

Protein Design & Engineering Conference



29th - 30th May 2018 | Dorint Hotels and Resorts,
Main Taunus Zentrum, 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 **29th & 30th May, 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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MARKETSANDMARKETS

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
Uppsala, Sweden



Reinhard Sterner, Professor,
Biochemistry, University of
Regensburg, 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 Ofra, Professor,
Bar Ilan University, Israel



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

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DAY 1, TUESDAY, 29TH MAY 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 Regensburg, 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, Afflogic, 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 development 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

Identification of novel biomarkers for disease diagnosis using proteome microarray approach

17:50

Closing Remarks by the Chair

18:00

End of Day 1

Media Partners



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DAY 2, WEDNESDAY, 30TH MAY 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 specificity 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 Uppsala, Sweden

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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

Yanay Ofran, Professor, **Bar Ilan University, Israel**

15:55

Evening Refreshments & End of Conference

Supporting Associations:

