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30 June – 1 July 2011
Hamburg, Germany



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Advances in Biodetection & Biosensors

Day One - Thursday 30 June 2011

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08.00 **Registration**

Session: Next Generation Biosensors and Biodetection Techniques

09:30 **Keynote Presentation**

Borrowing from Nature - Next Generation Biomimetic Analytical Platforms

Dermot Diamond, Professor, Dublin City University

The 'Internet of Things' envisages ubiquitous networks of millions of embedded sensors. Currently chem/bio-sensing are peripheral to this vision due to the complexity of the technology. To bridge the gap between current capability and future demand, new concepts in molecular sensing will emerge underpinned by revolutionary breakthroughs in materials science.

10.00 **Beyond Glucose: The Move Towards System Integration in Biosensors**

Jeff Newman, Advanced Biosciences MSc Programme Director, Cranfield University

10:30 **Coffee Break and Networking in the Exhibition Hall**

11:15 **Capacitive Biosensors for Ultrasensitive Analyses**

Bo Mattiasson, Professor, Department of Biotechnology

A capacitive biosensor with high sensitivity is presented. Assays of bacterial toxins and viral capsid proteins have been carried out with high sensitivity. The technology and the results will be presented.

11.45 **An Integrated Intracellular Optical and Extracellular Electrochemical Sensing Platform for the Study of Reactive Oxygen Species (ROS) Based Cellular Interactions**

Philip Manning, Scientist, Institute of Cellular Medicine, University of Newcastle

This presentation summarises the development of an integrated sensing platform that allows the simultaneous and real-time detection of reactive oxygen species production in both intracellular and extracellular environments.

12.15 **Technology Spotlight**

12:30 **Lunch and Networking in the Exhibition Hall**

13:30 **Poster Session**

14:15 **Advances in Biosensor Based Capabilities of Detecting Food Contamination**

Christopher Elliott, Director, Institute of Agri-Food and Land Use, Queen's University Belfast

The need for rapid detection of food contaminants is of immense importance to protect consumers and the integrity of the food supply chain. Biosensor technologies can help deliver this. An overview of current progress and remaining challenges will be presented.

14:45 **Chemical Restriction Length Polymorphism (CLFP) for Detection and Characterization of Bacterial Pathogens**

Byron Brehm-Stecher, Assistant Professor, Iowa State University

15:15 **Coffee Break and Networking in the Exhibition Hall**

16:00 **Investigating the Kinetics of cAMP Accumulation in Human Primary Cells Using a Live-Cell cAMP Biosensor**

Elizabeth Rosethorne and Steven Charlton, Promega

16.30 **Probing of NAD(P)H Availability in Living Yeast Cells Using a Microfluidic Electrochemical Sensor Array**

Natalie Kostesha, Post Doc, DTU Nanotech, Technical University of Denmark

The presented work is focused on the development and application of such miniaturized electrochemical sensors for simultaneous real-time monitoring of the dynamics of intracellular redox processes in genetically modified yeast cells.

17.00 **Title to be Confirmed**

Sina Bavari, Chief of Immunology, United States Army Medical Research Institute of Infectious Diseases

17.30 **Drinks Reception**

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Prearrange meetings with other delegates or follow up with them after the event.

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Advances in Biodetection & Biosensors

Day Two - Friday 1 July 2011

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Session: Point of Care and Field Ready Pathogen Detection Devices

09.30 **Keynote Presentation**

Recent Advances in Detection and Biosensors

Chris Lowe, Director, Institute of Biotechnology, University of Cambridge

10:00 **Molecular Pathogen Detection and the Challenge of Preanalytics for POCT**

Till Bachmann, Head of BioChip Research, University of Edinburgh

MDx at point of care at competitive costs remains an unmatched task which is mostly defined by the requirement of molecular detection technologies for highly processed and pure samples. We addressed this task at the level of sensitivity, specificity, and kinetics of the implemented biochip technologies.

10:30 **Coffee Break and Networking in the Exhibition Hall**

11:15 **BSI Performs Rapid and Quantitative Serological Assays: Prospects For Use in the Near-Patient Setting and the Field**

Darryl Bornhop, Professor of Chemistry, Vanderbilt University

11:45 **Magnetic Bead-Based Lab-on-a-chip systems For Rapid Detection and Identification of Avian Influenza Virus**

Bang Dang Duong, Senior Scientist and Head of Research Group, National Veterinary Institute, Technical University Of Denmark

12:15 **Lunch and Networking in the Exhibition Hall**

13:30 **Poster Session**

14:15 **Diagnostics Using Nanobioelectronics Based Sensing Systems**

Arben Merkoci, ICREA Research Professor, Nanobioelectronics & Biosensors Group, Catalan Institute of Nanotechnology
Recent advances in the field of nanobioelectronics based sensing systems that use either labeling with nanoparticles or even label-free technologies such as nanochannels will be shown. The developed devices have special interest for point of care diagnostics between other industries

14.45 **switchSENSE – A Novel Biosensing Principle to Detect and Analyze Molecules on a Chip**

Ulrich Rant, Group Leader, Technische Universität München

15:15 **Coffee Break and Networking in the Exhibition Hall**

16:00 **Biotests for Hazard Characterization of Waste**

Reinhilde Weltens, VITO

Biotests are used for hazard assessment of a variety of waste materials to demonstrate how biotests can provide information on the intrinsic toxicity of waste and how their results can be used for hazard classification of waste.

16.30 **Optical Classification of Human Embryonic Stem Cells**

Tracy Melvin, Researcher, University of Southampton

Optical approaches have been explored to enable the undifferentiated to be distinguished from differentiated stem cells. Our methods combine optical measurements, modelling and data analysis. This technique provides a novel approach with the potential for identification and sorting of stem cells.

17.00 **Close of Conference**

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AMT

Advances in Microarray Technology

Day One - Thursday 30 June 2011

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08:00 **Registration**

09:00 **Strengths and Weaknesses of Microarrays in Diagnostics**

Bertrand Jordan, Founder/Coordinator, Marseille-Nice Genopole

The common perception that microarrays are superseded by NGS doesn't take into account many features of clinical work. Microarrays may assess many entities of clinical interest besides DNA and definitely have a future in some of these fields.

Session: Advances in Protein Arrays

09:30 **Keynote Presentation:**

Immunoassays in Multiplex for Biased and Unbiased Proteomic Research

Thomas Joos, Professor, University of Tuebingen

This presentation discusses a simple and efficient way to overcome current limitations of multiplexing sandwich immunoassays and a strategy to cover a wide range of any given proteome with a minimal set of antibodies.

10:00 **Proteomic Profiling of Autoimmunity on Antigen Microarrays**

Peter Nilsson, Associate Professor, KTH - Royal Institute of Technology

The massive number of antigens produced within the Human Protein Atlas are systematically printed on microarrays and utilized for discovery of new autoimmunity targets with screening of disease oriented plasma and CSF samples.

10:30 **Coffee and Networking in Exhibition Hall**

11:15 **Unlocking Biomarker Discovery - Design of Antibody-Based Microarrays for High-Throughput Disease Proteomics**

Christer Wingren, Associate Professor and Lecturer, Department of Immunotechnology, Lund University

Unlocking the proteome and delivering biomarkers to the clinic will be critical for early and improved diagnosis, prognosis, and classification. Our recombinant antibody-based micro- and nanoarrays designed for high-throughput disease proteomics and applications thereof will be presented.

11:45 **Protein Microarray Technologies - Analysis of Signaling Networks in Tumours**

Markus Templin, Head of Assay Development, NMI at the University of Tuebingen

Complex data sets generated from limiting sample material allow the identification of differences in activation of signaling networks directly on the protein level. Protein microarray analysis during anti-cancer drug development will demonstrate the power of the technology.

12:15 **Lunch and Networking in Exhibition Hall**

13:15 **Poster Viewing**

14:15 **A Systematic Investigation of Candidate Breast Cancer Progression-Associated Biomarkers Identified from Omic Screens: Leveraging Antibody-Based Proteomics**

William Gallagher, Vice-Principal for Research and Innovation and Associate Professor of Cancer Biology, University College Dublin

A key bottleneck in the translation of discoveries from transcriptomic and proteomic screens into clinically viable diagnostics relates to current deficits in relation to antibody availability. This presentation provides a case example of how antibody-based proteomics can be applied to transition candidate breast cancer progression-related biomarkers from such omic screens.

14:45 **Kidney & Liver Biomarker Toxicity Identification from Gene Expression Data via Incorporation of Biological Network Information**

Robert Russel, Professor of Protein Evolution, University of Heidelberg

I will discuss our efforts to discover biomarkers for liver and kidney toxicities using gene expression data and an innovative biological interaction network based in silico approach which highlights new and old candidates.

15:15 **Coffee and Networking in Exhibition Hall**

16:00 **Silicon Chips with Dual Label-Free and Fluorescence Detection for High Sensitivity Diagnostic Protein Microarrays**

Marina Cretich, Researcher, Istituto di Chimica del Riconoscimento Molecolare (ICRM) C.N.R.

In this work, we propose a new silicon chip for protein microarray development, fabrication and validation. The chip allows, within a single experiment on the same surface, label-free imaging of the arrayed protein probes coupled with high sensitivity fluorescence detection of the molecular interaction counterparts.

16:30 **Protein Powered Drug Discovery**

Leonidas Alexopoulos, Group Leader, Systems Biology and Bioengineering Lab, National Technical University of Athens

High throughput proteomic technologies and systems biology algorithms are combined to construct signaling pathways for normal and diseased cells, identify drug mode of action, and predict drug toxicity and efficacy.

17:00 **Drinks Reception**

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AMT

Advances in Microarray Technology

Day Two - Friday 1 July 2011

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- 09:00 **Keynote Presentation:**
From Microarrays to NextGen and Models to Exotics
Andrew Cossins, Professor and Director of Institute of Integrative Biology and Centre for Genome Research, Liverpool University
- Session: Advances in DNA Arrays**
- 09:30 **Array CGH: Applications in the Clinical Setting**
Lisa White, Associate Professor and Director of the BCM Microarray Core Facility, Baylor College of Medicine
We present seven years of our aCGH experience utilizing arrays for postnatal, prenatal and cancer genetic testing.
- 10:00 **Proteomics at High Content using DNA Microarray Technology**
Larry Gold, Chairman, Somalogic
- 10:30 **Coffee and Networking in Exhibition Hall**
- 11:15 **A Microarray-Based NASBA for Diagnostic RNA Analytics**
Thomas Brandsetter, Group Leader, University of Freiburg
There is strong clinical need for a biochip platform which can analyze all relevant prognostic and therapeutic parameters simultaneously. For this purpose NASBA-on-microarray was developed and will be presented as multi-parametric microarray-based technique with the potential to perform real-time detection.
- 11:45 **MicroRNAs Studies on Aortic and Aortic Valve Diseases**
Salah Mohamed, Laboratory and Group Leader, UKSH Campus Luebeck
MicroRNAs are promising as potential biomarkers. For more thoroughly analysis of those promising biomarker candidates, the group is employing a state of art technology for highthroughput genomic screening to evaluate the differentially expressed microRNAs in aortic and aortic valve diseases.
- 12:15 **Lunch and Networking in Exhibition Hall**
- 13:30 **Poster Viewing Session 2**
Session: Novel Array Platforms, Technologies and Bioinformatics
- 14:15 **Rapid Multiplexed Analysis Based on Chemiluminescence Flow-Through Microarrays**
Michael Seidel, Chair for Analytical Chemistry and Group Leader in Bioseparation and Microarrays, Technische Universität München
We have developed a universal stand-alone platform for rapid multiplexed analysis based on flow-through chemiluminescence microarrays. Antibody-, DNA and small molecule microarrays were applied for analysis of bacteria, viruses, pharmaceuticals, and biotoxins in complex matrices.
- 14:45 **Recent Progress with Real-Time Microarrays**
Steve Blair, Associate Professor and Director of the Center for Microarray Technology, University of Utah
Instrumentation for real-time data acquisition from microarrays will be overviewed, along with a discussion of kinetics-based analysis methods. The prospects for quantitative data interpretation will be discussed in the context of heteroplasmy determination and methylation detection.
- 15:15 **Coffee and Networking in Exhibition Hall**
- 16:00 **The "Nuts and Bolts" of Microarray Based High Resolution Melting Analysis**
Siegfried Krainer, Research Scientist, Austrian Institute of Technology
The realization of High Resolution Melting analysis on microarray substrates combines insight into the thermodynamics of hybridization with a simplified process flow for application specific DNA sensors. A MEMS system with integrated amplification will be presented together with results on the hybridization kinetics and thermodynamics of different types of nucleic acids on microarrays.
- 16:30 **Overcoming Technical Bias in Clinical Microarray Measurements**
Aron Eklund, Assistant Professor, Technical University of Denmark
- 17:00 **Close of Conference**

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Advances in Protein Crystallography

Day One - Thursday 30 June 2011

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08:00 **Registration**

Session: Fragment Based Lead Discovery

09:00 **Keynote Presentation:**

Current Perspectives in Fragment-Based Ligand Discovery

Roderick Hubbard, Professor, University of York & Research Fellow, Vernalis

An overview of the current methods and applications of FBLD - what works and where there is a need for further innovation - illustrated with examples from drug discovery and chemical biology.

09:30 **From Fragments and Hot-Spots to Novel Lead Structures**

Gerhard Klebe, Professor, Philipps-University Marburg

General experience shows that small molecule fragments, thought as initial leads for a drug design project, assemble in an ordered fashion in protein binding sites. Usually they populate at the hot spots of binding in protein surface-exposed binding pockets. Therefore, their crystallographic characterization is usually successful and the obtained structures provide a valid starting point for a subsequent optimization by growing the initially discovered fragments in the binding pocket via the decoration with suitable side chains.

10:00 **Fragment Based Approaches to GPCRs**

John Christopher, Senior Scientist, Heptares Therapeutics

10:30 **Coffee Break and Networking in Main Exhibition Hall**

11:15 **Chemical Space as a Source for Fragments**

Jean-Louis Reymond, Professor, University of Bern

The ensemble of all possible molecules forms the so-called chemical universe, or chemical space, which is believed to contain at least 10^{E60} molecules up to a MW of 500 Da of possible interest for drug discovery. In de novo drug design one explores this chemical space by enumerating and scoring molecules in silico to select compounds for synthesis and testing. We have recently carried out an exhaustive enumeration of chemical space for small organic structures to form the Chemical Universe Database. The database contains one billion structures up to 13 non-hydrogen atoms. I will discuss the expansion of this enumeration up to 17 atoms, and a general method for mapping the chemical space covered by these structures and identifying analogs of useful fragments. I will also report latest results in using virtual screening of GDB-databases for drug discovery.

11:45 **Structure Biology to Understand Molecular Mechanisms in Tuberculosis**

Matthias Wilmanns, Head of Outstation, EMBL Hamburg

Tuberculosis has regained a global threat, mainly because of the emergence of hyper-resistant strains against front line antibiotics and a major problem in HIV co-infections. Classical target-oriented drug discovery has not fulfilled the premises because of the complexity of the infection process in the human host.

We have set up a program to determine a substantial, relevant fraction of the complete proteome of Mycobacterium tuberculosis in 3D, by solving high-resolution structures using X-ray crystallography. We will present examples where the knowledge of these 3D structures nevertheless provide important insight into molecular mechanisms, leading to potential drug discovery. We will also demonstrate on some examples, how structural biology can be used as a posteriori validation tool, i.e. for potential lead compounds where targets were initially unknown.

12:15 **Lunch and Networking in Main Exhibition Hall**

13:15 **Poster Presentations**

Session: Protein Chemistry and Crystallisation

14:15 **Keynote Presentation:**

Smart Materials for Protein Crystallisation

Naomi Chayen, Professor, Imperial College London

14:45 **Chaperone-Assisted Crystallography with DARPins**

Markus Grütter, Professor, University of Zurich

A recurring effort to crystallize a particular protein is to bind it non-covalently to a specific helper binding protein - a crystallization chaperone. There is a wide range of tools available nowadays but their handling is often not as convenient as required. A valuable addition to the present repertoire of binding proteins is the designed ankyrin repeat protein (DARPin) technology. The potential of these novel binding proteins is illustrated by co-crystal structures with a variety of target proteins, including a membrane protein. The usefulness of DARPins in crystallization, the potential for phasing through DARPins and other recent approaches will be presented.

15:15 **Coffee Break and Networking in Main Exhibition Hall**

16:00 **Crystallization and Structure Determination of Active and Inactive G Protein Coupled Receptors (GPCRs) using Stabilization Strategies**

Gebhard Schertler, Head of Biology and Chemistry,
Paul Scherrer Institut

16:30 **Latest Methods in Optimization of Crystallization by Combining in situ Light Scattering and Variation of Solution Contents**

Christian Betzel, Professor, University of Hamburg

A unique and advanced hardware combination supporting methods to induce nucleation by adding precipitants or other substances to optimize the crystallization process via a feedback loop will be presented together with results obtained of various proteins and different scenarios.

17:00 **Streamlining the Pipeline Towards Glycoprotein Structures**

Joanne Nettleship, Senior Scientist, Oxford Protein Production Facility

- High-throughput pipeline for glycoprotein production in HEK 293 cells.
- Parallelization and automation of expression screening.
- Glycan modification to aid glycoprotein crystallization.
- Automated large scale production and purification of secreted proteins.
- Use of transient transfection v's formation of a stable cell line.
- Antibody Fab's as co-crystallization chaperones.
- In situ diffraction for solving glycoprotein structures.

17:30 **Drinks Reception**



Advances in Protein Crystallography

Day Two - Friday 1 July 2011

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- 09:30 **Lessons of Diffraction Resolution and how the Structures of the Various Crustacyanins have been Solved**
John Helliwell, Professor of Structural Chemistry, University of Manchester
The coloration of the lobster shell derives from astaxanthin molecules with proteins in complex with apocrustacyanin A1 solved using softer X-rays, and refined at 1.4Å resolution, and the b-crustacyanin dimer complex at 3.2Å resolution. The α-crustacyanin complex of eight b-crustacyanins has been studied by EM and SAXS at 30Å resolution. Several relevant carotenoids have been investigated by chemical crystallography at 0.8Å resolution, and their colours in solution and the crystalline state also determined.
- 10:00 **Xaperone Assisted X-ray Crystallography: Turning on a G-protein-Coupled Receptor**
Jan Steyaert, Professor, Vrije Universiteit Brussel
Nanobodies that faithfully mimic the effects of G protein binding were used to obtain diffraction quality crystals and to solve the first structure of an active agonist-bound state of the human β2 adrenergic receptor.
- 10:30 **Coffee Break and Networking in Main Exhibition Hall**
- 11:15 **Improving Protein Crystallography with Acoustics for Crystallization Screening, Solution Quality Monitoring and Crystal Transfer**
Richard Ellson, Chief Technology Officer, Labcyte
Focused acoustics can transfer liquids and suspensions as well determine the quality and volume of crystallization solutions. Examples of protein crystallography work flows using acoustics will demonstrate miniaturization of screens, flexibility, and quality for a range of protein crystallography applications.
- Session: Crystallographic Computing**
- 11:45 **The wwPDB Common Deposition and Annotation Tool : how Deposition at the wwPDB will Change.**
Tom Oldfield, Team Leader, EBI
The Worldwide Protein Data Bank (wwPDB) common deposition and annotator project will release a common deposition tool at all wwPDB partners sites at the beginning of 2012. This tool will significantly change the process of deposition of macromolecular structure data for the scientific community and this talk will present the salient points for the depositor.
- 12:15 **Lunch and Networking in Main Exhibition Hall**
- 13:15 **Poster Presentations**
- 14:15 **The Collaborative Computational Project Number 4 (CCP4) - Towards New Challenges in Crystallographic Computing.**
Eugene Krissinel, Core Group Leader, CCP4
CCP4 is a community based resource in Protein Crystallography with ultimate goals to play a key role in the development of new crystallographic software for academic, not for profit, and for profit research, as well as in education and training of scientists, dissemination of new ideas, techniques and practice. In this talk, the current state of the Suite, new developments and new challenges arising will be discussed.
- 14:45 **Using Experimental Data Directly in Structure Solution**
Navraj Pannu, Assistant Professor, Leiden University
A multivariate likelihood function applied to the different steps of experimental phasing leads to solutions when current methods fail.
- 15:15 **Coffee Break and Networking in Main Exhibition Hall**
- Session: New Laboratory Instrumentation**
- 16:00 **Facilities for Macromolecular Crystallography at BESSY-II**
Manfred Weiss, Research Scientist, Helmholtz-Zentrum Berlin The Macromolecular Crystallography (MX) group at the Helmholtz-Zentrum Berlin (HZB) is operating three state-of-the-art beam lines for MX, which currently represent the most productive MX-stations in Germany. BL14.1 and 14.2 are energy tunable , while BL14.3 is a fixed-energy side station (13.8 keV). In the presentation, the beam line instrumentation as well as the available ancillary facilities will be presented and an overview of the experimental possibilities, which are possible, will be given.
- 16:30 **EMBL@PETRA3. An Integrated Facility for Structural Biology**
Thomas Schneider, Group Leader, EMBL Hamburg
EMBL is constructing an integrated facility for structural biology at the high-brilliance synchrotron PETRA III at DESY in Hamburg. Three beamlines for small angle X-ray scattering and X-ray diffraction will be operated together with on-site facilities for sample preparation and characterization and data evaluation.
- 17:00 **Close of Conference**

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Day One - Thursday 30 June 2011

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08.00 **Registration**

Session: Small Molecule Applications

09:30 **Keynote Presentation**

Automated Processing of Native Biofluids Up-Front to LC-MS/MS Analysis of Small Molecules

Karl-Siegfried Boos, Laboratory of BioSeparation, Medical Center of the University of Munich

The lecture describes front-end automation for LC-MS/MS analysis of drugs and endogenous compounds present in whole blood and blood plasma / serum as well as urine by applying a unique in-line thermal or cryogenic processing and / or on-line Solid Phase Extraction (SPE).

10.00 **Micro Separation LC-MS Methods for Improving Retrospective Detection of Drug Administration for Evidential Purposes**

Mark Parkin, Lecturer in Analytical Science, King's College London

Investigating multifaceted approaches utilising micro separation LC-MS methods for improving retrospective drug detection in both regular (blood or urine) and alternative (hair, sweat or saliva) biological matrices.

10:30 **Coffee Break and Networking in the Exhibition Hall**

11:15 **Functional Composite Phases for Biomolecule Extraction and Separations**

Brett Paull, Professor, Dublin City University

11.45 **Title to be Confirmed**

Tony Edge, Technical Manager, Thermofisher Scientific

12.15 **Technology Spotlight**

12:30 **Lunch and Networking in the Exhibition Hall**

13:30 **Poster Session**

Session: Protein Analysis

14:15 **Keynote Presentation**

Mass Spectrometry Based Translational Proteomics – From the Benchtop to the Bedside

Arthur Moseley, Director, Duke Proteomics Facility

This presentation evaluates the experimental design factors critical for success in biomarker proteomics. Importantly, it seeks to define both the mass spectrometry and the non-mass spectrometry experimental design factors necessary for successful biomarker proteomics projects in their journey from the Benchtop to the Bedside.

14:45 **Rapid and Sensitive Identification and Quantification of Fungal Cell Wall Glycoproteins**

Chris de Koster, Professor, University of Amsterdam

15:15 **Coffee Break and Networking in the Exhibition Hall**

16:00 **3D-Gel Electrophoresis, a New Development in Protein Analysis**

Robert Ventzki, Scientist, University of Greifswald

We present a new method for automated high-throughput analysis of DNA and proteins by electrophoresis in a 3D-geometry gel with online detection of laser-induced fluorescence, allowing the rapid, simultaneous, high-resolution analysis of a multitude of samples by 1D- or 2D-separation.

16.30 **Development of "Top-Down" and "Bottom-up" Approaches for the Determination of Milk and Egg Proteins in Spiked White Wine by on-line Liquid Chromatography/Tandem Mass Spectrometry**

Margarita Corrales Moreno, Post-doc, European Commission, Joint Research Centre, Institute of Reference Materials and Measurements

Method development: "top-down" and "bottom-up" approaches for the determination of milk and egg proteins in spiked white wine by on-line liquid chromatography/ tandem mass spectrometry

17.00 **Remote Open Access – The Lab2Lab™ Advantage**

Brian Everatt, Research Investigator, Novartis

This presentation will describe the system recently installed at Novartis, Horsham (UK) and demonstrate the typical throughput capability and time savings this introduces to the users, in addition to showing how it is possible to rationalize expensive equipment, reducing the cost of maintenance and support whilst increasing availability. It will show how the system can cope with failure of the analytical instrumentation by being able to redirect samples to working equipment, and the potential for future expansion.

17.30 **Drinks Reception**

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Day Two - Friday 1 July 2011

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Session: Informatics for MS

09.00 **We've Always had Data, so What's Changed? What's the Challenge and What's the Solution?**
John Langley, Head of Mass Spectrometry, University of Southampton

Session: Trapped Ions

09.30 **Keynote Presentation**
Current Role of Hyphenated Low and High Resolution Mass Spectrometry in Clinical and Forensic Toxicology.
Hans Maurer, Head, Department of Experimental and Clinical Toxicology, Saarland University

10:00 **Field Asymmetric Waveform Ion Mobility Spectrometry Combined With Mass Spectrometry for Structural and Trace Analysis**
Colin Creaser, Professor, Centre for Analytical Science
Combining field asymmetric waveform ion mobility spectrometry with mass spectrometry provides complementary separation of gas-phase ions on the basis of differential mobility and mass-to-charge. The combination allows enhance separations of mixtures including the separation of isobaric ions.

10:30 **Coffee Break and Networking in the Exhibition Hall**

Session: Novel Separation Techniques and Methodologies.

11:15 **Comprehensive Drug Metabolite Profiling Using Multidimensional Detection Techniques**
Hubertus Irth, Professor, VU University Amsterdam

11:45 **Novel Enrichment and Separation Methods for Bioanalysis**
Günther Bonn, Head of the Institute of Analytical Chemistry and Radiochemistry, Leopold-Franzens University innsbruck
Our research focuses on new developments in integrated sample preparation and separation systems including miniaturized solid-phase extraction (SPE), HPLC and capillary electrophoresis coupled to mass spectrometry.

12:15 **Lunch and Networking in the Exhibition Hall**

13:30 **Poster Session**

14:15 **Rapid Analysis of Plants by Ambient MS and On-Chip Sample Clean-up**
Teris van Beek, Associate Professor, WU Agritechology & Food Sciences
Pros and cons of ambient MS techniques for probing plants without any sample clean-up are discussed. Additionally rapid sample clean-up of alkaloid-containing plants by miniaturised three-phase microreactors is shown.

14.45 **New Support Materials for bio HPLC**
Peter Myers, Professor, University of Liverpool
This paper describes two approaches that have been taken in the University of Liverpool to develop new support materials for the analysis of biomolecules by HPLC.

15:15 **Coffee Break and Networking in the Exhibition Hall**

16.00 **Separation Performance of Modern HPLC Stationary Phases**
Attila Felinger, Professor, Department of Analytical and Environmental Chemistry, University of Pécs
The study of the mass transfer properties and thermodynamics of retention on modern fully porous and core-shell packing materials reveals the separation power of the latest generation of stationary phases. Results are presented focusing on the tools of stationary phase characterization.

16:30 **Automation and On-line Hyphenations for Trace Analysis**
Steven Wilson, Post-doc, University of Oslo

17.00 **Close of Conference**

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Day One - Thursday 30 June 2011

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08.00 **Registration**

Session: Growth Optimization for Food and Biofuels

09.30 **Keynote Presentation**

Metabolic Engineering of Transgenic Plants With the Omega-3 Long Chain Polyunsaturated Fatty Acid Biosynthetic Pathway - A Terrestrial Source of Fish Oils

Johnathan Napier, Research Leader, Rothamsted Research

10.00 **Systemic Protein and RNA Signaling in Flowering Induction**

Yiguo Hong, Professor, Hangzhou Normal University

In this presentation, I will discuss how to convert a plant flowering time integrator into a useful gene allele for molecular breeding of novel crops with increasing seed yields, as well as a new twist to reveal the nature of florigen.

10.30 **Coffee Break and Networking in the Exhibition Hall**

11.15 **Keynote Presentation**

Crop Biotechnology: Prospects and Opportunities

Jim Dunwell, Professor, University of Reading

This review summarizes important areas of activity in crop biotechnology likely to be exploited over the medium term (10–20 years), with an emphasis on agronomic traits.

Session: Systems-Based Approaches & Genomic Mapping in Plants

11.45 **Keynote Presentation**

The Use of High-Throughput Transcriptomics for Biomarker Development in Agriculture

Michael Pfaffl, Lecturer, Technical University of Munich

12.15 **Technology Spotlight**

12.30 **Lunch and Networking in the Exhibition Hall**

13.30 **Poster Session**

14.15 **The Search for New Genes Conferring Durable Disease Resistance**

John Walsh, Research Leader, Plant-Virus Interactions Group, University of Warwick

We have identified the major gene controlling broad-spectrum resistance to a plant virus. In collaboration with Syngenta Seeds, a gene-specific marker is now being used to introgress the resistance in to commercial plant lines. The nature of the resistance indicates that it may be durable.

14.45 **Phloem micro RNAs and Their Involvement in the Systemic Regulation of Stress Responses and Development**

Julia Kehr, Centre of Plant Biotechnology and Genomics, Polytechnic University of Madrid

This presentation will summarize the current knowledge about phloem micro RNAs and their long-distance mobility between organs. It will also discuss the potential roles their translocation plays during nutrient deficiency defense responses or the regulation of development.

15.15 **Coffee Break and Networking in the Exhibition Hall**

16.00 **Integration of Small RNA, mRNA and Degradome Profiling During Fruit Development**

Tamas Dalmay, Director of Research, Reader in Molecular and Cell Biology, University of East Anglia

Combined analysis of small RNA, mRNA and degradome profiles during tomato fruit development revealed many new microRNAs and microRNA targets. Correlation between microRNAs and their targets will be discussed.

16.30 **Transcriptional Control of Gene Expression by microRNAs**

Wolfgang Frank, Assistant Professor, University of Freiburg

17.00 **Visualization of Plant Sequence and Genotype Data and Analysis**

David Marshall, Head of Bioinformatics Group, SCRI

17.30 **Drinks Reception**

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Day Two - Friday 1 July 2011

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Session: Enhancing Plant Resistance to Disease

09.30 **Keynote Presentation**

Tipping the Balance: Sclerotinia Sclerotiorum Regulates Autophagy, Apoptosis and Disease Development by Manipulating the Host Redox Environment

Marty Dickman, Professor, Texas A&M University

What can be more fundamental than whether a given cell lives or dies? Our work with economically important necrotrophic phytopathogenic fungi has suggested that, whomever (plant vs. pathogen), controls the form cell death "wins" the battle.

10:00 **Keys to Durable Resistance Strategies in Crop Plants**

Richard Visser, Professor, Wageningen UR Plant Breeding

Potato is the world's third largest food crop yet it continues to endure late blight (LB), a devastating disease caused by the pathogen *Phytophthora infestans*. Exploiting plant genetic resistance in combination with knowledge of the pathogen's effector diversity will inform on the durability of Rpi genes and the best disease management strategy.

10:30 **Coffee Break and Networking in the Exhibition Hall**

11:15 **Map-Based Cloning of a Major Resistance Gene for Stripe Rust in Wheat**

Alan Schulman, Group Leader, Plant Genomics Lab, University of Helsinki

Wild emmer wheat (*Triticum dicoccoides*) is a particularly promising source of resistance to the wheat diseases. Our goal is to positionally clone Yr15 from *T. dicoccoides*, a key resistance gene to yellow rust. We have identified a BAC contig spanning this gene.

11:45 **Ulvan, a Sulfated Polysaccharide From Green Algae, Activates Plant Immunity and Protection Against Powdery Mildew Pathogens**

Bernard Dumas, Principal Investigator, University Paul Sabatier Toulouse III CNRS

12:15 **Lunch and Networking in the Exhibition Hall**

13:30 **Poster Session**

14:15 **Title to be Confirmed**

Phil Robinson, CEO, Kbiosciences

14:45 **From Lab to Farmers: Improving Disease Resistance in Durum Wheat**

Roberto Tuberosa, Professor, University of Bologna

15:15 **Coffee Break and Networking in the Exhibition Hall**

16:00 **Development of a Toolbox to Study Plant-Pathogen Interactions in Cereals**

Goetz Hensel, Senior Scientist, Leibniz-Institute of Plant Genetics and Crop Plant Research

16.30 **Disease Susceptibility as a Potential Target for Engineering Resistance?**

Ralph Huecklehoven, Chair of Phytopathology, Center of Life and Food Sciences Weihenstephan

Plant factors that are required for successful host infection by microbial pathogens might be targets

17.00 **Close of Conference**

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Prearrange meetings with other delegates or follow up with them after the event.

Check the event website for further information.

Lab-on-a-Chip

European Congress

Day One - Thursday 30 June 2011

Sponsored by
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08:00 **Registration**

09:00 **Keynote Presentation:**

Visualizing the flow in Lab on a Chip Devices

Ralph Lindken, Head of Microsystems and Fluid Mechanics Division, ZBT Duisburg

The efficiency of the design process of Lab-on-a-chip devices and their manufacturing costs can be improved by detailed a-priori knowledge of the fluid flow in the device. In this presentation we present the state-of-the-art tool for flow measurements micro-scale Particle Image Velocimetry (μ PIV) and we show how it improves the design process.

Session: Standardisation of Components

09:30 **Microfluidics – an Essential Tool for Product Development in the Life Sciences**

Holger Becker, Director, Microfluidic ChipShop GmbH

In the product development process of current systems in the Life Sciences and Diagnostics, microfluidics technology plays an instrumental role. In this presentation, with the help of examples of highly integrated microfluidic devices, we will highlight challenges and opportunities of using advanced miniaturization technologies in the product development process.

10:00 **Microfluidics Systems for Enhancing Life Science Applications such as in situ Hybridization and in vitro Stem Cell Cultures.**

Martin Dufva, Associate Professor, Technical University of Denmark

A library of miniaturized standardized components was realized for creating various compact, portable, robust and easy to use microfluidics systems. The component library is designated MainSTREAM and is used for dual in situ hybridization assays, microarray based genotyping, stem cell programming.

10:30 **Coffee Break and Networking in Main Exhibition Hall**

11:15 **Centrifugal Microfluidics for Assay Miniaturization on Commercially Available Instruments**

Roland Zengerle, Professor, University of Freiburg

Centrifugal microfluidics enables miniaturization, parallelization, integration and automation of biochemical assays. In addition the resulting lab-on-a-chip cartridges can be processed on commercially available instruments, like lab-centrifuges, real-time-PCR cyclers, or DVD drives.

11:45 **Keynote Presentation:**

Physical Tools for Probing Biological Complexity with Single-Cell Resolutions

Daniel Chiu, Professor, Washington University

This presentation describes some of the techniques that we have developed over the past years to study biological complexity at the single-cell level.

12:15 **Lunch and Networking in Main Exhibition Hall**

13:15 **Poster Presentations**

14:15 **Keynote Presentation:**

Droplet-based Microfluidic Strategies for High-Throughput Chemistry

Andrew DeMello, Professor, Imperial College London

My lecture will describe recent studies that are focused on exploiting the spontaneous formation of droplets in microfluidic systems to perform a variety of analytical processes, including cell-based assays, serial dilution, DNA binding assays and DNA amplification.

Session: Lab-on-a-Chip Applications: Sensing

14:45 **Integration of Femtosecond Laser Written Optical Sensors in a Lab-on-a-Chip**

Giulio Cerullo, Professor, Politecnico di Milano

We demonstrate the integration of femtosecond laser written optical waveguides and photonic devices in commercial fused silica lab-on-a-chips. We present applications to separation and detection of fluorescently labelled DNA fragments, and refractive index sensing with a 3D Mach-Zehnder interferometer.

15:15 **Coffee Break and Networking in Main Exhibition Hall**

16:00 **Integrated "BioCameras" in Chips**

Liv Furuberg, Chief Scientist, SINTEF Microsystems and Nanotechnology

We present a new optical biosensor principle for on-chip protein and DNA analyses for diagnostics. The biosensor generates a detectable signal from a few target molecules, has a high dynamic detection range and provides rapid results.

16:30 **Molecular Isolation on the Micro and Nanoscale**

Joshua Edel Senior Lecturer, Imperial College London

We report a novel method to fabricate nanopores with apparent diameters below 20 nm for biomolecular sensing.

17:00 **Lab-on-a-Chip Optical Biosensor for Enzyme Activity Sensing**

Karl-Heinz Feller, Head of Instrumental Analysis, University of Applied Sciences Jena

The commonly used assay for measuring glucose oxidase (GOx) and laccase (Lac) activity, based on spectrophotometric test using 2,2'-azinobis(-3 ethylbenzothiazoline-6-sulfononic acid) (ABTS) have been adapted to measure these enzyme activities in micro-structured devices.

17:30 **Drinks Reception**

Lab-on-a-Chip European Congress

Day Two - Friday 1 July 2011

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Session: Lab-on-a-Chip Applications: Point of Care

09:00 **Keynote Presentation:**

A System for Continuous Monitoring of Subcutaneous Glucose Based on Microfluidics and Microdialysis

Sabeth Verpoorte, Professor, University of Groningen

The surge in new diabetes patients caused by Western-style diet and a sedentary lifestyle continues to drive the development of glucose sensing technologies and portable monitoring systems. In this presentation, we consider the use of microfluidics coupled with microdialysis as the basis of a miniaturized system for continuous monitoring of glucose in subcutaneous tissue.

09:30 **Multifunctional Nanoparticles for an Integrated Microfluidic Diagnosis System**

Jörn Probst, Head of Life Science, Fraunhofer Institute

The great potential of nanoparticles in early diagnosis was recently demonstrated by a joint research project aiming to create a portable microfluidic diagnostic device capable of simultaneously detecting relevant biomarkers such as e.g. tumor-specific or cardiological markers with detection sensitivity even below 10⁻¹¹ mol/l.

10:00 **A Multiplexed Localized Surface Plasmon Based Biosensor Based on Gold Nanorings for Point of Care Applications**

Liesbet Lagae, Group Leader Functional Nanosystems, IMEC

A compact lab on chip system, cheap and easily parallelizable, was developed based on the localized surface plasmon resonance (LSPR) properties of gold nanoring covered substrates integrated with a multichannel microfluidic disposable and a compact CCD read out. The device was applied to simultaneously monitor the biomolecular interactions with label free and in real-time for both proteins and DNA. The investigation of the kinetic biomolecular interactions give a good indication how assay times could be further reduced of particular importance for point-of-care diagnostic applications. Furthermore, we will show the potential of these gold nanostructures for advanced LSPR sensing and Surface Enhanced Raman Scattering (SERS) spectroscopy.

10:30 **Coffee and Networking in Main Exhibition Hall**

Session: Cell and Particle Handling, Sample Preparation and Separation

11:15 **Rapid Clinical Diagnostics in a Continuous Flow Lab on a Chip**

Nicole Pamme, Senior Lecturer, University of Hull

We present a fast, highly versatile microfluidic platform which utilises mobile magnetic particles for performing surface-based assays in continuous flow within a fraction of the time required for conventional methods.

11:45 **Novel Strategies for Particle and Cell Handling and Detection on Centrifugal Microfluidic Platforms**

Jens Ducreé, Professor, Biomedical Diagnostics Institute, Dublin City University

This presentation highlights recent advances of high-efficiency particle capture, retention, counting, identification and aliquoting by making specific use of the centrifugal volume force, scale-matched geometrical features and integrated actuation. These lab-on-a-disc technologies leverage new applications such as the definition and counting of total particle numbers as well as multiplexed screening in bead and cell based assays implemented on low-complexity instrumentation.

12:15 **Lunch and Networking in Main Exhibition Hall**

13:15 **Poster Presentations**

14:15 **Applications of Microchip Acoustophoresis**

Thomas Laurell, Professor, University of Lund

Acoustophoresis allows non-perturbing manipulation and separation of cells in microfluidic systems. This opens the route to rapid processing of crude biological samples for medical diagnostics as well as other biofluids. The recent advancements of acoustophoresis and applications within life science will be overviewed.

14:45 **Chip-Compatible Sample Preparation for Early Diagnosis of Infectious Diseases**

Marion Ritzi-Lehnert, Head of Fluidics and Simulation Department, IMM Mainz

A major drawback of chip-based molecular diagnostic systems is their lack of an integrated sample preparation. The development of a chip-compatible sample preparation comprising not only the extraction, but also an efficient purification and pre-concentration of the target molecules is presented.

15:15 **Coffee and Networking in Main Exhibition Hall**

16:00 **Two-Dimensional Protein Separation in Microfluidic Devices**

Hugh Fan, Associate Professor, University of Florida

Two-dimensional protein electrophoresis has been implemented in plastic microfluidic devices. An array of microvalves was integrated for introducing different separation media. The total separation time was much shorter than the conventional approach.

16:30 **Polymeric Micro-Fabricated TiO₂-ZrO₂ Affinity Chromatography Microchip for Phosphopeptide Enrichment and Separation**

Angeliki Tserepi, Senior Researcher, NCSR Demokritos

We demonstrated a completely microfabricated affinity microcolumn on a polymeric chip design for the effective enrichment and separation of phosphopeptides using off-chip MALDI MS identification. The microcolumn exhibited large chromatographic capacity and can be used several times with reproducible results.

17:00 **Close of Conference**



Next-Gen Sequencing Europe

Day One - Thursday 30 June 2011

Sponsored by
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08:00 **Registration**

09:00 **Keynote Presentation:**

Next Generation DNA Sequencing Techniques and Applications

Wilhelm Ansorge, Professor, École Polytechnique Fédérale de Lausanne

Next generation DNA sequencing techniques are opening fascinating opportunities in life sciences. Commercially available DNA sequencing platforms, Single molecule Real-time methods, Nanopores (also Graphene), as well as other techniques under development are described and applications in bio-medical fields discussed.

Session: NGS Analysis in Disease Identification

09:30 **Revolution in Disease Gene Identification - Exome Sequencing**

Alexander Hoischen, Post Doctoral Researcher, Genomic Disorders Group, Radboud University Medical Centre Nijmegen

Exome sequencing has led to a revolution in disease gene identification. Recent breakthroughs show the potential of this technology and the unprecedented speed with which especially Mendelian disease genes are now identified.

10:00 **Title to be Confirmed**

Andrew Feber, Post Doctoral Researcher, University College London

10:30 **Coffee and Networking in Exhibition Hall**

11:15 **Cancer Methylome Profiling using Methyl-DNA Capture**

Arjen Brinkman, Research Associate, Department of Molecular Biology, Nijmegen Centre for Molecular Life Sciences

This talk will discuss: Methodology for NGS-based DNA methylation analysis in cancer, methylCap-seq technology for methylated-DNA capture and fractionation, small-scale and large-scale validation of MethylCap-seq, identification of differentially methylated regions within unique and repetitive regions of the genome and classification based on whole-genome DNA methylation profiles.

11:45 **Genomic Instability and the Evolution of Cancer**

Francesca Ciccarelli, European Oncology Institute, Principal Investigator

12:15 **Technology Spotlight:**

NGS Sample Prep Simplified - The Beckman Coulter Continuum of Automated Sample Preparation

Christoph Kreull, Marketing Manager Automated Solutions Europe, Beckman Coulter

12:30 **Lunch and Networking in Exhibiton Hall**

13:15 **Poster Viewing**

14:15 **Mate-Pair Sequence Analysis of Somatic and Germline Structural Variation in Human Genomes**

Wigard Kloosterman, Senior Post Doctoral Researcher, University Medical Center Utrecht, Dept Biomedical Genetics

Mate-pair sequencing is a powerful tool to detect structural genomic variation at high resolution. We are using this technology to understand the mechanisms and contribution of structural variation to congenital defects and cancer.

14:45 **Genetics of Coronary Artery Disease. From GWAS and Beyond**

Jeanette Erdmann, Professor and Head of the Working Group Cardiovascular Genomics, University of Lübeck

After the great success of genome wide association studies the time is now ready to apply next generation sequencing technologies to fully explain the genetic basis of coronary artery disease and myocardial infarction.

15:15 **Coffee and Networking in Exhibition Hall**

Session: Current and Future Challenges in NGS

16:00 **Nanoscience, Single Molecules and Genomics**

Kalim Mir, Group Head in Nanogenomics, Oxford University

This presentation will describe novel 3rd and 4th technologies that we are developing for the sequencing and long-range analysis of human genomic DNA, as part of the European Union READNA project.

16:30 **Color-encoded particles as a platform for next generation DNA sequencing**

Vera Gorfinkel, Professor, State University of New York, Genometrica Ltd.

A novel approach to high throughput DNA sequencing is presented, based on cycle sequencing of DNA molecules amplified on the surface of micro-beads encoded with compositions of quantum dots, and very fast, single-photon sensitive, and highly accurate detection and recognition of the beads' color codes.

17:00 **Evaluation and characterisation of a 3rd generation single molecule sequencer**

Michael Quail, Sequencing R and D Team Leader, Wellcome Trust Sanger Institute

Sanger Institute became the first laboratory within Europe to install a 3rd generation Sequencing platform. In this presentation we will detail the results obtained from our evaluation and characterisation of the Pacific Biosciences RS single molecule sequencer.

17:30 **Drinks Reception**



Next-Gen Sequencing Europe

Day Two - Friday 1 July 2011

Sponsored by



- 09:00 **Keynote Presentation:**
Southern African Genomes – Human History Written in DNA
Vanessa Hayes, Professor, JCVI
Recent genetic studies suggest Southern Africa as the birthplace of modern humans. We explore this history in the genomes of click-speaking Khoisan hunter-gatherers of the Kalahari desert, along with neighboring Bantu agro-pastoralists. A complex genetic profile of Southern Africa is beginning to emerge.
- Session: Gene Expression and Regulation**
- 09:30 **Genome-Wide Mapping of Chromatin Modifications**
Paul Hurd, Lecturer, Queen Mary University of London
The application of next-generation DNA sequencing to mapping histone modifications in the human genome will be discussed. Data will be presented describing the landscape of six histone tri-methylations and the relationship to gene transcription status.
- 10:00 **Characterisation and Identification of Genes Regulated by DNA Modification**
Richard Meehan, Chromosomes and Gene Expression Programme Leader, Human Genetics Unit, Medical Research Council
Analysis of DNA modification in vertebrates is at a crossroads with the recent identification of 5-hydroxymethylcytosine (5hC), a 6th base. I will discuss methods to distinguish between 5methylcytosine (5mC) and 5hC in DNA and their use in genome wide analysis.
- 10:30 **Coffee and Networking in Exhibition Hall**
- 11:15 **New NGS Strategies in Sample Preparation for High Sensitivity Identification of Gene Variations, Transcriptomes and Genomes**
Joakim Lundeberg, Professor, KTH Royal Institute of Technology
At the new Science for Life Laboratory, Stockholm we have improved the sample preparation for the major NGS platforms for more efficient use of the technology. This lecture will discuss some of these improvements and also demonstrate the use of NGS to perform molecular archeology, correlation of transcriptomes with proteomes and analysis of genomes.
- 11:45 **De Novo Assembly and Validation of a Metazoan Transcriptome by Massive Parallel Sequencing and Shotgun Proteomics**
Wei Chen, Senior Scientist and Group Leader, Berlin Institute for Medical Systems Biology, Max-Delbrück-Center for Molecular Medicine
- 12:15 **Lunch and Networking in Exhibition Hall**
- 13:30 **Poster Viewing Session 2**
- 14:15 **ChIP-Seq and RNA-Seq: From Sequence Tags to Target Genes and Beyond**
Hendrik Marks, Research Fellow, Department of Molecular Biology, Nijmegen Centre for Molecular Life Sciences
The experimental and bioinformatic workflow of ChIP-Seq/RNA-Seq, Publicly available software tools for ChIP-Seq applications, How to translate ChIP-Seq profiles into affected pathways.
- Session: NGS Optimisation**
- 14:45 **Optimized Library Preparation, an Essential Component of Next Gen Sequencing**
Masoud Toloue, Director of Genomic Research, Bioo Scientific
Strategies for massive parallel sequencing have revolutionized research across diverse scientific disciplines. Despite these advances, DNA and RNA sample preparations, one of the most important aspects of next generation sequencing, continue to use outdated, biased and cumbersome methods. We will describe our latest DNA and RNA library preparatory methods and how sequencing results benefit from these techniques.
- 15:15 **Coffee and Networking in Exhibition Hall**
- 16:00 **Implementation of Modular Automation for Next Generation Sequencing Library Production in a University Core Facility**
John Kenny, Post Doctoral Researcher and Translation Officer, Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool
This presentation will detail steps taken at a University-based core facility to increase throughput of sequencing DNA and RNA samples using next generation sequencing via the incorporation of automated methodologies.
- 16:30 **Optimization of Multiplex Deep Sequencing Applications**
Leonid Bystrykh, Researcher, UNCG University Groningen
For multiplex deep sequencing applications each sample must be easily discriminated on a basis of unique sample tags. Some strategies utilize Hamming binary codes. Because deep sequencing results are inherently noisy, used sample tags should be on a substantial minimal distance from each other. Otherwise correction of sequence errors and corresponding sequence results is neither possible nor meaningful. It will lead to cross contamination of the data. We have developed several primer design approaches which adapts to a variable extent of multiplexing, the complexity and length of the tag. Further, we employed a network strategy to assess quality and complexity of sequencing data. Limitations of the multiplexing strategy are further discussed.
- 17:00 **Close of Conference**



Screening Europe

HTS and Compound Management

Day One - Thursday 30 June 2011

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- 08:00 **Registration**
- 09:00 **Title to be Confirmed**
Dr Lorenz Mayr, Executive Director, Novartis
- 09:30 **Addressing the Challenge of Drug Safety in Early Discovery**
Dr Steve Rees, Director, Screening Compound Profiling GlaxoSmithKline
Drug toxicity is one of the major causes of attrition in preclinical and clinical development. GSK has developed a number of high throughput techniques to assess the potential for safety liabilities in chemical series in early discovery.
- 10:00 **Next Generation Plate Based Screening: Above and Beyond SAR Generation**
Dr Linda Kitching, Principal Scientist, Pfizer Global Research
The challenges of providing bespoke pharmacological assays across a broad target portfolio to drive target SAR and enhance the decision making process in a primary pharmacology group.
- 10:30 **Coffee Break and Networking in Main Exhibition Hall**
Session: Fragment Based Discovery
- 11:15 **Fragment-informed Lead Generation to Accelerate the Hit Identification for PDE10A Inhibitors: The Synergistic Combination of a Novel Fragment Screening Approach with high-throughput Screening**
Dr Stefan Geschwindner, Principal Scientist, AstraZeneca R&D
Using an innovative and efficient fragment-screening strategy in synergistic combination with an traditional HTS approach can achieve a significant acceleration of hit identification.
Session: Label Free Assays
- 11:45 **Innovative Label-free Technology Solutions Improving Efficiency in Drug Discovery**
Dr Fredrik Sundberg, Director of Global Pharma Market Development, GE Healthcare
Enabling technology solutions can impact both compound quality and overall productivity by providing more information on protein interactions. The use of innovative label-free assays can rapidly eliminate false-positive hits in screening, improve lead optimization and protein stability.
- 12:15 **Lunch and Networking in Main Exhibition Hall**
- 13:15 **Poster Presentations**
Session: Automation in Screening
- 14:15 **High Throughput in vitro Combination Profiling Using a Novel Cell-based Phenotypic Assay – A Preclinical Hypothesis Generation Tool**
Dr Eric Tang, Science Leader, AstraZeneca
Cancer is a multi-factorial disease and requires multiple therapeutic interventions to achieve significant clinical efficacy. Conventionally, combination treatments, mostly including chemotherapy agents, were often evaluated in the absence of a clear mechanistic hypothesis, either in off-label settings or more recently in early clinical trials. With the development of novel targeted agents, together with advances in technologies and better understanding of tumour biology, it has become feasible to perform combinations profiling studies across in vitro tumour cell panels from a variety of tissues and mutation backgrounds. The output from these high throughput combination campaigns will assist the generation and testing the biological hypothesis to prioritise synergistic combination agents to be evaluated in in vivo studies and early clinical opportunities. The high throughput screening technologies, workflow and rapid data visualisation will be discussed.
- 14:45 **Improving Efficiency in High Throughput Screening Operations with High-speed Identification of Problem Samples**
Dr Chris Walsh, Director, RTS Life Science
How intelligent vision technology is being used by CM and HTS groups to perform accurate non-contact volume measurement and precipitate detection in SBS format microtubes, to rapidly identify potentially problematic samples in library collections, and thereby minimise results variability, and reduce waste.
- 15:15 **Coffee Break and Networking in Main Exhibition Hall**
- 16:00 **Mass Spectrometry Based Detection Methods for High Throughput Applications**
Dr Kerstin Thurow, CEO, Center for Life Science Automation
The automation of different processes in life science laboratories saw a big development within the last 15 years. Current and future developments in these areas will be presented with examples including measurement, data analysis and automation.
- 16:30 **Right Compound- Right Amount - Right Place - Right Time. Moving to a Sound Compound Management Process**
Dr Toby Winchester, Senior Principle Scientist, Pfizer
This talk will include the processes involved in getting towards this steady state and the future steps needed to end the journey. The talk will include work on QC, investment in accurate liquid handling platforms such as acoustic systems (equipment and resource) and the essential IT integrations. The lessons learnt in this evolution and how to handle a file as large as Pfizer's. The talk will also involve Lean Six Sigma processes that got us close to this vision.
- 17:00 **Drinks Reception**



Screening Europe

HTS and Compound Management

Day Two - Friday 1 July 2011

Sponsored by



- 09:30 **A Strategy to Discover Inhibitors of Tyrosyl-DNA Phosphodiesterase 1 (Tdp1) as Anti-Cancer Agents**
Dr Wendy Lea, Research Scientist, NIH/NHGRI/NCGC
Tdp1 is a DNA repair enzyme, and its inhibitors can potentiate the efficacy of certain anti-cancer agents. A strategy to discover novel Tdp1 inhibitors is presented, including the development of a qHTS AlphaScreen assay and secondary assays for hit triaging.
Session: High Content Screening
- 10:00 **Automation for High Content Screening and Genome-Wide RNA-Interference (Screening Unit, FMP)**
Dr Jens Von Kries, Head of Screening, Leibniz Institute for Molecular Pharmacology
The open access technology platform for HTS at the Leibniz-Institut für Molekulare Pharmakologie is located on the Campus of the Max-Delbrück-Center in Berlin. The Unit already served more than 100 projects for identification of compounds modulating biological functions with state of the art automation and detection technologies.
- 10:30 **Coffee Break and Networking in Main Exhibition Hall**
- 11:15 **Lead discovery 2020**
Dr Everard Pap, Global Director Lead, Discovery, Sanofi-Aventis
This presentation will highlight major trends that will transform Lead Discovery in the next decade.
- 11:45 **12-lipoxygenase Regulation of Pro and Anti-thrombotic Effects in Human Platelets: Two Approaches to Novel Anti-platelet Therapy**
Prof Michael Holinstat, Assistant Professor of Medicine, Thomas Jefferson University
Novel anti-platelet therapies are needed to treat unwanted platelet aggregation leading to vessel occlusion and stroke. Our screens have identified several potential therapeutic targets to address this need including inhibition of 12-lipoxygenase and regulation of oxidized metabolites in the platelet.
- 12:15 **Lunch and Networking in Main Exhibition Hall**
- 13:15 **Poster Presentations**
- 14:15 **Sensors for Single Cell Isolation of Metabolite Producing Bacteria**
Dr Lothar Eggeling, Group leader, Forschungszentrum Juelich
Use of bacterial transcriptional regulators naturally sensing intracellular metabolites. Together with FACS it enables to select producers from mutant populations.
Session: Chemical Probes
- 14:45 **High Throughput Flow Cytometry for Small Molecule Discovery in the NIH Molecular Libraries Initiative and Beyond**
Prof Larry Sklar, Professor, University of New Mexico
The University of New Mexico Center for Molecule Discovery (U54MH084690, <http://screening.health.unm.edu/>) identifies and implements novel applications of the HyperCyt flow cytometry platform for high throughput small molecule discovery. Flow cytometry is recognized for its unique ability to analyze complex and multiplexed target populations in cell and molecular screening where multi-parameter analysis is beneficial.
- 15:15 **Coffee and Networking in Main Exhibition Hall**
- 16:00 **PubChem - the NIH Public Repository for Bioactivity Data**
Dr Yanli Wang, Associate Investigator, National Center for Biotechnology Information, National Library of Medicine
This presentation will describe the PubChem project, which is a public resource for archiving bioactivity results of small molecules and RNAi reagents from HTS experiments and chemical biology research. The PubChem project is an element of the NIH Molecular Libraries Program (MLP), and is hosted by the National Center of Biotechnology Information, a division of the US National Institutes of Health. PubChem currently contains 30 million chemical structures and 120 million biological test results.
- 16:30 **Innovative HTS Assay Development for Chemical Probe Discovery**
Dr Haian Fu, Professor & Director, Emory Chemical Biology Discovery Center, Emory University
Label-free biosensor assays offer unprecedented opportunities for compound profiling in cells without the need of artificially engineered reporters. Such innovative assay technologies and HTS platforms are expected to accelerate the discovery of oncogenic pathway modulators.
- 17:00 **Close of Conference**

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Screening Europe

HCS and Assays

Day One - Thursday 30 June 2011

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08:00 **Registration**

Session: Fragment Based Drug Discovery

09:00 **Fluorescence Lifetime Assays - An Attractive Addition to the Toolbox of Fragment Screening Technologies**
Dr Doris Hafenbradl, Senior Director Biology & Natural Products, Galapagos

Session: Label-free Assays

09:30 **Cosmetic Ingredients Tantalising TRPs - Validation of Novel TRP Modulators by Impedance-based Label-free Technology**

Dirk Sombroek, BRAIN - Biotechnology Research And Information Network

TRPs respond to a variety of diverse stimuli and their activation impacts on cellular physiology. Label-free impedance technology was applied to validate novel TRP modulators with high potential for cosmetic applications.

Session: High Content Screening

10:00 **Miniaturisation of Cell based Assays for High Content Screening Problems and Solutions**

Professor Anthony Davies, Head, Irish National Centre for High Content Analysis and Screening

In this presentation we will be covering a new and relatively straightforward means of setting up cell based assays for high content analysis in a micro array format.

10:30 **Coffee and Networking in Main Exhibition Hall**

11:15 **Title to be Confirmed**

Dr Urban Leibal, Group Leader, KIT Screening Centre, KIT Karlsruhe Institute of Technology

11:45 **Off-target Effects in an RNAi Screen: Seeing is Believing**

Dr Karol Kozak, Head, Computation Analysis, ETH Zurich

We present a bioinformatics tool for RNAi library analysis and the prediction of potential off-target effects that can be applied to high content screening data.

12:15 **Lunch and Networking in Main Exhibition Hall**

13:15 **Poster Presentations**

14:15 **Implementation of a High Content Screening Platform in Academia: Experiences and Challenges**

Dr Hakim Djaballah, Director, Memorial Sloan-Kettering Cancer Center

In this presentation we will discuss our efforts to build and operate a high content screening platform at the HTS Core Facility at Memorial Sloan-Kettering Cancer Center. My talk will cover instrumentation, types of assays we perform, data acquisition and storage, data analysis, meta data merging with images, and business rules as to data storage and access.

14:45 **From Acquisition to Analysis: Tools to Improve the High Content Screening Workflow for Stem Cell Assays**

Dr Ben Haworth, European Imaging Applications Specialist, Molecular Devices

15:15 **Coffee and Networking in Main Exhibition Hall**

16:00 **Re-inventing the HIV Cell Fusion Assay using High Content**

Dr Lisa White, Scientist II, Cellular Pharmacology Department, Merck

The HIV cell fusion assay is a surrogate system for detecting viral entry. A T-cell tropic HIV cell fusion assay was established using U2OS cells expressing the envelope glycoprotein gp160 from HIV NL4-3 (transduced by BacMam virus) and HeLa cells expressing CD4 and CXCR4. High content analysis of the cell fusion event is based upon a Gal4/VP16-activated beta-lactamase signal, using the Pathway855 (BD Biosciences) or the Acumen eX3 (TTP Labtech). Measurement of changes in morphology associated with cell fusion was combined with beta-lactamase activity to show robust assay statistics in 384-well and 1536-well plates.

16:30 **Advanced Toponomics Analysis of Cellular Assays and Tissue Sections**

Dr Thomas Berlage, Institute Director, Fraunhofer-Institute for Applied Information Technology

Advanced tools for high content image analysis increasingly hide technical detail, yet are getting more powerful to address complex cellular assays and tissue sections. Examples are reported from several recent collaborations.

17:00 **Kinetic Monitoring of Cellular cAMP/cGMP Signalling - A Challenging Tool for High-content Analysis of Living Cells**

Dr Reinhard Seifert, Chief Scientific Officer, Sibion Biosciences

Cyclic nucleotides are intracellular second messengers that control important physiological functions. The concentration of cyclic nucleotides is regulated by Gi/Gs coupled receptors, adenylyl cyclases, guanylyl cyclases, and phosphodiesterases. Therefore, over the past decades a huge variety of assays has been developed to identify drug candidates targeting the activity of those molecules. However, most of the assays are inappropriate to analyse the kinetics of activity and inhibition, desensitisation, or internalisation of a drug target in the presence or absence of drug candidates. In contrast, genetically encoded sensors that detect cyclic nucleotides are most suitable to overcome these limitations. The sensors allow monitoring the cellular cyclic nucleotide concentration within a period of seconds up to hours or days directly in living cells. Target activity can be monitored using a fluorescence read-out in a homogenous HTS format as well as in microscopy on a single cell level with cell lines, primary cells or tissue slices. Examples for high-content analysis will be presented to demonstrate the potential of the sensor technology directed to improve the identification of new drug candidates.

17:30 **Drinks Reception**

The logo features a stylized grid of green and blue circles, resembling a microarray or a cell culture plate, with a blue arrow pointing downwards from the center. To the right of the grid, the text "Screening Europe" is written in a large, white, sans-serif font, and "HCS and Assays" is written below it in a smaller, white, sans-serif font. The entire logo is set against a dark blue background.

Screening Europe

HCS and Assays

Day Two - Friday 1 July 2011

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- 09:30 **High Content Screening for Sytoskeletal Rearrangements**
Dr Maria Montoya, Head of Laboratory, Centro Nacional de Investigaciones Cardiovasculares
High Content Analysis has been developed for an RNA interference loss of function screening. Confocal fluorescence microscopy images were subjected to image processing, cell segmentation, and feature extraction for the classification of cytoskeletal phenotypes using machine learning based algorithms.
- 10:00 **A High Quality High Content Screening Assay for Intracellular Leishmania**
Dr Manu De Rycker, Screening Scientist, University of Dundee
We present the development of a high-content assay for intracellular Leishmania, a parasite with a significant worldwide health impact. The assay was used for a 100,000 compound screen, the results of which will be discussed.
- 10:30 **Coffee Break and Networking in Main Exhibition Hall**
- 11:15 **Challenges for High Content Analysis of Infectious Diseases**
Dr Anne Danckaert, Research Engineer, Institut Pasteur
High Content Analysis (HCA) is an emerging state of the art that has its roots in over one hundred years of biological imaging. It is only recently that its power as a scientific experimental tool has begun to be harnessed, facilitated mainly by a new generation of post genomic imaging, signal processing and computer science technologies. Arguably, among the most important of these systems tools is the engineering of image acquisition and processing into unbroken, and fully-automated sample handling workflow, making possible the acquisition and analysis of literally hundreds of thousands of images per day. Additionally, the analysis of complex cellular events and the emergence of systems biology require large scale experimental approaches that can take great advantages from the automated imaging systems that are being developed. Whereas a typical High Content Screening (HCS) application would tend to find the best compromise between throughput, speed and resolution, our approach focuses on more subtle features such as high resolution analysis of details cell features and live cell imaging to measure dynamics of cell functions. Here we describe our strategy for HCA of infectious diseases with emphasis on assay development aimed to contextualize physiologically and clinically relevant conditions. Using a primary cell paradigm; we present our methodology, addressing the challenges therein, notably, automation of the HCA process and the statistical variation.
- 11:45 **High Content Screen for Inhibitors of Cell Migration in Cancer Metastasis Using Adenoviral Knock-down**
Dr Remko de Pril, Principal Scientist, Galapagos
Enhanced cell migration is a hallmark of metastatic cancer cells. The propensity of cancer cells to close an open wound in a cell monolayer is thought to predict this ability. Using our adenoviral shRNA knock-down library we have established a high-throughput wound healing assay to identify novel genes involved in cell migration. Therefore, a 96-pin scratch tool was designed to apply a constant mechanical scratch-wound in the cellular monolayer. We used transmitted light imaging for segmentation and quantification of the scratch wound that remained open. Genes whose knock-down inhibit cell migration can be identified by their effect on the open wound. Using this approach we demonstrated that two knock-down constructs targeting a known player in motility, CXCR4, inhibit wound healing, validating our set-up. Using this wound healing assay we have identified a number of novel genes associated with cancer cell motility. These targets are currently validated for their effect in 3D invasion using Boyden chambers. As our adenoviral knock-down libraries focus on drugable targets, these validated targets can quickly be employed to generate small molecule compounds or antibody therapeutics targeting cancer metastasis.
- 12:15 **Lunch and Networking in Main Exhibition Hall**
- 13:15 **Poster Presentations**
- 14:15 **The Potential of High Content Imaging in Primary Screening**
Mrs Daniela Siebert, Scientist, Novartis
The presentation will show the approaches taken in the Lead Finding Platform at Novartis to adapt High Content Imaging to High Throughput Screening and will illustrate the instrumentation, data management and automation established to perform a full deck primary HCS.
- 14:45 **Can Machine Intelligence Help? Classification and Regression Models for High Content Screening**
Dr Peter Horvath, Head of Image and Data Analysis, ETH Zurich
The audience will learn pros and contras of classical machine learning techniques and see how new methods can help in HCS analysis. An open-source tool will be proposed offering all the methods presented during the talk.
- 15:15 **Coffee Break and Networking in Main Exhibition Hall**
Session: Automation in Screening
- 16:00 **Ultra Low Volume Liquid Handling: Picoliter and Nanoliter Applications in Biosensors, Microarrays, Lab-On-A-Chip and HCS**
Dr Holger Eickhoff, Chief Executive Officer, Scienion
Saving precious samples and reagents are key to minimize costs in pharmaceutical screening and the development of new diagnostic tests. Handling small amounts of liquids with tiny dead volumes is a key part to achieve this.
- 16:30 **Title to be Confirmed**
Professor Torston Schoneberg, Professor, Leipzig University
- 17:00 **Close of Conference**



World Biobanking Summit

Day One - Thursday 30 June 2011

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08:00 **Registration**

Session: Umbilical Cord Blood Banking

09:00 **Keynote Presentation**

Umbilical Cord Blood Collection, Processing and Storage.

Mary-Beth Fisk, Vice President, Texas Blood and Tissue Bank

Objectives:

- To review methods for umbilical cord blood processing/cell isolation.
- Define technologies for cryoprotection, freezing and storage of cells.
- Illustration of experiences with cord blood collection modes.
- Outline current statistical data related to transplantation and other clinical uses for cord blood in the regenerative medicine arena.

09:30 **Knowledge vs Opinion: Their Role in Patient Choice**

Rajan Jethwa, CEO, Virgin Health Bank, Doha

Umbilical cord blood stem cells have huge potential, both currently for transplant surgeons and in the future for potential autologous cell-based therapies. Virgin moved into the arena over four years ago and is unique in offering a choice of banking models. However, increased public opinion of this industry has raised the discussion of controversial issues surrounding storage and subsequent usage. Dr Jethwa will discuss Virgin's aims within the sector and discuss why enabling parental choice is key to Virgin's strategy.

10:00 **Cord Blood Banking Market Analysis**

Enal Razvi, Biotechnology Analyst, Select Biosciences

In this presentation, we will describe our most-recent market analysis of the cord blood banking space and frame it into the broader cellular therapy marketplace. Both qualitative and quantitative market trends are presented in this talk.

10:30 **Coffee Break and Networking in Main Exhibition Hall**

11:15 **The Bavarian Red Cross Blood Donor BioBank - the First Successful Combination of Blood Donation and Biobanking**

Christine Zoglmeier, Project Manager Biobank, The Bavarian Red Cross Blood Donor BioBank

As the first blood bank, the Bavarian Red Cross Blood Bank has implemented a novel concept combining blood donation and biobanking. Its BioBank samples are uniquely positioned to address research issues related to the early diagnosis of slowly progressing diseases.

11:45 **Title to be Announced**

Niels Kruize, Director, KBiosciences

12:15 **Lunch and Networking in Main Exhibition Hall**

13:15 **Poster Presentations**

Session: Sample Storage and Collection

14:15 **The Fraunhofer Technology Platform: Sustainable Integrated Biobanking for Biomedical Applications**

Heiko Zimmermann, Professor, Fraunhofer Institute of Biomedical Engineering

The Fraunhofer Society Germany has developed through its institute IBMT together with industrial partners a fully integrated biobank platform comprising cryobiological, IT, and storage solutions for high quality cryo-biobanking at temperatures below -150°C. The presentation will describe the components of the platform as well as the use case of the HIV Specimen Cryorepository of the Bill & Melinda Gates Foundation.

14:45 **The Future of Bio-Sample Storage is Here to Stay - Not in the Cold but at Room Temperature!!!**

Rolf Muller, Chief Scientific Officer and President, Biomatrix, Inc

We will present technologies and methods derived from nature (biomimicry) applied to transporting and storing a wide range of biological samples, from purified gDNA and RNA, to more complex mixtures in blood, tissue and cell lines at ambient room temperature.

15:15 **Coffee Break and Networking in Main Exhibition Hall**

Session: Legal, Ethical & Regulatory Considerations

16:00 **Biobanking : An Attempt at a Global Regulatory Approach**

Marc Martens, Senior Associate, Bird & Bird LLP

The presentation will examine the typology of biobanks and their respective regulatory framework, and will then examine several current legal issues the biobanks are facing (among others, the presentation will focus on privacy issues, ownership rights and informed consent). Finally, on the basis of a case study, the presentation will address the import and export of human biological material, will examine whether a legal harmonization is needed and/or possible in that respect.

16:30 **Bioethics and Regulations for the Global Biobanking Field**

Timo Faltus, Legal Researcher, Leipzig University

The presentation explains the legal framework for running a biobank in the European Union in general and especially under German law. Therefore, the presentation will give an overview of European Advanced Therapy Medicinal Products Regulation (ATMP Regulation) and the European Tissue Directive in the field of biobanking. Additionally, the presentation describes the legal requirement for international and transnational cooperation in the biobanking field. Finally, the presentation will highlight the pitfalls regarding the range of the informed consent in biobanking.

17:00 **Human and Nonhuman Biobanking Regulations. An International Framework**

Elena Salvaterra, Senior Researcher and Jurist Doctor, Scientific Institute Eugenio Medea

Since its origin, the debate on biobanking has concentrated on regulations addressing the collection, storage and use of biological materials and associated data. This presentation seeks to represent the evolution of regulations on biobanking by reporting not only the paramount of laws and guidelines addressing human biobanks but also describing specific regulations covering animal and vegetable specimen collections.

17:30 **Drinks Reception**



Day Two - Friday 1 July 2011

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Session: Biobanking for Cancer Research; Challenges, Opportunities and Developments

09:00 Keynote Presentation

Wither Biobanking for Cancer? Building Our Reserves or, a Spending Spree?"

Malcolm Mason, Professor, University of Cardiff

It has been said that "the only good biobank is an empty one", implying that all samples should be fully utilised, but is this true? How should the tensions balance between building up large numbers of samples with good clinical annotation, versus encouraging the scientific community to use what we have now? How many samples do we need before enough is enough?

09:30 Hospital Integrated Biobanking and Prospective Cancer Biobanking (U-Can)

Anna Beskow, Director, Uppsala Biobank

Uppsala Biobank has a biobank service that is integrated in the existing hospital infra structure. Uppsala Biobank supports research where an example is U-Can, a cancer research infra structure project where samples and data are collected routinely from cancer patients in hospital care.

10:00 Research Biobanking to the Benefit of Personalized Medicine in Oncology

Antje Stratmann, Scientist, Global Biomarker Research, Bayer-Schering

Collaboration with medical doctors is crucial to built up a pharma research biobank. Both the underlying concept - compliant with socioethical considerations and deploying biotechnology's best practice - as well as some real-life biomarker case studies will be presented.

10:30 Coffee Break and Networking in Main Exhibition Hall

11:15 Isolation and banking of Circulating Tumor Cells (CTC)

Christer Ericsson, Senior Research Scientist, Karolinska Institute

Circulating tumor cells (CTC) are cancer cells from solid tumors that are found in the peripheral blood. Some may seed metastases. They provide a new opportunity to estimate prognosis, predict treatment and to follow the efficacy of the treatment.

11:45 Utilising Informatics to Add Value to Banked Samples

Jane Rogan, Business Manager, Manchester Cancer Research Centre Biobank

Informatics can mean anything from sample tracking to relating clinical data to samples. This talk will describe what we mean when we say informatics and how we've used it to our benefit.

12:15 Lunch and Networking in Main Exhibition Hall

13:15 Poster Presentations

Session: Quality Assurance, Standardisation and Harmonisation of Biobanks

14:15 Rapid, Standardized Tissue Acquisition and Comprehensive Data Collection: A Prerequisite for Cancer Research and Drug Development

Hartmut Juhl, CEO, Individumed

The talk will cover several aspects for modern biobank infrastructures, standardisation of operating procedures and collection of validated clinical data for research purposes. Sensitive points for generating fresh or freshly preserved biospecimen will be demonstrated such as intra- and postsurgical ischemia time and examples for the impact of processing variables on tissue data will be shown. The talk will also cover the importance of availability of comprehensive clinical data and data about tissue processing and how they can be used to perform cost efficient target discovery and drug development.

14:45 Accelerating Scientific Discovery by Harmonizing Biobanking Practices Worldwide

Pasquale De Blasio, President, European, Middle-Eastern and African Society of Biopreservation and Biobanking

Health research relies heavily on access to large-scale high quality biospecimens collections containing minimal clinical information (genotypic, clinical, exposure, lifestyle, biomarkers). Harmonization among Biological Resource Centres (BRCs) Worldwide is critical for accelerating clinical discovery.

15:15 Coffee Break and Networking in Main Exhibition Hall

16:00 Rubbish In – Rubbish Out. Protocols for Assessing Tissue Quality at Source

Gerry Thomas, Professor of Molecular Pathology, Imperial College London

The quality of human tissue that is made available for research is highly variable. This presentation will focus on key elements to enable tissue banks to develop mechanisms to assess the biological quality of their samples prior to release to researchers.

16:30 Human Stem Cell Lines: Challenges for Long Term Delivery

Glyn Stacey, Director, UK Stem Cell Bank

Many research labs can rapidly provide collaborators with rapid samples of cells from their work. However in sourcing such research materials there are a number of critical issues that researchers should be aware of including potential microbial contamination, cell line cross-contamination, variation in ethical regulations in different regions and intellectual property issues. If not addressed properly each of these can lead to serious problems for the researcher. Stem Cell Banks committed to public supply of stem cell lines are valuable resources to enable researchers to obtain access to many different cell lines which have been subjected to minimum standards of quality control and best practice. This presentation will give an overview of the key issues mentioned above, how the UK Stem Cell Bank manages these and the international standards that are being developed for such biobanks.

17:00 Close of Conference

Registration Form

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[†] Check web site for deadline [°] For non profit institutions only

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