Protein Design & Engineering Conference

Bridging the technological gap between protein evolution, targeted therapeutics and analytical techniques

8th - 9th October 2018 | Frankfurt, Germany

Event Overview

Protein-based drugs are a fast-growing class on the pharmaceutical market, with thousands of candidates in development. State-of-the-art technologies in computational protein design and experimental protein engineering are needed to accelerate the process of biotherapeutic design. Industrial meetings on drug design frequently miss the new computational and experimental methodologies introduced by a few academic labs around the world. On the other hand, university environment rarely allows for high-throughput testing of the new technologies. To bridge this gap between industry and academia, we initiated the meeting on Protein Design and Engineering and assembled a panel of world-class scientists.

MarketsandMarkets is coming up with the **Protein Design & Engineering Conference** to be held in **Frankfurt, Germany** on **8th & 9th October, 2018.** We invite to join us to experience the live case studies and discussions from the experts of industry and institutes across the globe. The meeting should stimulate exchange of ideas and collaborative research between industry and academia.

Who Should Attend?

From Pharmaceutical, Bio-pharmaceutical and Therapeutics companies:

Senior Scientists/ Principal Scientists/ Project Leaders/Heads in:

- Molecular Biology
- Drug discovery
- Protein biochemistry
- Protein engineering
- Therapeutics
- Protein production
- Antibody discovery
- Biologics
- Protein technologies
- Medicinal chemistry
- Biotherapeutics
- Systems Biology
- Purification & analytics

From Universities and Research institutes:

Professors/ Assistant Professors/ Researchers/ Scientists/ Principal Scientists in:

- Molecular Biology
- Bio-molecular Engineering
- Bio-chemistry
- Biophysics
- Bio-chemical engineering
- Bio-medical engineering
- Functional Genomics
- Genome Biology
- Structural Biology
- Systems Biology
- Proteomics & protein analysis
- Protein engineering
- Metabolomics
- Medical oncology

Key Highlights

- **Structural** methods in **drug design**
- Protein **design and analysis**
- **Structure** based drug development
- Proteome **microarray** based approach
- Design **binding** specificity
- **Human-like recombinant** antibodies
- **Glycoengineered** antibodies

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Advisory Committee

Julia Shifman, Associate Professor, The Hebrew University of Jerusalem, Israel

Expert Speaker Panel

Julia Shifman, Associate Professor, The Hebrew University of Jerusalem, Israel

Eva-Maria Strauch, Research Assistant Professor, Department of Biochemistry, University of Washington, USA

Mathieu Cinier, Scientific Director, Affilogic, France

Simon Huet, R&D Project Manager, Affilogic, France

Stefan Zielonka, Senior Scientist, Merck, Germany

Ylva Ivarsson, Associate Professor, University of Uppasala, Sweden

Reinhard Sterner, Professor, Biochemistry, University of Regenburg, Germany

Arne Skerra, Professor, TUM School of Life Sciences Weihenstephan, Germany

Mette Rosenkilde, Professor, University of Copenhagen, Denmark

Yariv Wine, Assistant Professor, Tel Aviv University, Israel

Michael Hust, Professor, Technical University of Braunschweig, Germany

Birte Hoecker, Full Professor, Biochemistry, University of Bayreuth, Germany

Christian Griesinger, Professor, Max Planck Institute for Biophysical Chemistry, Germany

Yanay Ofran, Professor, Bar Ilan University, Israel

Laura Von Schantz, Senior Scientist, Alligator Bioscience AB, Sweden

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DAY 1, MONDAY, 8TH OCTOBER 2018

08:00 **Registration**

08:55 **Welcome note from MarketsandMarkets**

09:00 **Opening Remarks from the Chairman**

COMPUTATIONAL AND EVOLUTIONARY BASED PROTEIN DESIGN

09:10 **Protein engineering through combined computational and directed evolution approaches**

- Developed computational saturated mutagenesis protocol for predicting effects of mutations on binding
- This method could be used for design of focused libraries of protein bindings
- Using the computational/combinatorial approach we engineer high-affinity and highly specific binders for one type of Matrix Metalloproteinases

Julia Shifman, Associate Professor, **The Hebrew University of Jerusalem, Israel**

09:40 **Ancestral sequence reconstruction is an efficient tool for protein design and the analysis of protein-protein interactions**

- Primordial enzymes can be resurrected by ancestral sequence reconstruction
- Resurrected enzymes are thermostable and active
- Ancestral sequence reconstruction can help to analyze protein-protein interactions

Reinhard Sterner, Professor, Biochemistry, **University of Regenburg, Germany**

10:10 Solution Provider Presentation; Please contact at saumyo.ghosh@marketsandmarkets.com

10:40 **Morning Refreshments | Poster Presentations | One-to-One Networking**

11:25 **Protein design from evolutionary building blocks**

- Natural proteins evolved from sub-domain sized fragments
- Even different protein folds share evolutionary conserved subunits
- New protein hybrids can be build based on the same principle

Birte Hoecker, Full Professor, Biochemistry, **University of Bayreuth, Germany**

11:55 **Designer Proteins: Targeting Protein-Pathogen Interactions**

- General strategy for the computational design of homo-oligomeric protein assemblies with binding functionality precisely matched to homo-oligomeric target sites
- Summary on the generation of de novo designed small protein libraries as a basis for next-generation therapeutics and diagnostics
- How we can take the design of binding proteins to the next level using completely customized proteins against pathogens

Eva-Maria Strauch, Research Assistant Professor, Department of Biochemistry, **University of Washington, USA**

12:25 Solution Provider Presentation; Please contact at saumyo.ghosh@marketsandmarkets.com

12:55 **Lunch | Poster Presentations | One-to-One Networking**

13:55 **Panel Discussion: Protein engineering: a new frontier for biological therapeutics**

- Advantages
- Disadvantages

NEW SCAFFOLDS AND TARGETS FOR PROTEIN THERAPEUTICS

14:25 **Optimization of Nanofitin hits driven by epitope determination from in vitro assays and structural prediction**

- Presentation of the Nanofitin technology with focus on oral administration route
- Case study on anti-inflammatory Nanofitins in gastrointestinal disease
- Hits optimization through iterative in vitro and in silico cycles
- Highlight of new mechanism of interaction by interface mapping and docking

Simon Huet, R&D Project Manager, **Affilogic, France**

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14:55	**Engineering of shark-derived vNAR single domain antibodies** • The adaptive immune system of sharks comprise a unique heavy chain-only antibody isotype referred to as IgNAR • The variable domain of IgNAR (vNAR) displays several peculiar features making it attractive for biotechnological and biomedical applications • The generation of high-affinity vNAR antibody domains as well as bispecific and pH-dependent vNAR fragments • Additionally, also the generation of anti-idiotypic vNAR domains will be explained **Stefan Zielonka,** Senior Scientist, **Merck, Germany**
15:25	**Novel Biopharmaceuticals through Protein Design: Anticalins and PASylation** • Anticalins are binding proteins based on the natural lipocalin scaffold that offer a promising alternative to antibodies, having reached the clinical development stage in multiple indications • PASylation provides a biological alternative to PEGylation and allows the delepment of biobetter proteins/peptides with extended plasma half-life and enhanced action in diverse therapeutic applications • Apart from target affinity and specificity, tuning of the circulation half-life has become an important parameter for the design of modern biological drugs as well as in vivo diagnostic agents **Arne Skerra,** Professor, **TUM School of Life Sciences Weihenstephan, Germany**
15:55	**Evening Refreshments | Poster Presentations | One-to-One Networking**
16:40	Solution Provider Presentation; Please contact at saumyo.ghosh@marketsandmarkets.com
16:55	**The Molecular Landscape of ADA Following Treatment with Biologics** • While mAbs hold significant promise for improving human health however, repeated administration of mAb often leads to the induction of undesirable Anti-Drug Antibodies (ADA) • The mechanisms that lead to induction of ADAs and the molecular composition of the ADAs are unknown • We developed a new immunoassay to determine ADA level and their neutralizing capacity • We have found that mAb infusion mounts a vaccine like response reflected in a rapid rise of lymphocytes 7-10 days post-infusion • B Cells were isolated at the peak response post-infusion and their repertoire features were determined by Next Generation Sequencing **Yariv Win,** Assistant Professor, **Tel Aviv University, Israel**
17:25	**Predicting and designing interaction between proteins and other molecules** • While modelling of protein interaction has improved greatly over the years, most models of protein interaction are still wrong • We show how wrong models can dramatically improve the prediction of interactions between proteins and other molecules, including DNA, RNA, small molecules and antibodies • We show how these predictions can be used to design new proteins with specific functions and the prediction phenotypes of genome sequences **Yanay Ofran,** Professor, **Bar Ilan University, Israel**
17:50	**Closing Remarks by the Chair**
18:00	**End of Day 1**

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DAY 2, TUESDAY, 9TH OCTOBER 2018

08:15 **Registration**

08:55 **Welcome note from MarketsandMarkets**

09:00 **Opening Remarks from the Chairman**

09:10 **NMR spectroscopy and protein structures and dynamics**

- NMR spectroscopic techniques to study small molecule/protein interactions
- NMR spectroscopic techniques to capture kinetics of conformational interconversions
- Folding kinetics
- Recognition kinetics

Christian Griesinger, Professor, **Max Planck Institute for Biophysical Chemistry, Germany**

PROTEIN ENGINEERING BY DIRECTED EVOLUTION TECHNIQUES

09:40 **Established and novel Family B GPCRs drug targets for metabolic diseases**

- Discovery of the first GIPR antagonist with efficacy in humans
- GIPR designed to reveal the role of GIP in pathophysiological conditions like obesity and T2D

Mette Rosenkilde, Professor, **University of Copenhagen, Denmark**

10:10 **Nanofitin technology with focus on drug conjugate and multi-specifics applications**

- Focus on the advantages of scaffold technologies with respect to size and modularity - highlights of the specificty of the Nanofitin technology
- Case study on drug conjugate
- Case study on bispecific application
- Case study on immune check point inhibitor

Mathieu Cinier, Scientific Director, **Affilogic, France**

10:40 Solution Provider Presentation; Please contact at saumyo.ghosh@marketsandmarkets.com

10:55 **Morning Refreshments | Poster Presentations|One-to-One Networking**

11:55 **Developability engineering of therapeutic monoclonal and bispecific antibodies**

- Establishing a developability engineering platform
- Lead optimization strategies using structure based focused libraries
- Screening for different types of stability

Laura Von Schantz, Senior Scientist, **Alligator Bioscience AB, Sweden**

12:25 Solution Provider Presentation; Please contact at saumyo.ghosh@marketsandmarkets.com

12:40 **Panel Discussion: Different types of protein structures and their behavior**

- Process
- Interaction levels
- Applications

13:10 **Lunch|Poster Presentations | One-to-One Networking**

14:25 **Discovery of short linear motif-mediated interactions through phage display of intrinsically disordered regions of the human proteome**

- A large part of the human proteome is intrinsically disordered. The disordered regions are enriched in short motifs that serve as docking sites for peptide binding domains. These interactions are typically transient and difficult to capture through most conventional high-throughput methods
- I will describe a novel approach for the large-scale profiling of domain-motifs interactions called Proteomic Peptide Phage Display (ProP-PD), that allows the interrogation of domain-motif interactions on a proteome-wide scale

Ylva Ivarsson, Associate Professor, **University of Uppasala, Sweden**

14:55	**Fighting Pathogens and Toxins with human and human-like recombinant Antibodies** • Recombinant human antibodies • Phage display • Pathogens • Toxins **Michael Hust,** Professor, **Technical University of Braunschweig, Germany**
15:25	**Role of ribosomes in altering the folding of a multidomain protein**
15:55	**Evening Refreshments & End of Conference**

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