8th Annual Next Generation Sequencing Congress
4th Annual Single Cell Analysis Congress

10-11 November 2016, London, UK

Day 1 Stream 1 – Advances in NGS Platforms and Key Therapeutic Applications
- DNA, RNA & proteins sequencing technologies
- Effective sample preparation
- Assessment of NGS technologies and platforms
- Latest innovations: gene editing technologies in NGS
- Applications of NGS in medicine and therapeutic case studies:
  - Cancer
  - Immunotherapy
  - Biomarkers
  - Genomic medicine
  - Infectious diseases
  - HIV

Day 1 Stream 2 – NGS Data Management and Bioinformatics
- Developments in NGS data analysis techniques and technologies
- Comparison in practical use of NGS platforms and software
- Integration of ‘omic’ data sets
- Genetic and genomic data analysis
- Advanced bioinformatics & computational genomic analysis tools
- Big Data, & cloud computing & data storage strategies in NGS

Day 2 Stream 1 – NGS Clinical Applications & Diagnostics
- NGS in the clinic: case studies including cancer and tumour testing
- Using NGS for precision & personalised medicine
- Supporting clinical decision-making through genomic sequencing
- Novel technology and platforms for NGS data analysis
- Integration of technologies and data sets

Day 2 Stream 2 – Applications and Technologies in Different Therapeutic Areas
- Case studies: oncology, immunotherapy and autoimmune diseases
- Methods for single cell isolation, capture & purification
- Single cell analysis tools including PCR analysis technologies
- Clinical applications & future perspectives
- High throughput in-situ sequencing approaches
- Microfluidics technologies and advances in applications
- The potential applications of single cell manipulation

Day 2 Stream 3 – Overcoming Single Cell Analysis Challenges
- Sample preparation for single cell analysis
- Bioinformatics challenges:
  - Calling copy number variations
  - Single cell data-handling
  - Identifying mutated genes in tumor samples
  - Improving the accuracy of quantitative analysis of transcripts
- Data analysis and interpretation hurdles
- Strategies and applications for single cell gene expression study

Day 3 Stream 1 – Insights on the Future of NGS & Targeted Sequencing
- Future directions of NGS
- Targeted sequencing technologies and applications
- Clinical applications and future perspectives

Day 3 Stream 2 – NGS Applications in Infectious Diseases
- Applications of NGS in infectious diseases
- Microbiome analysis
- Viral genomics
- Metagenomics

Day 3 Stream 3 – NGS Solutions for Immunology
- NGS applications in immunology
- Autoimmune diseases
- Immune cell profiling

Day 4 Stream 1 – Therapeutic Applications of NGS
- Therapeutic applications of NGS in oncology
- Clinical trials
- Precision medicine

Day 4 Stream 2 – NGS in Genomics
- NGS applications in genomics
- Genome sequencing
- SNP analysis

Day 4 Stream 3 – Clincal Applications and NGS Standards
- Clinical applications of NGS
- Quality control and standards
- Regulatory considerations

Day 5 Stream 1 – NGS for Drug Development
- NGS applications in drug discovery
- Lead optimization
- Compound screening

Day 5 Stream 2 – NGS Technology Applications
- NGS applications in technology development
- Bioinformatics tools
- Next generation sequencing platforms

Day 5 Stream 3 – NGS Analytical Challenges
- Analytical challenges in NGS
- Sequence quality control
- Data interpretation

Benefits to Attending
- Hear from and meet with the key innovators in next generation sequencing and single cell analysis. Attendees include: Professor of Genomics, University of Southampton; Professor of Chemistry, George Washington University; Professor of Cell Biology, Paris Descartes University
- Discover collaborative solutions to next generation sequencing challenges. This prestigious congress brings together key opinion leaders to discuss topic areas ranging from advancements in next generation sequencing platforms & technologies, novel NGS data analysis techniques and NGS case studies in the clinic
- Learn more about the application of next generation sequencing in medicine. Hear therapeutic case studies from cancer, immunotherapy, HIV and infectious diseases
- Discuss the latest innovations in single cell analysis. Case studies include the areas of genomics, transcriptomics & proteomics, metabolomics, bioinformatics and data interpretation
- Examine novel advancements in single cell applications and technologies. The conference will cover using single cells in different therapeutic applications and updates in microfluidics technologies
- A high quality programme devised with the help of our esteemed advisory board. Presentations will cover areas including latest innovations in gene editing technologies in NGS, single cell RNA sequencing technologies and advances in circulating single tumor cells
- Co-located with the highly anticipated 2nd Annual Genome Editing Congress

Complimentary Webinars:
- Advances In Rapid Transgeneration Adaptation, 13th September 2016
- Single Cell Analysis Research: Case Studies, 14th September 2016
- Advances In Genome Editing, 15th September 2016

Register for free - email marketing@oxfordglobal.co.uk

2016 Speakers Include:

Akos Vertes
George Washington University

Päivi Saavalainen
University of Helsinki

Nic Mermod
University of Lausanne

Meet Senior Decision Makers
450 delegates from leading research & academic institutions, clinical research institutions, food & nutrition companies as well as major pharmaceutical and biotech companies will attend the event. Delegate job titles include:

Next Generation Sequencing
Developmental Biology
Genomics
Bioinformatics

Single Cell Analysis
Cellular Biology
Gene Expression
Bioengineering

Discover New Solutions
Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Services to be discussed include:

Sequencing Technologies
NGS Data Analysis
NGS Data Generation
Bioinformatics Development

Diagnostics Technologies
Microfluidic Solutions
Molecular Profiling
Single Cell Analysis Products

For booking details & registration fees please refer to the last page or visit: www.nextgenerationsequencing-congress.com/marketing
2016 8th Annual Next Generation Sequencing Congress Confirmed Speakers Include:

- Jane Wilkinson, Senior Director, Broad Genomics Alliance Management, Broad Institute
- Edward Oakeley, Global Head ASI Informatics, Novartis Pharma AG
- Miika Ahdesmäki, Associate Principal Scientist, AstraZeneca
- Tim Hubbard, Head of Genome Analysis, Genomics England / King's College London
- Nickolas Papadopoulos, Professor of Oncology, Johns Hopkins
- Antoine van Kampen, Professor Medical Bioinformatics, Academic Medical Center (AMC), University of Amsterdam (UvA)
- Shamima Rahman, Professor of Paediatric Metabolic Medicine, UCL Institute of Child Health
- Nic Mermod, Professor, University of Lausanne
- Sarah Ennis, Professor of Genomics, University of Southampton
- Filip Van Nieuwerburgh, Professor, Ghent University
- Jurg Bahler, Professor of Systems Biology, University College London
- Hubert Smeets, Professor in Clinical Genomics with focus on Mitochondrial Diseases, Maastricht University
- Dhavendra Kumar, Professor, University of South Wales and Consultant in Clinical Genetics, University Hospital of Wales
- Ole Lund, Professor, Technical University of Denmark
- Jonathan Strefford, Professor of Cancer Molecular Genetics, University of Southampton
- Niels Tommerup, Professor, University of Copenhagen
- Anthony V Moorman, Professor of Genetic Epidemiology, Newcastle University
- Ettore Capoluongo, Professor and Head of Laboratory, Catholic University of Sacred Heart
- Alberto Paccanaro, Professor in Machine Learning & Computational Biology, Royal Holloway, University of London
- Timothy Ravasi, Professor, Bioscience, King Abdullah University of Science & Technology
- Rob Krams, Professor of Molecular Bioengineering, Imperial College London
- Ross McManus, Professor in Molecular Medicine, Trinity College Dublin
- Noam Shomron, Head of Genomics Research Team, Tel Aviv University
- Sven Nahnsen, Head of Quantitative Biology Center, Eberhard Karls University, Tübingen
- Patrick Descombes, Head of Functional Genomics, Nestle Institute of Health Sciences
- Vicki Chalker, Head, Respiratory and Vaccine Preventable Bacteria Reference Unit, Public Health England
- Christopher Woelk, Associate Professor and Director of the Genomics Core, University of Southampton
- Mikael Rørdam Andersen, Associate Professor, Technical University of Denmark
- Abdul Khalid Siraj, Senior Scientist / Deputy Director, King Faisal Specialist Hospital and Research Centre

2016 Co-located 4th Annual Single Cell Analysis Congress Confirmed Speakers Include:

- Patrizia Paterlini-Brechot, Professor of Oncology/Molecular Biology, University Paris Descartes, Paris, France
- kos Vertes, Professor of Chemistry and Professor of Biochemistry & Molecular Biology, George Washington University
- Aldo Jesorka, Professor, Chalmers University of Technology
- Michael Rieger, Professor, Goethe University of Frankfurt
- Neil Avent, Professor of Molecular Diagnostics and Transfusion Medicine, Plymouth University
- Yaron Shav-Tal, Professor, Bar-Ilan University
- Jörg Vogel, Professor, University of Würzburg
- Giuseppe Battaglia, Professor, University College London
- Andrew Ewing, Professor, University of Gothenburg and Director, Center for Bioanalytical Chemistry, Chalmers University of Technology
- Raffaele Calogero, Professor, University of Torino
- Patrik Ernfors, Professor, Karolinska Institutet
- Claus Nerlov, Professor, University of Oxford
- Saheer Gharbia, Professor and Head of Genomic Research, Public Health England
- Valerie Taly, Group Leader and CNRS Research Director, INSERM / Paris Descartes University
- David Wood, Professor of Engineering, Durham University
- Jonathan Chubb, Professor and Group Leader, MRC LMCB and Department of Cell and Developmental Biology, University College London

If you’re on Twitter, make sure to follow us @xgenseq and join the Congress conversation on #xgenseq16

For more information please contact marketing@oxfordglobal.co.uk
2016 Co-located 4th Annual Single Cell Analysis Congress Confirmed Speakers Continued:

- Samuel Marguerat, Group Head, MRC Clinical Sciences Centre / Imperial College London
- Päivi Saavalainen, University Researcher, University of Helsinki
- Christian Depeursinge, Adjunct Professor, University of Lausanne
- Pamela Pinzani, Associate Professor, University of Florence
- Björn Önfelt, Associate Professor, Karolinska Institutet
- Catherine Alix-Panabières, Director of the Laboratory of Rare Circulating Human Cells (LCCRH), University Medical Center of Montpellier
- Jose Gutierrez-Marcos, Associate Professor, University of Warwick
- Stephan Lorenz, Head of Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute
- Joshua B. Edel, Senior Lecturer in Micro and Nanotechnology, Imperial College London
- Erez Mills, Senior Scientist, Weizmann Institute of Science
- Esther Mellado, Research Assistant, Wellcome Trust Centre for Human Genetics (University of Oxford)

2016 Co-located 2nd Annual Genome Editing Congress Confirmed Speakers Include:

- Barry Rosen, VP and Senior Principal Scientist, AstraZeneca
- Danilo Maddalo, Laboratory Head, Novartis Oncology
- Morten Frodin, Professor, University of Copenhagen
- Stephen Hart, Professor in Molecular Genetics, UCL GOS Institute of Child Health
- Virginijus Siksnys, Professor, Vilnius University
- Tara Moore, Director of Biomedical Sciences Research Institute, Ulster University
- Uta Griesenbach, Professor of Molecular Medicine, Imperial College London
- Zsuzsanna Izsvák, Group Leader, Max Delbrück Center for Molecular Medicine
- Eric Paul Bennett, Associate Professor, University of Copenhagen
- Keith Foster, Associate Professor in Translational Medicine, University of Reading
- Zoltan Ivics, Head of Division, Paul Ehrlich Institute
- Pentao Liu, Senior Group Leader, Wellcome Trust Sanger Institute
- Helene Fastrup Kildegaard, Senior Researcher and Co-PI, Technical University of Denmark, DTU Biosustain
- A. Francis Stewart, Professor, Technische Universitaet Dresden
- Peter Rugg-Gunn, Group Leader, Babraham Institute
- Victor Turcanu, Senior Lecturer in Allergy, King’s College London
- Rafael J. Yáñez-Muñoz, Reader in Advanced Therapy and Director of Planning and Resources, Royal Holloway, University of London
- Aleksandar Vojta, Assistant Professor, University of Zagreb
- Hiroshi Nishimatsu, Assistant Professor, The University of Tokyo

2016 Vendor Speakers Include:

- Steve Siembieda, Vice President Commercialization, Advanced Analytical
- Christophe Lancrin, Group Leader, EMBL
- Xin Liu, Principle Scientist, Sphere Fluidics
- Ruth Kläver, Scientist Product Development, QIAGEN
- Wieland Keilholz, Field Applications Specialist, BD Genomics
- Jean-Noel Billaud, Principal Scientist, QIAGEN
- Sara Gonzalez-Hilarion, Product Manager and Scientific Support Specialist, Takara Bio Europe
- Neil Ward, Marketing Manager UK & Ireland, Illumina
- Yannis Pitsiladis, Professor of Sport and Exercise Science and Director, FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research

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<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>07.30 – 08.20</td>
<td>Registration</td>
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<tr>
<td>08.20 – 08.25</td>
<td>Oxford Global’s Welcome Address</td>
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<td>08.25 – 08.30</td>
<td>Chairperson’s Opening Address: TBS</td>
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<td>08.30 – 09.00</td>
<td>Co-located Event Keynote Address: The 100,000 Genomes Project</td>
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<td>Tim Hubbard, Head of Genome Analysis, Genomics England / King’s College London</td>
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<td>8th Annual Next Generation Sequencing Congress</td>
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<td></td>
<td>NGS Data Management And Bioinformatics</td>
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<td>Stream Chair: TBC</td>
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<tr>
<td>09.00 – 09.30</td>
<td>Stream Keynote Address: Mitochondria-related Disease, Transmission And</td>
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<td>Toxicity: A Tale Of 2 Genomes</td>
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<td>• Next-generation sequencing of mtDNA and the exome in mitochondrial</td>
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<td>• De novo mtDNA mutations and inherited mtDNA mutations in</td>
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<td>zebrafish and humans</td>
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<td>• mtDNA variants and the risk of radiation induced lung toxicity in</td>
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<td>Hubert Smeets, Professor in Clinical Genomics with focus on Mitochondrial</td>
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<td>Diseases, Maastricht University</td>
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<td>4th Annual Single Cell Analysis Congress</td>
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<td>Single Cell Analysis, Transcriptomics And ‘Oms</td>
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<td>Stream Chair: Daniel Liber, Business Development, Director, Wafergen</td>
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<tr>
<td>09.30 – 10.00</td>
<td>The Path To Successful Sequencing Includes Accurate Nucleic Acid Analysis</td>
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<td>• Improve library preparation and decrease overall preparation costs by</td>
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<td>assessing genomic DNA and RNA extraction quality</td>
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<td>• Accurately size and quantify large fragment and standard library</td>
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<td>smears through proper data imaging</td>
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<td>• Eliminate data loss, increase efficiencies and reduce labour with</td>
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<td>Steve Siembieda, Vice President Commercialization, Advanced Analytical</td>
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<td>10.00 – 11.20</td>
<td>Morning Coffee &amp; Refreshments, Poster Presentation Sessions, One to One</td>
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<td>Meetings x3</td>
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<tbody>
<tr>
<td>11.20 – 11.50</td>
<td><strong>Illumina Technology From Research To The Clinic</strong></td>
<td>Neil Ward, Marketing Manager UK &amp; Ireland, Illumina</td>
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<td><strong>De Novo Genome Assembly In The Cloud</strong></td>
<td>Edward Oakeley, Global Head ASI Informatics, Novartis Pharma AG</td>
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<td><strong>Detection, Characterisation And Ex Vivo Expansion Of Viable Circulating Tumor Cells</strong></td>
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<td>11.50 – 12.20</td>
<td><strong>Combining Data On Gene Expression And Biological Pathways With Genome Mapping And High Throughput Sequencing</strong></td>
<td>Niels Tommerup, Professor, University of Copenhagen</td>
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<td><strong>Determination Of The Putative Affinity Distribution Among Expanded B Cells Determined By RNAseq Repertoire Sequencing</strong></td>
<td>Antoine van Kampen, Professor Medical Bioinformatics, Academic Medical Center (AMC), University of Amsterdam (UvA)</td>
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<td><strong>Metabolites, Vital Signs And Cell Cycle Studied In Single Cells</strong></td>
<td>Akos Vertes, Professor of Chemistry and Professor of Biochemistry &amp; Molecular Biology, George Washington University</td>
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<td>12.20 – 12.50</td>
<td><strong>Use Of Genomics In Bacterial Reference Microbiology For Respiratory And Systemic Pathogens</strong></td>
<td>Vicki Chalker, Head, Respiratory and Vaccine Preventable Bacteria Reference Unit, Public Health England</td>
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<td><strong>Genomic And Phenotypic Diversity In Fission Yeast</strong></td>
<td>Jurg Bahler, Professor of Systems Biology, University College London</td>
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<td><strong>Dissecting Hematopoietic Stem- And Progenitor Cell Populations Using Molecular And Functional Single Cell Approaches</strong></td>
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<tr>
<td>12.50 – 13.50</td>
<td>Lunch</td>
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### Delegates are welcome to attend the co-located presentations

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<tr>
<th>Time</th>
<th>Session</th>
<th>Presentation</th>
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<tr>
<td>13.50 – 14.20</td>
<td><strong>For more information please contact <a href="mailto:marketing@oxfordglobal.co.uk">marketing@oxfordglobal.co.uk</a></strong></td>
<td><strong>Solution Provider Presentation</strong>&lt;br&gt;<strong>DNASTAR®</strong>&lt;br&gt;Software for life scientists&lt;br&gt;<strong>Raimo Tanzi</strong>, Chief Commercial Officer, Menarini Silicon Biosystems</td>
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<td>14.20 – 14.50</td>
<td><strong>For more information please contact <a href="mailto:marketing@oxfordglobal.co.uk">marketing@oxfordglobal.co.uk</a></strong></td>
<td><strong>Rapid Transgeneration Adaptation Of A Reef Fish To Climate Change</strong>&lt;br&gt;<strong>Timothy Ravasi</strong>, Professor, Bioscience, King Abdullah University of Science &amp; Technology</td>
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<td>14.20 – 14.50</td>
<td><strong>For more information please contact <a href="mailto:marketing@oxfordglobal.co.uk">marketing@oxfordglobal.co.uk</a></strong></td>
<td><strong>Electrochemistry And Mass Spectrometry Imaging In Cells And Vesicles</strong>&lt;br&gt;<strong>Andrew Ewing</strong>, Professor, University of Gothenburg and Director, Center for Bioanalytical Chemistry, Chalmers University of Technology</td>
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| 14.50 – 15.20 | SMARTer® Way For RNA-seq From Single-cells And Other Challenging Samples | - Powered by SMART and LNA technologies, our latest kits for NGS push the limits of sensitivity enabling to obtain the highest quality sequencing data from the most difficult samples, including single cells, pico-input amounts of RNA, degraded RNA samples (FFPE) and small RNAs  
- Expanding applications for SMART technology have led to innovative tools for immune profiling, targeted RNA-Seq and ChIP-Seq  
- In this talk we will present newly-developed methods that leverage the strengths of the SMARTer approach for single-cell RNA-seq and other challenging NGS applications  
Sara Gonzalez-Hilarion, Product Manager and Scientific Support Specialist, Takara Bio Europe |
|          | Solution Provider Presentation                                           | Solution Provider Presentation                                                      |
| 15.20 -15.50 | Solution Provider Presentation                                          | Jean-Noel Billaud, Principal Scientist, QIAGEN                                    |
|          | The presentation will cover:                                            | - How blood stem cells are crucial cells for the continuous formation of blood cells throughout life and how they are formed from the vasculature during embryogenesis  
- Challenges associated with studying this process in vivo due to very low cell number available and how we are using single cell transcriptomics approaches to understand the generation of this very important cell type  
Christophe Lancrin, Group Leader, EMBL |
<p>| 15.50 – 16.30 | Afternoon Refreshments, Poster Presentation Sessions, One to One Meetings x2 | Afternoon Refreshments, Poster Presentation Sessions, One to One Meetings x2        |</p>
<table>
<thead>
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<tbody>
<tr>
<td>16.30 – 17.00</td>
<td>An Integrative ‘Omics’ Solution To The Detection Of Recombinant Human Erythropoietin And Blood Doping</td>
<td>Yannis Pitsiladis, Professor of Sport and Exercise Science and Director, FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research</td>
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<td>PAST: The history of drugs in sport – the problem with the current approach</td>
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<td>Utilizing The Connectivity Map To Inform HIV Cure Strategies</td>
<td>Christopher Woelk, Associate Professor and Director of the Genomics Core, University of Southampton</td>
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<td>Latency reversing agents (LRAs) are used in shock and kill strategies to cure HIV</td>
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<td>Many LRAs discovered using high throughput screens have unknown mechanism of action (uMOA)</td>
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<td>We have developed pipelines to annotate drug mechanism of action using the connectivity map and gene expression profiles, as well as for the discovery of new LRAs</td>
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<td>A Network Medicine Approach To Quantify Distance Between Hereditary Disease Modules On The Interactome</td>
<td>Alberto Paccanaro, Professor in Machine Learning &amp; Computational Biology, Royal Holloway, University of London</td>
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<td>Bacterial Cells Tomography By Digital Holography: An Emerging Technology For Cell Investigation</td>
<td>Christian Depeursinge, Adjunct Professor, University of Lausanne</td>
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<td>For cell and tissue imaging, new technologies are presently emerging which are not based on fluorescence. They do not require tagging and offer easy and quick access to biological matter and cells in particular. The data delivered to the biologists and physicians are complementary and are also intrinsically quantitative. In this presentation, we present a short review of our works and other works as well regarding tomographic imaging of dielectric object, biological cells in particular. The complex electromagnetic wavefield scattered by the specimen, can be obtained by reconstruction of digital holograms or by other methods sometime described as “Quantitative Phase Imaging” (QPI). This approach leads to a growing modality in microscopy, which will find its own path in addition to light intensity based imaging methods like fluorescence. By itself, quantitative phase is acknowledged to provide a wealth of data on the sizes and composition of the specimen by the analysis of the optical pathlength and the refractive index with its dispersion law. Significance of these data has been improving recently in biology and medicine. The exploitation of phase data permits the improvement of the image resolution and new criteria must be envisaged to quantify resolution. From the reconstructed complex wavefield, it is possible synthesizing the aperture of a virtual microscope up to 2n, offering super-resolution images. Live images of micro-organisms and neurons with resolution around 100 nm have been obtained.</td>
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<td>17.30 – 18.00</td>
<td><strong>Short And Long Sequencing Reads From Bacteria To Plant Genomes</strong>&lt;br&gt;Our laboratory is exploiting the respective characteristics of short and long reads sequencing technologies in research areas ranging from bacterial to plant genomes characterization and analysis.</td>
<td>Patrick Descombes, Head of Functional Genomics, Nestle Institute of Health Sciences</td>
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<td><strong>Whole-genus Association Analysis – Using Hundreds Of Microbial Genomes For Linking Of Phenotype To Genotypes</strong>&lt;br&gt;• Comparative genomics with large numbers of genomes&lt;br&gt;• Applying microbial genomes for elucidation of primary metabolism, secondary metabolism, and secretomes, among other things&lt;br&gt;• Studies of microbial speciation through pan-genus analysis</td>
<td>Mikael Rørdam Andersen, Associate Professor, Technical University of Denmark</td>
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<td><strong>Quantifying Allelic mRNA Expression Of Tagged Endogenous Genes Within Single Cells</strong>&lt;br&gt;• New approach for tagging endogenous genes and detection of their transcribed mRNAs&lt;br&gt;• The technique is used for single molecule mRNA imaging in single cells&lt;br&gt;• This approach allows to distinguish between mRNAs transcribed from different alleles within the same cell</td>
<td>Yaron Shav-Tal, Professor, Bar-Ilan University</td>
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<td>18.00 – 18.30</td>
<td><strong>Genomic Profiling Of Thyroid Cancer</strong>&lt;br&gt;• Papillary thyroid carcinoma (PTC) is most common in Saudi Arabia, where it is only second to breast cancer as the most common cancer among females.&lt;br&gt;• Genomic profiling of PTC from Saudi Arabia has not been attempted previously. We performed whole-exome sequencing of 101 PTC samples and the corresponding genomic DNA to identify genes with recurrent somatic mutations&lt;br&gt;• Additional 785 samples then sequenced for detected recurrent somatic mutations by using a next-generation gene-panel approach.&lt;br&gt;• In addition to BRAF, N-RAS, and H-RAS, which have previously been shown to be recurrently mutated in PTC, our analysis highlights additional genes, including thyroglobulin (TG)&lt;br&gt;• Further analysis of metastatic PTC tissue revealed significant enrichment for TG mutations, demonstrating unknown role of TG somatic mutations in the pathogenesis of PTC and its malignant evolution</td>
<td>Abdul Khalid Siraj, Senior Scientist / Deputy Director, King Faisal Specialist Hospital and Research Centre</td>
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<td><strong>Integrating Data, Tools, And Infrastructure To Provide For Efficient Collaboration And Management In Large-scale Biomedical Research</strong>&lt;br&gt;• Data management for high-throughput experiments&lt;br&gt;• Fully automated process from project design to the data archive&lt;br&gt;• Scalable mining and searching of NGS data</td>
<td>Sven Nahnsen, Head of Quantitative Biology Center, Eberhard Karls University, Tübingen</td>
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<td><strong>Nanotechnological Solutions To Single Cell Imaging</strong>&lt;br&gt;• Introduction to live cells imaging and assays&lt;br&gt;• How to access the cell interior using nanoparticles&lt;br&gt;• Different approach to dynamically probe the cell interior</td>
<td>Giuseppe Battaglia, Professor, University College London</td>
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<td>18.30 – 19.00</td>
<td><strong>Big Data And Genomics: Halting Breast Cancer Metastasis</strong>&lt;br&gt;• Metastasis is the primary cause for mortality in breast cancer though it lacks effective treatment strategies&lt;br&gt;• We performed big data analysis on multiple data-sets identifying new players in the metastatic pathway and possible methods to regulate them&lt;br&gt;• We show that breast cancer metastasis can be prevented by local delivery of small RNAs to tumor site in mice&lt;br&gt;• Our work will permit a more effective individualized anti-metastatic breast cancer therapy</td>
<td>Noam Shomron, Head of Genomics Research Team, Tel Aviv University</td>
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<td><strong>Development Of A Multipurpose Microgripper Device For Individual Cell Capture And Analysis</strong>&lt;br&gt;• Single cell manipulation&lt;br&gt;• Adaptable for any microscope platform&lt;br&gt;• Complete with control electronics and software</td>
<td>David Wood, Professor of Engineering, Durham University</td>
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<td>19.00 – 19.30</td>
<td>Delegates are welcome to attend the co-located presentations</td>
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<td>19.30</td>
<td>Networking Drinks – Sponsored by and End of Day One</td>
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Technical improvements in single-cell perturbation, live-cell imaging and single-cell sequencing are enabling the detailed dissection of heterogeneous cell states. Combining all three modalities with new platforms such as the Polaris lab-on-chip, we are performing temporal studies of CRISPR-edited macrophages to better understand their responses to inflammatory perturbation. We analysed the genetic features ('nature') and micro-environmental factors ('nurture') of heterogeneity in single cells, cultured in perfect isolation, and studied the relationship between transcriptomics and cell signaling interactions. We will present some genetic effects found in macrophages to be likely microenvironmental specific, indicating the importance of both nature and nurture contributions to be considered in particular single-cell studies.

Esther Mellado, Research Assistant, Wellcome Trust Centre for Human Genetics (University of Oxford)
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<th>Conference Room:</th>
<th>Stream Chair:</th>
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| 08.30 – 09.00 | **Keynote Address:**  
The Clinical Application Of Cancer Genomics: The Example Of Mature B-cell Malignancies  
- Mature B-cell malignancies as excellent model systems to study cancer genomics will be introduced  
- NGS technologies have identified a plethora of clinically relevant genomic lesions in these diseases  

Jonathan Strefford, Professor of Cancer Molecular Genetics, University of Southampton |

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<tr>
<th><strong>8th Annual Next Generation Sequencing Congress</strong></th>
<th><strong>4th Annual Single Cell Analysis Congress</strong></th>
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<tr>
<td>NGS Clinical Applications &amp; Diagnostics</td>
<td>Applications And Technologies In Different Therapeutic Areas</td>
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<td>Stream Keynote Address:</td>
<td>Stream Keynote Address:</td>
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<td>Detection Of Somatic Mutations In Biological Fluids</td>
<td>Deciphering, By Single-cell Sequencing, The Subpopulation Organization Of Innate T-cells</td>
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</table>
| - Somatic mutations are cancer specific biomarkers that reveal the presence of cancer when present in biological fluids  
- The number of tumor derived DNA molecules with somatic mutations is very small compared to that of DNA molecules with wild type sequence making their detection challenging and required the development of sensitive methods for their detection  
- Accurate detection of rare mutations in biological fluids provides the opportunity to develop non-invasive tests for the clinical management of cancer patients  

Nickolas Papadopoulos, Professor of Oncology, Johns Hopkins |

| Morning Coffee & Refreshments, Poster Presentation Sessions, One to One Meetings x2 |
|--------------------------------------------------|--------------------------------------------|
| 09.30 – 10.00 | Microfluidic Picodroplets – An Enabling Platform For Biological Discoveries  
- Introduction of Sphere Fluidics’s Picodroplet technologies and instrument platforms  
- Discussion about applications in Biopharmaceutical Discovery & Development and others  

Xin Liu, Principle Scientist, Sphere Fluidics |

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### 11.00 – 11.30
**NGS Technology: How It Has And Will Improve Precision Medicine In Acute Lymphoblastic Leukaemia**

During this talk I will:
- Describe how NGS has and will contribute to deciphering the genomic landscape of acute lymphoblastic leukaemia
- Outline the somatic genetic abnormalities that are and will soon be used as prognostic and predictive biomarkers in the management of patients with acute lymphoblastic leukaemia
- Discuss the future role of NGS in deciphering the biology of acute lymphoblastic leukaemia and delivering precision medicine in the clinic

**Anthony V Moorman, Professor of Genetic Epidemiology, Newcastle University**

### 11.30 – 12.00
**Continuous Observation Of Hematopoietic Stem Cell Fate Decision Control At Single Cell Resolution**

- Time-lapse microscopy-based tracking of stem cell behavior
- Tracking of stem cells and their progeny for many generations
- Molecular control of hematopoietic stem cell self-renewal and differentiation

**Michael Rieger, Professor, Goethe University of Frankfurt**

### 12.00 – 12.30
**Evaluation Of Tumour BRCA Testing Methodology Across Clinical Labs Shows Great Variability In Approaches And Analytics**

- As part of correctly identifying patients eligible for novel therapies such as olaparib, a PARP inhibitor, clinical labs have to establish accurate detection and calling of germline and somatic variants in BRCA and other cancer related genes
- An evaluation of 10 clinical diagnostics laboratories across the world revealed wide differences in the choice of DNA capture protocols as well as bioinformatics analyses
- An internal dissection of the data received from the laboratories showed that although no false positives were reported by the labs, false negatives were cause often by differences in bioinformatics, variant classification, automated nomenclature, database limitations and in the background levels of noise in each data set

**Miika Ahdesmäki, Associate Principal Scientist, AstraZeneca**

### 12.30 – 13.30
**Lunch**

### 11.00 – 11.30
**Imaging Transcriptional Dynamics In Single Living Cells**

- Imaging transcription pulses in living cells using live cell fluorescence imaging
- Quantitative analysis of pulsing data reveals mechanisms of transcriptional regulation
- Imaging in mutant backgrounds reveals the causes of specific regulatory features

**Jonathan Chubb, Professor and Group Leader, MRC LMCB and Department of Cell and Developmental Biology, University College London**

### 11.30 – 12.00
**Solution Provider Presentation**

### 12.00 – 12.30
**Advances In High-Throughput Single Cell RNAseq**

- Automation & protocol improvements of the Smartseq-2 and Nextera protocols
- Lessons learnt: advice on experimental design and controls for single cell RNAseq experiments
- Tracking solution for 100’s of experiments across 1000’s of cells

**Stephan Lorenz, Head of Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute**

### 12.30 – 13.30
**Dual RNA-seq Unveils Noncoding RNA Functions In Host–Pathogen Interactions**

- Full transcriptomes of both a bacterial pathogen and its eukaryotic host
- All classes of coding and noncoding RNA detected during infection
- Fast long noncoding RNA response

**Jörg Vogel, Professor, University of Würzburg**
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<th>Time</th>
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<tr>
<td>13.30 – 14.00</td>
<td>Mike Hawes, Chief Executive Officer, Dolomite Bio</td>
<td>QIAscout: Overcoming Challenges In Single Cell Isolation</td>
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<td>• QIAscout is an effective and fast method to isolate viable single cells ensuring minimal manipulation of the cellular status</td>
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<td>• This novel single cell isolation method works in conjunction with inverted microscopes and is the ideal method to separate single cells for further downstream analysis or cultivation of clonal sub-populations</td>
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<td>• Single cell isolation with QIAscout is compatible with multiple downstream applications such as whole genome and transcriptome amplification methods, PCR and NGS</td>
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<td>Ruth Kläver, Scientist Product Development, QIAGEN</td>
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<td>14.00 – 14.30</td>
<td>Elucidation Of The Molecular Basis Of Human Mitochondrial Disease</td>
<td>The Biopen: Microfluidic Superfusion Of Adherent Single Cells</td>
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<td>Shamima Rahman, Professor of Paediatric Metabolic Medicine, UCL Institute of Child Health</td>
<td>• Technology foundation: microfluidic chip technology featuring hydrodynamic confinement and flow switching</td>
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<td>• Application examples: brain tissue, muscle fibers, single cell enzymology</td>
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<td>• Innovation: multiprobe/multistep experiments, integrated viability testing</td>
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<td>Aldo Jesorka, Professor, Chalmers University of Technology</td>
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<td>14.30 – 15.00</td>
<td>Shallow Whole Genome Sequencing Is Well Suited For The Detection Of Translocations In Human Blastocysts</td>
<td>Single Cell Transcriptome Profiling Of Human Leukocyte Populations</td>
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<td>Filip Van Nieuwerburgh, Professor, Ghent University</td>
<td>• We utilize the high-throughput Drop-seq RNA-seq method by Macosco et al (2015)</td>
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<td>• We study various human leukocyte populations both from healthy donors and in various autoimmune conditions</td>
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<td>• A modified version of the method to capture also the clonality, i.e. the T and B cell receptor variable sequences is under development</td>
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<td>Päivi Saavalainen, University Researcher, University of Helsinki</td>
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<td>Impact Of Growth And Cell Size On Fission Yeast Gene Expression In Single Cells</td>
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<td>• mRNA expression levels and transcription rates scale with cell size and growth</td>
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<td>• Single cell RNA-seq reveals the molecular heterogeneity of fission yeast cells as a function of growth</td>
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<td>Samuel Marguerat, Group Head, MRC Clinical Sciences Centre / Imperial College London</td>
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<td>Fetal Erythroid Surface Biomarkers – Targets For Fatal Cell Enrichment From Maternal Blood</td>
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<td>• The selection of fetal nucleated red cells as targets for fatal cell isolation</td>
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<td>• differential proteomics of fetal cells compared to adult red cells</td>
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<td>• Characterisation of fetal erythroid Hsp60 as a candidate biomarker</td>
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<td>Neil Avent, Professor of Molecular Diagnostics and Transfusion Medicine, Plymouth University</td>
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<td>15.00 – 15.30</td>
<td>Afternoon Refreshments, Poster Presentation Sessions</td>
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<td>15.30 – 16.00</td>
<td>Case Studies In Personalised Diagnostics – Pre-clinical Diagnoses And New Phenotypes For Old Genes</td>
<td>Sarah Ennis, Professor of Genomics, University of Southampton</td>
<td>Valerie Taly, Group Leader and CNRS Research Director, INSERM / Paris Descartes University</td>
<td>Erez Mills, Senior Scientist, Weizmann Institute of Science</td>
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<td>16.00 – 16.30</td>
<td>BRCA1/2 Somatic Analysis In Ovarian Cancer Patients: Are We Ready For Routine Setting?</td>
<td>Ettore Capoluongo, Professor and Head of Laboratory, Catholic University of Sacred Heart</td>
<td>Valter Ernfors, Professor, Karolinska Institutet</td>
<td>Joshua B. Edel, Senior Lecturer in Micro and Nanotechnology, Imperial College London</td>
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**Droplet-based Microfluidics For Single Cell Analysis**
Droplet based microfluidics allows to perform single cell experiments with high efficiency and high throughput. We will illustrate capabilities of newly developed microfluidic platforms for single cell encapsulation, phenotypic characterization and sorting. Finally, we will emphasize on its potential applications for cancer research and resistance to treatment analysis.

**Host And Pathogen Simultaneous Single-cell Transcriptome Analysis Reveals Interacting Sub-populations During Infection**
The interaction between a pathogen and a host is a highly dynamic process in which both agents activate complex programs. Single-cell RNA-Seq is typically limited to the polyadenylated component of the transcriptome, thereby preventing the study of both the host and intracellular bacterial pathogens. Here, I will introduce a single-cell RNA-Seq method that simultaneously captures both host and pathogen transcriptomes. I will present application of this method to study the transcriptomes of individual mouse macrophages along with that of their intracellular pathogen Salmonella typhimurium, and identify their sub-population structure and expression heterogeneity throughout infection. Further, I will demonstrate the ability to study the biological significance of these sub-populations, most importantly the relationships among the co-existing sub-populations, their molecular details and the interplay between host and bacteria subpopulations. I will introduce novel insights into the biology of infection through the molecular study of both host and bacterium in individual encounters.

**Novel Strategies For The Detection Of Single Molecules Using Multiphase Microfluidics**
Analytical Sensors plays a crucial role in today’s highly demanding exploration and development of new detection strategies. Whether it be medicine, biochemistry, bioengineering, or analytical chemistry the goals are essentially the same: 1) improve sensitivity, 2) maximize throughput, 3) and reduce the instrumental footprint. In order to address these key challenges, the analytical community has borrowed technologies and design philosophies which has been used by the semiconductor industry over the past 20 years. By doing so, key technological advances have been made which include the miniaturization of sensors and signal processing components which allows for the efficient detection of nanoscale object. One can imagine that by decreasing the dimensions of a sensor to a scale similar to that of a nanoscale object, the ultimate in sensitivity can potentially be achieved - the detection of single molecules. This talk highlights novel strategies for the detection of single molecules using multiphase microfluidics.

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<td>16.30 – 17.00</td>
<td><strong>Genomic Epidemiology</strong>&lt;br&gt;• European collaboration in COMPARE, a large EU project with the intention to speed up the detection of and response to disease outbreaks among humans and animals worldwide through the use of new genome technology: <a href="http://www.compare-europe.eu">http://www.compare-europe.eu</a>&lt;br&gt;• Online methods at the Center for Genomic Epidemiology (CGE) for analysis and comparison of isolates and metagenomic samples&lt;br&gt;• Collaboration at Global Microbial Identifier (GMI) to develop a global system to aggregate, share, mine and use microbiological genomic data</td>
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<td><strong>Mutational Analysis Of Single Circulating Tumor Cells By Next Generation Sequencing</strong>&lt;br&gt;• CTCs are a real-time “liquid biopsy” of the tumor reflecting the disease complexity at any stage of cancer progression&lt;br&gt;• Technical advances have enabled molecular analyses at the single-cell level allowing the profiling of rare cancer cells in clinical samples&lt;br&gt;• Several steps are needed to achieve the analysis of CTCs at the single-cell level. The procedure is not yet integrated in a single device, but implies the performance of CTC selection, whole genome amplification and single cell sequencing. Each phase can be conducted by several approaches that can be combined in different workflows&lt;br&gt;• On the basis of the results obtained in a pilot study on breast cancer, single CTC sequencing seems to hold promise for future clinical applications by the development of cancer diagnostics focused on non-invasive disease management aimed at personalized medicine</td>
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<td><strong>Updates In Single Cell Data Analysis</strong>&lt;br&gt;Jose Gutierrez-Marcos, Associate Professor, University of Warwick</td>
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<td>17.00 – 17.30</td>
<td><strong>Coeliac T Cell Interiors: Insights From Transcriptomics</strong>&lt;br&gt;• Case control transcriptomic study&lt;br&gt;• Transcriptome of purified CD4+ T cells&lt;br&gt;• Identification of transcriptional control networks&lt;br&gt;• BACH2 as an important regulator of T cell development in coeliac disease</td>
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|         | **Immune Surveillance At The Single Cell Level**<br>• Microchip tools for studies of immune cell heterogeneity<br>• Serial killing by individual natural killer cells and T cells<br>• Ultrasound-mediated formation 3D "microtumors"
• Applications in cancer research and cell therapy |
|         | **Delegates are welcome to attend the co-located presentations** |

Ole Lund, Professor, Technical University of Denmark

Pamela Pinzani, Associate Professor, University of Florence

Ross McManus, Professor in Molecular Medicine, Trinity College Dublin

Björn Önfelt, Associate Professor, Karolinska Institutet

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Identifying A New Mechanosensitive Gene Network By Fusing World-wide Studies

Blood flow is an essential contributor to plaque growth, composition and initiation. It is sensed by endothelial cells, which react to blood flow by expressing >1000 genes. The sheer number of genes implies that one needs genomic techniques to unravel their response in disease. Individual genomic studies have been performed but lack sufficient power to identify subtle changes in gene expression. In this study, we investigated whether a systematic meta-analysis of available microarray studies can improve their consistency.

We identified 17 studies using microarrays, of which 6 were performed in vivo and 11 in vitro. The in vivo studies were disregarded due to the lack of the shear profile. Of the in vitro studies, a cross-platform integration of human studies (HUVECs in flow cells) showed high concordance (>90%). The human data set identified >1600 genes to be shear responsive, more than any other study and in this gene set all known mechanosensitive genes and pathways were present. A detailed network analysis indicated a power distribution (e.g. the presence of hubs), without a hierarchical organization. The avg. cluster coefficient was high and further analysis indicated an aggregation of 3 and 4 element motifs, indicating a high prevalence of feedback and feed forward loops, similar to prokaryotic cells.

In conclusion, this initial study presented a novel method to integrate human-based mechanosensitive studies to increase its power. The robust network was large, contained all known mechanosensitive pathways and its structure revealed hubs, and a large aggregate of feedback and feed forward loops.

Rob Krams, Professor of Molecular Bioengineering, Imperial College London

Next Generation Sequencing In Rare Inherited Cardiac Conditions

- Diagnostic challenges of rare inherited cardiac conditions
- Experience with multi-gene next generation sequencing diagnostic panels
- Multi-disciplinary management of rare inherited cardiac conditions

Dhavendra Kumar, Professor, University of South Wales and Consultant in Clinical Genetics, University Hospital of Wales

For more information please contact marketing@oxfordglobal.co.uk
Next Generation Sequencing Congress | Single Cell Analysis Congress
Conference: 10-11 November 2016, Novotel London West, UK
www.nextgenerationsequencing-congress.com
www.singlecell-congress.com

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