roush, Ph.D., Senior Investigator, BioProcess, Protein Purification Development, Merck Research Labs

Joey M. Studts, Ph.D., Director, Protein Science, Boehringer Ingelheim Pharma GmbH & Co
PEGS SUMMIT-AT-A-GLANCE

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<td><strong>Biologics Partnering Forum</strong>*</td>
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<td>Difficult to Express Proteins</td>
<td>Characterization of Biotherapeutics</td>
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**DINNER SHORT COURSES***

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<th>Wednesday</th>
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<tr>
<td>Engineering Antibodies</td>
<td>Optimizing Protein Expression</td>
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<td>Immunogenicity</td>
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* Separate Registration Required

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**BIOLIGICS PARTNERING FORUM**

**EMERGING ANTIBODY & PROTEIN ENGINEERING**

**APRIL 28 - 29, 2012**

The Boston Park Plaza Hotel & Towers | Boston, MA

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**REASONS TO ATTEND:**

**NETWORK AND FOSTER BUSINESS** with the companies that are going drive biologics growth over the next decade, as well those interested in funding its expansion

**IN-DEPTH PRESENTATIONS** focused on promising technology platforms and innovative approaches in antibody therapies and protein engineering

**LEADING EARLY-STAGE COMPANIES** hand-picked to present by top biologics experts on our Program Advisory Board

**BIG PHARMA, INDUSTRY EXECUTIVES, INVESTORS’** representatives in attendance, open to further business collaborations

**COVERAGE INCLUDES:**

- *In Vivo* Transgenic Antibody Platforms
- *In Vitro* Antibody Development Platforms
- Antibody Tools
- Novel Antibody Products in Development
- Bi-Specific and Multi-Specific Antibody Technologies
- Fusion Proteins
- Protein Diversity
- Human-Derived Antibodies
- Novel Protein Scaffolds
- Screening and Design Platforms for Protein Engineering

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**PROGRAM ADVISORY BOARD:**

- **Brian Atwood, M.B.A.,** Managing Director, Versant Ventures
- **Sharon Cload, Ph.D.,** Vice President, Adnexus, Bristol Myers Squibb
- **Jon Ellis, Ph.D.,** Vice President, Business Development, Biopharmaceutical R&D and Platform Technology & Science, GlaxoSmithKline
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- **Thomas Li, Ph.D.,** Senior Director, Technology, Roche Diagnostics
- **Kia Motesharei, Ph.D.,** Vice President, Business Development & Alliance Management, Dyax Corp.
- **Hilde Revets, Ph.D.,** Senior Research Fellow, Technology, Ablynx
- **Barry Springer, Ph.D.,** Head of External Research and Innovation, Biologics Research, Johnson & Johnson
- **Charles Wilson, Ph.D.,** Vice President, Global Head of Strategic Alliances, Novartis Institutes for Biomedical Research
- **Gordon Wong, Ph.D.,** Vice President, Business Development, Biogen-IDEA

To view the complete Partnering Forum agenda and other details, please visit: [PEGSummit.com/Antibody-Engineering-Partnering](https://www.PEGSummit.com/Antibody-Engineering-Partnering)
### SHORT COURSES*

#### SUNDAY, APRIL 29

**MORNING 10:00am - 1:00pm**

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<td>SC1</td>
<td>Phage and Yeast Display Libraries</td>
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<td>SC2</td>
<td>Techniques for Antibody Selection &amp; Screening</td>
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<td>SC4</td>
<td>Engineering Optimized Biotherapeutics</td>
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<tr>
<td>SC5</td>
<td>Translational Strategies for Development of Monoclonal Antibodies Part I: Focus on Early Discovery</td>
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**AFTERNOON 2:00 - 5:00pm**

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<tr>
<td>SC6</td>
<td>Alternate Display Technologies</td>
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<td>SC7</td>
<td>Use of HT Sequencing for Antibody Library Generation and Selection</td>
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<td>SC8</td>
<td>Engineering of Bispecific Antibodies</td>
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<td>SC9</td>
<td>Biosimilars: Development, Regulation and Prospects</td>
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<td>SC10</td>
<td>Translational Strategies for Development of Monoclonal Antibodies Part II: Focus on Non-Clinical Development to Clinic</td>
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<tr>
<td>SC11</td>
<td>Molecular Imaging on Tissues Using Mass Spec</td>
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#### TUESDAY, MAY 1

**DINNER 6:00 - 9:00pm**

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<tr>
<td>SC12</td>
<td>Asia-U.S. Biotech Alliances: Opening Up New Opportunities for Pre-Clinical Development of Biologics</td>
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<td>SC13</td>
<td>Light Scattering – Theory, Do’s &amp; Don’ts, and Data Interpretation</td>
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#### THURSDAY, MAY 3

**DINNER 5:30 - 8:30pm**

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<td>SC14</td>
<td>Antibody Conjugate Therapeutics Challenges</td>
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<td>SC15</td>
<td>Advances in Immunogenicity Assays</td>
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*Separate Registration Required

Please visit our website at PEGSummit.com for course details.

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### HOTEL & TRAVEL INFORMATION

**CONFERENCE HOTEL**

The Boston Park Plaza Hotel & Towers  
50 Park Plaza at Arlington Street  
Boston, MA 02116  
T: 617-426-2000

Discounted Room Rate: $199 s/d  
Discounted Room Rate Cut-off Date: March 30, 2012

Please visit our conference website to make your reservations online or call the hotel directly to reserve your sleeping accommodations. You will need to identify yourself as a Cambridge Healthtech Institute conference attendee to receive the discounted room rate with the host hotel. **Reservations made after the cut-off date or after the group room block has been filled (whichever comes first) will be accepted on a space- and rate-availability basis. Rooms are limited, so please book early.**

**TRAVEL INFORMATION**

For additional travel information and discounts, visit the hotel and travel page of the conference website.

Reserve your hotel room and **SAVE $100 off your conference registration***  

*You must book your reservation under the Cambridge Healthtech/PEGs room block for a minimum of four nights at The Boston Park Plaza Hotel & Towers. The $100 discount is per room.
Harnessing Innovation to Improve Expression and Function

**DIFFICULT TO EXPRESS PROTEINS**

**SUNDAY, APRIL 29**

4:00 - 6:00 pm Main Conference Registration

**MONDAY, APRIL 30**

7:00 am Registration and Morning Coffee

**8:30 Chairperson’s Opening Remarks**

- **8:40 FEATURED PRESENTATION**
  
  **Overcoming Challenges of Difficult to Express Proteins**
  
  Jeff Culp, Ph.D., Associate Research Fellow, Primary Pharmacology Group, Pfizer Worldwide Research and Development

  We will examine the production of an 80 amino acid protein (or peptide) and as our understanding of biology and disease evolves, challenges increase to deliver biologically relevant proteins for use with all Drug Discovery tools. Mammalian, insect and bacterial expression systems must be leveraged. Proper protein characterization is critical to eliminate potential mistakes. Successful examples will be presented for proteins intended for use in target screens, NMR, crystalization and biophysical characterization.

- **9:10 Peptide Surfactants for Cell-Free Production of Functional G Protein-Coupled Receptors**
  
  Shuguang Zhang, Ph.D., Associate Director, Center for Biomedical Engineering, Massachusetts Institute of Technology

  We report using peptide surfactants in commercial *E. coli* cell-free systems to rapidly produce milligram quantities of soluble G protein-coupled receptors (GPCRs). The GPCRs expressed in the presence of the peptide surfactants were soluble and had α-helical secondary structures, suggesting that they were properly folded. These short and simple peptide surfactants may be able to facilitate the rapid production of GPCRs, or even other membrane proteins, for structure and function studies.

- **9:40 Expression of the Transmembrane Domain of the Human APP Binding Protein LR11 for “in Situ” NMR Structural Analysis**
  
  Fang Tian, Ph.D., Assistant Professor, Department of Biochemistry and Molecular Biology, College of Medicine, Pennsylvania State University

  Information about protein structure in biological environment is scarce. To date, most membrane structure determinations have been carried out in detergent preparations and synthetic lipid bilayers. Using a new MBP expression vector, we successfully expressed the transmembrane domain of the human APP binding protein LR11 at high yields for a direct structural characterization in native Escherichia coli membranes.

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

- **11:10 Engineering Membrane Proteins for Better Expression in *E. coli***
  
  Morten Narholm, Ph.D., Senior Scientist, Novo Nordisk Center for Biosustainability, Technical University of Denmark

  In this study we show that fusion of an N-terminal peptide to a poorly-expressed membrane protein of *E. coli* origin can significantly improve over-expression levels. Further, we could mimic the effect of the N-terminal peptide by re-engineered the 5′ mRNA with favorable synonymous mutations. These simple changes significantly improve over-expression of the native protein and provide a design principle for engineering better expressing membrane proteins.

- **11:40 Crystallization Chaperone Strategies for Membrane Proteins**
  
  Jennifer A. Maynard, Ph.D., Assistant Professor, Chemical Engineering, University of Texas Austin

  From G protein-coupled receptors to ion channels, membrane proteins represent over half of known drug targets, yet structure-based drug discovery is hampered by the lack of available three-dimensional models. Here, we present a novel, generic solution: development of a toolbox of engineered antibodies recognizing short peptides to chaperone crystallization of membrane proteins presenting the peptide ligand in a permissive loop.

- **12:00 NOVEL HOSTS AND PLATFORMS**

  - **2:00 Chairperson’s Remarks**
    
    Paul Wengender, Founder & CEO, Blue Sky BioServices

  - **2:05 Retention of Thrombin Inhibitory Activity by Recombinant Serpins Expressed as Integral Membrane Proteins Tethered to the Surface of Mammalian Cells**
    
    William P. Sheffield, Ph.D., Professor, Departments of Pathology and Molecular Medicine, McMaster University

    Both TR- and AR-α11 PI M358R were enriched in the integral membrane fraction of transfected COS-1 or HEK 293 cells, and formed inhibitory complexes with thrombin, although less rapidly than soluble α1(1) PI M358R. Two of three thrombin-inhibitory serpins retained functionality when expressed as integral membrane proteins. Our findings could be applied to create and screen hypervariable serpin libraries expressed in mammalian cells, or to confer protease resistance on engineered cells in vivo.

  - **2:35 A Novel Expression and Purification Platform for the Production of Soluble Human Lysozyme in *E. coli***
    
    John Lampa, Chemical and Biomolecular Engineering, Thayer School of Engineering, Dartmouth College

    Pre-clinical assessment of novel lysozyme variants requires a robust, efficient, and scalable expression system. *E. coli* is accessible, efficient and a scalable platform, but expression of soluble lysozyme is toxic to these cells. To capitalize on the numerous benefits of this bacterial host, we have developed an anti-toxin co-expression system that yields a 1000-fold increase in soluble lysozyme relative to prior reports.

  - **3:05 Daedalus: A Robust, Turnkey Platform for Rapid Production of Decigram Quantities of Active Recombinant Proteins in Human Cell Lines Using Novel Lentiviral Vectors**
    
    Ashok Bandaranayake, Ph.D., Associate, Department of Biochemistry, Albert Einstein College of Medicine

    We describe a novel system for the rapid production of recombinant mammalian proteins, including immune receptors, cytokines and antibodies, in a human cell line culture system. The inclusion of minimized ubiquitous chromatin opening elements in the transduction vectors is key for preventing genomic silencing and maintaining the stability of decigram levels of expression.

  - **3:35 Expression of a Self Assembling Immune Adjuvant and Antigen Targeting Fusion Protein to Accelerate the Development of New Vaccines for Emerging Infectious Diseases**
    
    Mark C. Poznansky, M.D., Ph.D., Director, Vaccine and Immunotherapy
αDF generates an Effective and translatable Angiogenic Factor-1. Computational Protein Design to re-Engineer stromal cell-Derived mutations, which can produce chemical heterogeneity in the target protein associated with target protein activity produces selective pressure leading to properties of the proteins themselves as the major obstacles to success. Toxicity suitable for structural studies and that the biochemical and conformational properties of E. coli at moderate levels We present evidence that, at least for the target proteins included in our study, Physiological response to membrane Protein Overexpression in Physicochemical Properties of secretory cargo Play Critical Roles in Shaping the Maximum Secretory Capacity Haruki Hasegawa, Ph.D., Senior Scientist, Department of Protein Science, Amgen, Inc. What will determine the maximum secretory capacity of a cell? Is it simply the collective ability of intrinsic cellular machinery? By analyzing a striking cellular phenotype that inadvertently illustrates the limits of protein synthesis, trafficking, and secretion, we will highlight the importance of physicochemical properties of secretory cargo that shape the maximum secretory capacity of CHO cells. 9:30 Data Mining High-Throughput Studies to Establish the Influence of RNA Sequence on Protein Expression Grégory Boel, Ph.D., Senior Scientist, Department of Biological Sciences, Cornell University; Northeast Structural Genomics Consortium While codon usage can strongly influence protein expression level, most exercises in codon optimization fail to yield any improvement. We used the large-scale experimental database of the Northeast Structural Genomics Consortium to evaluate the influence of RNA sequence on protein expression level in E. coli. This analysis has provided a variety of new insights in addition to verifying some previously inferred principles. Analytical metrics have been developed to predict whether redesign of RNA sequence is likely to improve expression.

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

ISSUES OF FOLDING AND OVEREXPRESSION

10:45 Physiological Response to Membrane Protein Overexpression in E. coli
John F. Hunt, Ph.D., Associate Professor, Department of Biological Sciences, Columbia University
We present evidence that, at least for the target proteins included in our study, there is no inherent obstacle to IMP overexpression in E. coli at moderate levels suitable for structural studies and that the biochemical and conformational properties of the proteins themselves are the major obstacles to success. Toxicity associated with target protein activity promotes selective pressure leading to preferential growth of cells harboring expression-reducing and inactivating mutations, which can produce chemical heterogeneity in the target protein population.

11:15 Computational Protein Design to Re-Engineer Stromal Cell-Derived Factor-1 (SDF) Generates an Effective and Translatable Angiogenic Polypeptide Analog
John McArthur, Jr., Ph.D., Post Doctoral Researcher, Woo Laboratory, Hospital of the University of Pennsylvania
Exogenous administration of recombinant SDF enhances neovascularogenesis and cardiac function after MI. Smaller analogs of SDF may provide translational advantages including enhanced stability and function, ease of synthesis, lower cost, and potential modulated delivery via engineered biomaterials. In this study, computational protein design was used to engineer an SDF polypeptide analog that more efficiently induces EPC migration and improves post-MI cardiac function, and thus offers a more clinically translatable neovascularogenic therapy.
We use a dynamic model to explore ~10^4 combinations of process and cell line development. We will discuss the aspects of the international community’s efforts at developing an infrastructure to support, host, and disseminate genome-scale data related to CHO cell lines.

We describe a novel cell line, CAP-T® derived from human amniocytes, as host in transient protein production, and the establishment of suitable protocols for transfection and expression of recombinant proteins. Moreover, we show comparative analyses of expression to the well-known HEK293 and CHO transient protein production platforms. In brief, the addition of the CAP-T® cells to the repertoire of cell lines amenable to transient protein production clearly enhances the chances of success.

The importance of biologics as well as knowledge gained from decades of therapies led to challenges and opportunities in the field of biomanufacturing. The technological platform Algebiosys™ developed by Agencis leverages microalgae capabilities to achieve consistent and qualitative glycoproteins expression. To demonstrate the versatility offered by our microalgal cell line, proofs of concept including monoclonal antibodies and recombinant viral antigens will be presented with emphasis on glycosylation properties.

We describe a novel cell line, CAP-T® derived from human amniocytes, as host in transient protein production, and the establishment of suitable protocols for transfection and expression of recombinant proteins. Moreover, we show comparative analyses of expression to the well-known HEK293 and CHO transient protein production platforms. In brief, the addition of the CAP-T® cells to the repertoire of cell lines amenable to transient protein production clearly enhances the chances of success.
Proteases are a class of drug targets for which wide ranging approaches for production are required due to their heterogeneity. The Expertise Protease Platform has over the years gained significant experience in the production of often highly complex, human and viral proteases, using E. coli, insect and mammalian expression systems. This talk will attempt to provide an insight into our experiences, positive as well as negative.

9:35 Production of an AGC Kinase in the Pfizer La Jolla Parallel Protein Production Platform

Carán N. Cronin, Ph.D., Head, Parallel Protein Production Group, Pfizer Global Research & Development

The Parallel Protein Production Platform that has been established at Pfizer’s La Jolla, California site was applied to the production of a recombinant AGC kinase. Multiple expression constructs of this AGC kinase were passaged through E. coli, baculovirus/insect cells, and mammalian expression systems in order to optimize protein production. An overview of the process and the results of this study will be presented.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing

OPTIMIZING PROCESSES

11:05 Optimizing Effectiveness when Expressing Proteins for Drug Discovery

Krista Bowman, Ph.D., Senior Scientific Manager, Structural Biology, Genentech, Inc.

We have implemented a fairly high-throughput generic approach to increase not only our efficiency but also our effectiveness in successfully producing proteins for drug discovery. We have combined techniques such as small scale E. coli and baculovirus infections in multivell blocks, analysis of expression level following single affinity capture and elution from Ni-NTA Phytips, and analytical fluorescent size exclusion chromatography to gain insight into protein aggregation and general behavior, multimerization, or complexation.

11:35 Applying a Platform Approach to Pre-Clinical Protein Production: Evaluating Options and Streamlining Processes

Anne London, Ph.D., Investigator II & Lab Head, Mid-Scale Protein Production, Novartis Institutes for BioMedical Research, Inc.

Pre-clinical protein production is a broad discipline, with expectations and goals differing from project to project. Fast and efficient production of recombinant proteins is necessary with all requests, but challenges arise with differing maturity of programs (initial antigen production to late-stage in vivo material) and QC specifications (how “pure” is pure enough?). Here we present case studies reflecting our approaches to develop a platform capable of adapting to fit all production requests, with emphasis on cell line evaluation and impurity clearance.

12:05 pm End of Conference
9:35 Purification Strategies for Bispecific DART Proteins and Derivatives
Syd Johnson, Ph.D., Vice President, Antibody Engineering, MacroGenics, Inc.
Single domain antigen binding fragments or Nanobodies are well expressed in bacteria, easily purified, highly soluble, very stable and highly specific for their cognate antigen. Results will be presented where our Nanobodies are employed to purify their antigen from complex mixtures by affinity chromatography or in a one-step Chip. The specific antigen capturing is practical in vivo as was demonstrated by non-invasive imaging, and in vivo detoxification experiments of envenomed mice.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing

OPTIMIZING PURIFICATION PROCESSES

10:50 Purification of Recombinant Antibodies by Hydroxyapatite Chromatography – Potential and Pitfalls
Frank Hilbrig, Ph.D., Chair, Process Biotechnology, University of Bayreuth
Chromatographic hydroxyapatite is a highly biocompatible, non-toxic material that naturally presents a patterned structure of diverse interaction points on its surface. Highly selective “pseudo-affinity” binding of proteins including antibodies has been reported for this material. The talk will discuss the basis for this selectivity and how to exploit this knowledge for the set up of efficient antibody purification processes. The integration of such a hydroxyapatite step into a multi-step isolation scheme will also be discussed together with possible pitfalls.

11:20 Streamlining Simultaneous Development of Late Stage Purification Processes for Two Different Antibodies: A Case Study
Lilia Nunez, Ph.D., Associate Scientist, Purification Development, Genentech
Processes for two Different Antibodies have become commonplace in the purification of monoclonal antibodies, particularly for proof of concept studies. More recently, high throughput screening has further accelerated early stages of process development, and has also started to play an important role in the development of late stage and commercial processes. When combined, both platform knowledge and high throughput screening can streamline process development where timelines are constricted or when only limited resources are available. Simultaneous development of two or more purification processes, however, has been rarely explored as a tool for the acceleration of development timelines. A case study will be presented for the simultaneous development of late stage purification processes of two antibodies with different purification properties.

11:50 Purification Process Development of a Recombinant Monoclonal Antibody Expressed in Glycoengineered *Pichia pastoris*
Sandra Rios, Ph.D., Senior Scientist, Downstream Process Development, Merck Research Laboratories
A robust and scalable purification process was developed to generate antibodies of high purity and sufficient quantity from glycoengineered *Pichia pastoris*. Protein A affinity chromatography and alternative chromatography steps were used to capture the antibody from the culture supernatant. Cation exchange and mixed mode chromatography using an optimized NaCl gradient efficiently removed process- and product-related impurities. Antibody produced from glycoengineered *P. pastoris* was comparable to its commercial counterpart in heterotetramer folding, physical stability and binding affinity.

12:20 pm Increasing Options to Meet Drug Development & Manufacturing Challenges
Richard Pearce, M.Sc. DipM, Director of Strategy Development, EMD Millipore
In this presentation we introduce the concept of “Open-Sourcing”, an alternative view of how knowledge, expertise and resources can be accessed and delivered to speed the journey to the clinic.

12:50 Luncheon Presentation (Sponsorship Opportunity Available) or Lunch on Your Own

INSIGHTS INTO BIOPROCESSES

1:35 Chairperson’s Remarks

1:40 Structural/Functional Tools Helping to Design Robust Purification Processes
Guy de Roo, Ph.D., Project Leader, DSP Synthon BV
A combination of high-throughput screening, design of experiments and structural modeling was applied to study the impact of different pH, salt and buffer composition on the propensity of antibodies to form aggregates, degradation products and oxidized/deamidated species. The obtained information allows for selection of a more optimal design space resulting in the development of more robust purification processes.

2:10 Understanding Chromatography Fouling in Therapeutic Protein Manufacture
Daniel G. Bracewell, Ph.D., Senior Lecturer, The Advanced Centre for Biochemical Engineering, Department of Biochemical Engineering, University College London
Chromatography performance is inherently susceptible to feed stream characteristics and fouling processes. To understand the operation in a process context it is necessary to understand how fouling impacts performance and lifetime. In this work, scanning electron microscopy and confocal laser scanning microscopy are used to investigate fouling during the manufacture of a therapeutic protein.

OVERCOMING PURIFICATION CHALLENGES

2:40 Affinity Purification of a Framework 1 Engineered Mouse/Human Chimeric IgA2 Antibody from Tobacco
Markus Sack, Ph.D., Senior Scientist, Fraunhofer Institut für Molekularbiologie und Angewandte Oekologie IME, RWTH Aachen
Despite their therapeutic potential, IgA formats are currently underexploited in the development of antiviral and anticancer drugs and for topical mucosal applications, mainly because they are difficult and expensive to purify. We engineered a protein-L binding site into the variable light chain domain of a chimeric IgA2 to simplify downstream processing. Transiently expressed IgA2 variants were efficiently recovered from tobacco leaves by protein-L affinity chromatography while retaining their antigen binding affinity, making them more amenable to further process development.

3:10 Validation and Application of a Novel EF Hand Affinity Tag and Nanoparticle-Based Technology for Purification and Clean Up of Antibody Fragments and Whole IgG Proteins
David O’Connell, Ph.D., Senior Scientist, Conway Institute of Biomolecular & Biomedical Research, School of Medicine, University College Dublin
We have developed a novel EF hand-based fusion vector system that we have engineered to express scFv fusion proteins. We will present a case study data showing the enhanced functionality of the scFv when purified with nanoparticles bearing the second hand of the system. Stability, efficacy and multifunctionality of the purified protein will be addressed.

BREAKTHROUGH TECHNOLOGIES

3:40 Molecular Modeling of the Affinity Chromatography of Monoclonal Antibodies
Carlo Cavallotti, Ph.D., Associate Professor, Dipartimento di Chimica, Materiali e Ingegneria Chimica “G. Natta,” Politecnico di Milano
The critical step of purifying mAbs usually involves the efficient, but highly expensive, protein A affinity chromatography process. Recently, molecular modeling has been used to investigate at the microscopic scale the interaction between mAbs and affinity materials with the intent of understanding the nature of this process and determining rational guidelines for its optimization. The current status of these studies is the subject of this presentation.

4:10 ETRAP Selection of Specific Polyclonal Antibody Epitopes
Dan L. Crimmins, Ph.D., Senior Scientist, Department of Pathology and Immunology, Division of Laboratory and Genomic Medicine, Washington University School of Medicine
ETRAP (efficient trapping and purification) is a one-step affinity column procedure to isolate specific epitopes from GST protein polyclonal antibodies. After spot-peptide membrane array linear epitope mapping, the intensely immunostained spots are decoded, the corresponding sequences synthesized to contain a non-native N-terminal cysteine, and a column then prepared. This purification removes antibodies to GST and selects antibodies specific to the peptide epitope.

4:40 End of Conference
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Co-locate your user-group meeting with PEGS 2012. CHI will help market the event, manage logistical operations, develop the agenda, and more.

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