







qPCR & Next Generation Sequencing Congress
16th & 17th November 2009


Day 1 – Monday 16th November 2009

08.10	REGISTRATION & COFFEE – Palm Court Lobby	Next Generation Sequencing Congress- Adelphi Room 1 & 2
		
08.30	Chairman's Opening Address Len Keenan, Account Manager, Integromics UK	Chairman's Opening Address Dr Robert Nutter, Sr. Staff Applications Scientist, SOLiD Transcriptomic Applications, Applied Biosystems
08.40	Keynote Address The Role qPCR in Drug Discovery and Development <ul style="list-style-type: none"> • Biomarker profiling to afford personalized healthcare • RNA biomarkers in clinical genomics applications and molecular diagnostics • Evolution of qPCR methodology <p>Dr Patricia McLoughlin, Head of Genomics Basel, F Hoffmann-La Roche Ltd</p>	Keynote Address Next Generation Sequencing: Its Role in Infectious Disease Drug Discovery <ul style="list-style-type: none"> • Rapid DNA sequencing now allow whole genome approaches to study novel, multi-gene, drug resistance pathways in pathogenic bacteria and viruses • Old methods of drug discovery, such as whole cell screening, can be re-invented by using whole genomic sequences to reveal mechanisms of drug/target action • Finally, next generation DNA sequencing technology will help us understand more fully, the diversity of viral and bacterial pathogens in clinical settings <p>Dr James Brown, Director Computational Biology for Infectious Diseases, GSK</p>
9.10	Investigating Mechanisms of Gene Regulation in Drug Safety Sciences <ul style="list-style-type: none"> • Integrating the epigenome with gene expression data • Assessing mechanisms of toxicity using novel approaches <p>Dr Olivier Grenet, Group Head Genome Biology, Investigative Toxicology, Translational Sciences Novartis Pharma</p>	Solution Provider Presentation Using Ultrahigh Throughput Sequencing to Revolutionize our understanding of RNA structure and Function <ul style="list-style-type: none"> • Sequencing is unsurpassed for discovery of novel RNA structures. • The discoveries made thus far already are changing our understanding of the role RNA plays in gene expression. • Improved bioinformatic tools will now be needed to take full advantage of this technology. <p>Dr Robert Nutter, Sr. Staff Applications Scientist, SOLiD Transcriptomic Applications, Applied Biosystems</p> 
9.40	Solution Provider Presentation The Next Generation in Hot Start PCR - CleanAmp™ dNTPs <ul style="list-style-type: none"> • Introduction the novel concept of thermolabile dNTP protecting groups as applied to Hot Start activation schemes in PCR • Demonstration of the versatility of CleanAmp™ dNTPs as they can be used to convert any DNA polymerase into the corresponding Hot Start version • Presentation of synergistic benefit when CleanAmp™ dNTPs are used in combination with other approaches to Hot Start activation in PCR <p>Dr Natasha Paul, Senior Staff Scientist, Trilink Biotechnologies</p> 	Solution Provider Presentation Re-sequencing of the Human Genome on the 454 Genome Sequencer FLX System <p>The Genome Sequencer FLX System (GS FLX), powered by 454 Sequencing, is a next-generation DNA sequencing technology featuring a unique mix of long reads, exceptional accuracy, and ultra-high throughput. It has been proven to be the most versatile of all currently available next-generation sequencing technologies, supporting many high profile studies in over 7 applications categories. GS FLX users have pursued innovative research in <i>de novo</i> sequencing, re-sequencing of whole genomes and target DNA regions, metagenomics, and RNA analysis. 454 Sequencing is a powerful tool for human genetics research, having recently re-sequenced the genome of an individual human, currently re-sequencing the complete human exome and targeted genomic regions using the NimbleGen sequence capture process, and detected low frequency somatic mutations linked to cancer.</p> <p>This presentation will provide a short overview about the 454 Sequencing technology, and will focus on applications possible to address with the Genome Sequencer FLX system, with special emphasis on human re-sequencing. It will also provide information</p>






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		<p>on the newest product developments, including the 2010 launch of kits allowing to generate read lengths of >800 - 1000 bases on the today's FLX instrument.</p> <p>Dr Marcus Droege, Global Marketing Director Genome Sequencing, Roche Applied Science</p> 
<p>10.10</p>	<p>qPCR Applications on the Path to Novel Bone Anabolic Drug Targets</p> <ul style="list-style-type: none"> • Quantification of drug target expression and tissue profiling • In vivo qPCR gene expression analyses in hard tissues like bone • qPCR expression assays for compound screening <p>Dr Hansjoerg Keller, Senior Research Investigator, Novartis</p>	<p>PANEL DISCUSSION Fitting the Requirements of Drug Discovery Process</p> <p>A new generation of sequencing technologies will increase the speed and lower the cost of sequencing, and promises to expand the utility of sequencing in drug discovery and development. The panellists are invited to share their experiences in development of next generation sequencing applications in the drug discovery process, the state of the technology and the issues and challenges facing its application.</p> <p>Moderator: Dr Robert Nutter, Sr. Staff Applications Scientist, SOLiD Transcriptomic Applications, Applied Biosystems</p> <p>Panellists: Dr David Dow, Group Leader, Molecular and Cellular Technologies, GSK</p> <p>Dr David Taylor, Discovery Platform Manager, Microbiology, Unilever</p> <p>Dr James Brown, Director Computational Biology for Infectious Diseases, GSK</p>
<p>10.35</p>	<p>MORNING REFRESHMENTS – Exhibition Room – Palm Court</p>	
<p>11.05</p>	<p>The Use of qPCR in Clinical Research</p> <p>Dr Victor Turcanu, Lecturer in Paediatric Allergy, King's College London, Division of Asthma, Allergy and Lung Biology, Guy's Hospital</p>	<p>Solution Provider Presentation Illumina Genome Analyzer System - The Most Widely Adopted Next Generation Sequencing System</p> <p>Whether you need to sequence an entire genome or a large candidate region, the Illumina Genome Analyzer is today's most productive and economical sequencing tool. The Genome Analyzer delivers unprecedented volumes of high-quality data rapidly and economically, with a simple workflow and minimal sample input..</p> <ul style="list-style-type: none"> • Leverage single or paired-end reads for a wide range of genome sequencing applications. <p>-Discover and confirm SNPs -Identify chromosomal rearrangements, including Copy Number Variations (CNVs) -Map break points -Detect rare variants</p> <ul style="list-style-type: none"> • The Genome Analyzer can generate highly accurate results in under a week, with the fastest and least labor-intensive workflow of any sequencing technology. • DNA sequencing with the Genome Analyzer delivers: <ul style="list-style-type: none"> -superior accuracy - more accurate reads per run than any other massively-parallel sequencing method -highest throughput - gigabases of data per run with the smallest amount of starting material and the lowest cost per base compared to other technologies -simplest workflow - single-operator driven process and walk-away automation with minimal hands-on time per run <p>Dr Stephanie Brooking, European Segment Manager, Sequencing, Regional Marketing-Europe, Illumina</p> 

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<p>11.35</p>	<p>Current Technologies in qPCR Diagnostics: Old Concept for New Application in Absolute Q-PCR</p> <ul style="list-style-type: none"> • Absolute determination of the number of copies for a DNA marker can result of a greater value for minimal residual disease (MRD) evaluation in hemopoietic neoplasms. • Absolute quantification of given DNA targets, remains technically difficult due to the lack of a methodology able to comprehensively account for accurately quantification of target copy number. However, the quantity of DNA target sequences in the samples can be assessed with a reasonable accuracy using proper external standards, i.e. plasmid DNA containing the target sequence, PCR-amplified target sequences and healthy DNA. • Method to build an external standard curve made of a recombinant plasmid DNA, quantified itself by Fine-competitive PCR, allow fine-standardization of absolute Q-PCR, long-term stability of the standards, affordable molecular tests and gene copy accuracy. In addition, this method to quantify external standard curve is suitable for use in any q-PCR platforms (Taq-Man, SYBR green etc). <p>Dr. Raffaele Di Francia, Lab of Molecular Hematology, Institute of Tumors G. Pascale</p>	<p>Pushing the Limits of Next Generation Sequencing</p> <p>Dr Dan Turner, Head of Sequencing Technology Development, Wellcome Trust Sanger Institute</p>
<p>12.00</p>	<p>miQPCR - A Novel Approach for Expression Profiling of microRNA based on RNA-linker Ligation</p> <ul style="list-style-type: none"> • MicroRNAs are evolutionary conserved, small non-coding RNAs with a critical role in controlling the expression of protein coding genes • Expression profiling of microRNAs is challenged by several factors including short template length and closely relate sequence • MiQPCR, is a novel T4-RNA ligase-based approach for cDNA synthesis which enables fast, accurate and sensitive microRNA expression profiling by using RT-PCR <p>Dr Mirco Castoldi, Postdoctoral Fellow, Hentze Group, EMBL Heidelberg, Germany</p>	<p>Separating Wheat from Chaff –Molecular Elucidation of Genetic Factors Underlying Mental Retardation by Genome Partitioning and Large Scale Next-Generation Sequencing</p> <p>The recent introduction of massive parallel sequencing technology has revolutionized genomic research. These so-called next-generation sequencing platform can sequencing DNA orders of magnitude faster and at much lower cost than traditional Sanger method. However, even with the dramatically improved efficiency, presently available instruments do not allow to resequence the complete genome from a large number of human patients in economically realistic manner. Therefore, robust methods to isolate relevant genomic regions fro targeted sequencing are required.</p> <p>In this study, we evaluated different genome partitioning strategies including droplet-based PCR from RainDance Technologies, solution hybrid selection from Agilent Technologies and chromosome sorting. With different strengths, they are eventually combined to identify genetic factors underlying mental retardation.</p> <p>Dr Chen Wei, Head of Genomics Platform, Berlin Institute for Medical Systems Biology, Max-Delbrueck-Center for Molecular Medicine, Berlin, Germany</p>
<p>12.25</p>	<p>Real Time Quantitative PCR for Molecular Diagnosis in Viral Infection: Exemplified for Simian Virus 40</p> <ul style="list-style-type: none"> • Simian virus 40 (SV40) is a potent tumour virus, and mounting evidence suggests it is an emergent human pathogen • Prospective studies are needed to determine the prevalence of SV40 infection in different populations and to access how the virus is transmitted from person to person. Until now there has been a lack of standardized and sensitive tests for SV40 to perform these important studies • We developed a RQ-PCR assay to establish the clinical diagnosis of SV40 infections in a wide spectrum of specimens. This can be easily expanded to other viruses. Therefore our RQ-PCR assay is a sensitive and specific approach to analyse infectious diseases and malignancies <p>Susanne Heinsohn, University Hospital Hamburg-Eppendorf, Clinic for Hematology and Oncology</p>	<p>Solution Provider Presentation “Scalable DNA Fragmentation using Novel Nuclease Digestion”</p> <ul style="list-style-type: none"> • NEBNext™ dsDNA Fragmentase™ is an enzyme-based solution to generating random, representative DNA fragmentation. A unique blend of engineered nucleases promotes scalable fragmentation from a variety of sample sources • A root level examination of the kinetics of nucleotide incorporation by DNA polymerases has illuminated the mechanism for accurately copying a DNA template. Further studies of modified polymerases and nucleotides have provided additional insight into determinants of fidelity, and have guided engineering of the essential components of DNA sequencing platforms. Examples of insights obtained by kinetic studies will be presented <p>Dr William E. Jack, Research Director, New England Biolabs</p> 


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12.55	LUNCH – Exhibition Room – Palm Court	
13.50	<p>Solution Provider Presentation Considerations for reducing variance in qPCR research</p> <ul style="list-style-type: none"> • Discussion of the common steps taken to complete a qPCR assay • Discuss steps that can be taken in order to minimize the variation throughout the protocol • Discuss the ways in which these steps can be optimised to reduce the overall time of a qPCR protocol <p>Dr Ian Kavanagh, Research and Development Manager, Thermo Scientific Genomics</p> 	<p>Solution Provider Presentation Update on Tools for NextGen DNA shearing (Covaris), Advances in Emulsion PCR and Cost Efficient, High Throughput In-silico & In-situ SNP Assays for NextGen SNP Validation</p> <ul style="list-style-type: none"> • Advances in NextGen DNA shearing using Covaris Adaptive Focussed Acoustics (AFA) • Advances in Emulsion PCR, HydroCycler and emulsion bag/MTP formats • Advances in Cost Efficient, High Throughput In-silico & In-situ SNP Assays for NextGen SNP Validation using KBiosciences KASP technology <p>Dr Niels Kruize, Sales Director, KBiosciences Ltd</p> <p>Sponsored by:</p> 
14.20	<p>The Use of Individual Amplification Curves in the Analysis of Quantitative PCR Data</p> <ul style="list-style-type: none"> • The paper describes the analysis of qPCR data, starting with the raw fluorescence data, and will discuss • The need for a correct baseline subtraction • The need to use the real PCR efficiency per amplicon • A data analysis approach based on the analysis of (groups of) single samples <p>Dr. Jan .M. Ruijter, Image and Data Analyst, Dept. Anatomy and Embryology, Academic Medical Centre, Amsterdam</p>	<p>Solution Provider Presentation Next Generation Sequencing - Comprehensive Methods for Data Analysis</p> <ul style="list-style-type: none"> • Live demonstration for an integrated analysis strategy for • ChIP Seq • RNA Seq <p>Dr. Martin Seifert, Chief Executive, Technology & Marketing, Genomatix</p> 
14.45	<p>Design and Analysis of qPCR Data with Mixed Models</p> <p>Dr Sami Hokkanen, Senior Biostatistician, Research & Translational Statistics, Biostatistics & Support Functions, R&D, Orion Pharma</p>	<p>Exploring the Potential Applications of Next Generation Sequencing in Molecular Genetic Diagnostics</p> <p>Dr Ann Curtis, Northern Genetics Service, Newcastle Hospitals NHS Foundation Trust</p> <p>Dr Jonathan Coxhead, Institute of Human Genetics, Newcastle University</p>
15.15	<p>Solution Provider Presentation RealTime Ready - Function tested custom qPCR-Assays for Gene Expression Analysis on the LightCycler Platform</p> <ul style="list-style-type: none"> • New: RealTime ready custom qPCR Assays and Panels for Human Gene Expression Analysis • Flexible and customized assay selection and panel configuration with web-based Order Portal • All qPCR Assays are function tested for reliable performance • LightCycler® 1536 Real-Time PCR System – High throughput - redefined <p>Dr Ralf Mauritz, Director R&D, Roche Diagnostics GmbH</p> 	<p>Solution Provider Presentation Microfluidics and Next-Generation Sequencing</p> <ul style="list-style-type: none"> • Introducing the Fluidigm microfluidic technology • The use of digital PCR in sequencing rare samples • Elimination of library preparation • Microfluidics for sample multiplexing <p>Dr Martin Pieprzyk, Worldwide Product Manager, Fluidigm Corporation</p> 

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15.45	<p>Is Your Cp/Ct Telling You the Truth</p> <p>Dr. Chaminda Salgado, Head of PCR Services, Pharmaceutical Analysis, NDA Analytics</p>	<p>Highly Sensitive Detection of Genomic Instability using Next-Generation Sequencing</p> <ul style="list-style-type: none"> • Genomic instability and cancer • Ultradeep sequencing of cancer genome • Statistical treatment and error control <p>Dr Francesca Ciccarelli, Group Leader, European Oncology Institute, Milan, Italy</p>
16.10 16.35	<p>AFTERNOON REFRESHMENTS – Exhibition Room – Palm Court</p>	
16.35		<p>Panel Discussion & Presentation Implementation of HighThroughput Next Generation Sequencing DNA Research in the UK</p> <ul style="list-style-type: none"> • Overview of the Medical Research Council project • Technology Considerations <p>Moderator: Stephanie Brooking, European Segment Manager, Sequencing, Regional Marketing-Europe, Illumina</p> <p>Panellists: Scottish Hub- Dr Mark Blaxter, Principal Investigator, University of Edinburgh, Gene Pool North England Hub- Professor Neil Hall, Principal Investigator, University of Liverpool West England Hub- Dr David Buck, Head of Genomic Services, Wellcome Trust Centre for Human Genetics (WTCHG)</p>
17.05	<p>Effective Approaches on Generating, Normalising, Visualisation of Gene Expression Data</p> <ul style="list-style-type: none"> • Diversity of QPCR applications in drug discovery • Global expression data base for cell lines and tissues <p>Dr Rolf Studer, Senior Lab Head Molecular Biology Core Unit, Actelion</p>	<p>Comparison of Solexa High Throughput Sequencing and Affymetrix Microarrays in Transcriptomics Study of <i>Drosophila Melanogaster</i></p> <ul style="list-style-type: none"> • The FlyAtlas project • Comparison of gene expression results from microarrays and sequencing data • Investigating gene structure and alternative splicing <p>Dr Pawel Herzyk, DNA, Arrays, Bioinformatics, Sir Henry Wellcome Functional Genomics Facility, University of Glasgow</p>
17.30	<p>Whole Process Quality Assurance of a Fully Automated qPCR-based Gonococcal Analysis</p> <ul style="list-style-type: none"> • Neisseria gonorrhoea is a major sexually transmitted bacteria and its low viability in transport media, led us to develop a real-time PCR to improve the diagnosis. • We have developed a fully automated, system for nucleic acid purification, amplification and detection in collaboration with Hamilton robotics which improves tracability and decreases hands-on time as a fully walk away system. • The very sensitive Real-time PCR methods in use today can detect a single copy of DNA and therefore a single bacteria. In order to rely on results of our tailored robotic system, we evaluated a system for whole process quality assurance <p>Dr Stig Ove Hjelmevoll, Scientist, Department of Microbiology and Infection Control, University Hospital of North Norway</p>	<p>Next-Generation Sequencing in Epigenetic Research</p> <ul style="list-style-type: none"> • Advantages of NGS in epigenetic research • ChIP-Seq delivers data-rich epigenomic maps • The landscape of histone tri-methylation in the human genome <p>Dr Paul J. Hurd, Lecturer in Molecular Biology & Biochemistry, School of Biological and Chemical Sciences, Queen Mary University of London</p>
17.55	<p>Classical and Real time Immuno-PCR: Use and Limits</p> <ul style="list-style-type: none"> • Background signal • Choice of specific antibodies • Gel electrophoresis vs real time PCR <p>Dr EIMoualij Benaissa, Scientific Director, Center of Research on Prions Proteins CRPP, Institute of Pharmacy, University of Liege</p>	<p>Comparison of Solexa High Throughput Sequencing and Affymetrix Microarrays in Transcriptomics Study of <i>Drosophila Melanogaster</i></p> <ul style="list-style-type: none"> • The FlyAtlas project • Comparison of gene expression results from microarrays and sequencing data • Investigating gene structure and alternative splicing <p>Dr Pawel Herzyk, DNA, Arrays, Bioinformatics, Sir Henry Wellcome Functional Genomics Facility, University of Glasgow</p>

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18.20		<p>Solution Provider Presentation Enrichment of Resequencing Targets Using Microdroplet-based PCR</p> <ul style="list-style-type: none">• Overview of RainDance technology• The Sequence Enrichment assay• Targeted resequencing results <p>Dr Steve Picton, Senior Commercial Application Scientist, RainDance Technologies, Inc.</p> 
18.50	CLOSE OF CONFERENCE	

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Day 2- Tuesday 17th November 2009

08.10	REGISTRATION & COFFEE- Palm Court Lobby qPCR Congress – Adelphi Room 3 	Next Generation Sequencing Congress- Adelphi Room 1 & 2 
08.20	Chairman's Opening Address – Dr. Chaminda Salgado, Head of PCR Services, Pharmaceutical Analysis, NDA Analytics	Chairman's Opening Address Dr Marcus Droege, Global Marketing Director Genome Sequencing, Roche Applied Science
08.25	QPCR in the Context of Other Genomic Technologies - Integration into the Drug Discovery Process <ul style="list-style-type: none"> • Target discovery and validation • siRNA analysis • Marker discovery Dr Paul E. Kroeger, Senior Group Leader, Neuroscience & Pain Discovery, Abbott Laboratories	Next .5 Generation Sequencing: Selective Resequencing on Custom DNA Microarrays using CycLIC Chemsitry <ul style="list-style-type: none"> • Targeted approach combines selective capture from genomic DNA with sequencing • Rapid resequencing of regions of interest from GWAS with simple workflow • 99.8% raw accuracy at 1x coverage • Software allows increased accuracy through filtering and confidence scoring Dr David L.V. Bauer, University of Oxford, Wellcome Trust Centre for Human Genetics
08.50	Expression Profiling with QPCR in Drug Discovery: Distribution of the Phosphodiesterase Gene Family Members in 24 Human Tissues <ul style="list-style-type: none"> • Validating a set of reference genes for expression studies in a variety of human tissues • The distribution of phosphodiesterase (PDE) gene family members in 24 human tissues • What does the expression profile of PDEs tell us about targeting these enzymes for drug discovery? Dr Viktor Lakics, Senior Research Scientist - Neurodegeneration DHT, Lilly UK	08.50 Interactive Seminar While drastically improving the ability to generate more and better results in significantly less time, data generated by next-generation sequencers and other life science instruments also place a tremendous burden on your IT infrastructure. Well-suited to handling the lower volume of files generated by legacy sequencing machines, older IT solutions cannot keep pace with the demands of next-generation sequencers, resulting in lower performance, slow response times, storage capacity at maximum utilization and increasingly difficult data management. Working together as trusted partners, HP and Quantum provide advanced storage solutions that support the demanding workloads of next-generation genome sequencers and other high-powered life science instruments. Offering high-performance platforms, years of industry experience and a dedicated support staff, scientific researchers can trust our IT solutions to simplify data management for faster workflows and reduced storage costs and to intelligently manage the growing data management challenge.
9.20	qPCR A Powerful Tool For Intestinal Microbiota Monitoring – A Cross Species Study <ul style="list-style-type: none"> • Description of the species' choice (Human, Rabbit and Porc) • Description of the Bacterial flora choice • Pitfalls of DNA extraction from stool • Absolute quantification by real time PCR Dr Afif Abdel Nour, Associate Professor, Molecular Biotechnology, qPCR Expert, Institut Polytechnique LaSalle Beauvais	40 minutes Presentation - Petabyte-scale Storage Solutions for Today's Life Science Research <ul style="list-style-type: none"> • Managing exponential growth of data • Simplifying the storage ecosystem • New sequencers requiring smarter infrastructure (including Data Protection and DR) Dr Roberto Fabbretti, IT Manager, Swiss Institute of Bioinformatics Genopode, University of Lausanne 20 minutes Q&As  
9.45	qPCR GMP Applications: Contamination Detection in the Biopharmaceutical Industry: <ul style="list-style-type: none"> • Issues faced in the implementation of Molecular Biology methods • GMP requirements and validation guidelines • Routine use of qPCR as integration of classical testing Dr Emiliano Toso, Molecular Biology Lab Head, Non- Clinical Development, Merck Serono	Coping with 'Le Deluge' - Boosting ChIPseq Analysis using Self Organising Maps <ul style="list-style-type: none"> • 'De novo' motif finding using Self-Organising Maps • Filtering ChIPseq datasets for high signal-to-noise reads • From Clouds to Cards: the computational options Dr Aaron Golden, Lecturer, College of Engineering and Informatics, Enabling Technologies, National Centre for Biomedical Engineering Science, NUI, Galway

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10.10	<p>High Resolution Melting Analysis in Cancer Diagnosis</p> <ul style="list-style-type: none"> • Basic aspects of HRMA • Application for the detection of somatic mutations • Methylation specific-HMRA <p>Professor Claudio Orlando, Clinical Biochemistry Unit, Dept. of Clinical Physiopathology, University of Florence</p>	<p>Bioinformatics Support for Next Generation Sequencing: A Core Facility Perspective</p> <ul style="list-style-type: none"> • Automated data processing supported by LIMS and high performance computing • Secondary analysis pipelines for short-read data • Managing projects and workload <p>Dr Matthew Eldridge, Head, Computational Biology Core, Cancer Research UK (Cambridge Research Institute), Cambridge UK</p>
10.35 MORNING REFRESHMENTS - Exhibition Room – Palm Court		
11.05	<p>MicroRNA profiling in the Malignant Mesothelioma: Diagnostic and Therapeutic Application</p> <p>Malignant Mesothelioma (MM) is a rare and aggressive tumour of serosal cavities linked to asbestos exposure. Improved detection methods for diagnosis of this type of neoplastic disease are essential for an early and reliable detection and treatment. Thus, focus has been on finding tumour markers used for non-invasive detection of MM. There is emerging evidence of abnormal levels of microRNAs (miRNAs) in tumours. While some miRNAs commonly exhibit altered amounts across tumours, often, different tumour types produce unique patterns of miRNAs, related to their tissue of origin. The miRNA isolated from fresh-frozen biopsies of MM was profiled for the expression of 88 miRNAs involved in cancer by qPCR miRNA array. Unique patterns of altered levels of miRNA production provide fingerprints that may serve as molecular biomarkers for tumour diagnosis, classification, prognosis and prediction of therapeutic responses.</p> <p>Dr Marco Tomasetti, Investigator, Department of Molecular Pathology and Innovative Therapies, Polytechnic University of Marche, Italy</p>	<p>High-throughput Small RNA Sequencing in Acute Myeloid Leukaemia (AML)</p> <ul style="list-style-type: none"> • Distribution of microRNAs and small non-coding (snc)RNAs in AML • Dysregulation of microRNAs (miRNAs) in acute myeloid leukaemia AML • Discovery of novel species of microRNAs and other sncRNAs <p>Dr. Silvana Debernardi, Senior Postdoctoral Research Fellow, Medical Oncology Centre, Barts & The London School Of Medicine</p>
11.30	<p>Solution Provider Presentation LNA-based Real-Time PCR in Cancer Diagnostics</p> <p>Dr Ditte Andreasen, Senior Scientist, R&D, Exiqon</p> 	<p>Solution Provider Presentation The Agilent Technologies SureSelect™ Platform for Target Enrichment</p> <ul style="list-style-type: none"> • Enables you to focus your sequencing efforts on a subset of the genome • Uses long oligonucleotides to capture genomic material of interest • Protocols available for both Illumina and Solid workflows <p>Dr Ruth Burton, Applications Specialist, Agilent</p> 
12.00	<p>Validation Studies of Mitotic Kinases</p> <ul style="list-style-type: none"> • qPCR analysis is an indispensable tool to study target knockdown after antisense or siRNA validation of a pharmacological drug target • Various examples of orthogonal target validation of essential mitotic kinases are given using mRNA knockdown strategies as well as pharmacological inhibitors • Kinome-wide screening efforts will be used to show the value of qPCR techniques to identify novel putative drug targets • Target validation using mRNA knockdown technologies combined with qPCR is most successful in target classes with a tightly regulated protein turnover such as regulatory proteins of the cell cycle <p>Dr Mathias Schmidt, Associate Principal, Strategic Planning and Business Support, Nycomed GmbH</p>	<p>Developments in RNA-seq and in SNP Characterization in Resequencing</p> <ul style="list-style-type: none"> • Calling SNPs in RNAseq and in resequencing gene enriched genomes (“exomes”) • Coding and non-coding SNPs with functional effect • Predicting functional SNPs within gene sequences <p>Dr Joaquin Dopazo, Head of the Bioinformatics and Genomics Department, Centro de Investigacion Principe Felipe</p>

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12.25	<p>Design and Optimisation of RT qPCR Experiments</p> <p>Prof. Mikael Kubista , Head Laboratoř Genové Expresie, Biotechnologický ústav AV ĀR</p>	<p>Next Generation Sequencing of B- and T-cell Receptor Rearrangements</p> <ul style="list-style-type: none"> • Amplification protocols for quantitative analysis of rearrangements • Bioinformatic workflow of BCR and TCR analysis • Results of sequencing BCR and TCR in human and mouse samples <p>Dr Niek de Vries, Team Leader, Dept. Clinical Immunology & Rheumatology FOCIS & EULAR Center of Excellence, University Hospital Amsterdam, The Netherlands</p>
12.50	<p>LUNCH – Exhibition Room – Palm Court</p>	
13.50	<p>Case Study: Development of An Ex-vivo Pharmacodynamic Assay for CAM-3001, A New Potential Therapy for the Treatment of Rheumatoid Arthritis</p> <p>Dr Jo Woods, Senior Research Scientist, MedImmune</p>	<p>Next-Generation Sequencing of Bacteria- Bugs to Data to Discoveries</p> <ul style="list-style-type: none"> • Application of NGS to bacteria • How far to go with assembly, closure, finishing, annotation...? • Discoveries made and those to come <p>Dr. Lori Snyder, Senior Lecturer in Biotechnology, Kingston University</p>
14.15	<p>Transcription Changes in Peripheral Blood Cells- Applications for Neuropsychiatric Disorders</p> <ul style="list-style-type: none"> • Transcription changes are measured in human peripheral blood using qPCR. • A focused, hypothesis driven approach and small gene set was used. • Changes in transcription patterns can be used to differentiate subject groups. • Goal is to identify transcription patterns that will predict appropriate treatment and treatment outcome <p>Dr Roman Artymyshyn, Principal Scientist, Target Discovery and Assessment, Lundbeck Research</p>	<p>De Novo Sequencing and Transcriptomics Analysis of an Obligate Biotrophic Plant Pathogen, <i>Albugo candida</i></p> <p>Illumina sequencing, cDNA sequencing, expression profiling, genome sequencing, de-novo assemblies, genome annotation, quality controls, synteny analyses, detection of SNPs, heterozygosity.</p> <p>Dr. Eric Kemen, Post Doctoral Researcher, Sainsbury Laboratory</p>
14.40	<p>Solution Provider Presentation</p> <p>Novel Real-Time PCR Technologies from QIAGEN</p> <p>In his presentation, Dr. Thorsten Traeger will talk about two powerful techniques that take PCR to the next level. The first is multiplex, real-time PCR, where several targets are quantified simultaneously in the same reaction. PCR throughput is increased, precious sample material is conserved, and reliable normalization of target genes to a control gene is achieved. The second technique is high-resolution melting (HRM) analysis, which characterizes double-stranded PCR products based on their dissociation behaviour. Even PCR products which differ by a single base pair can be discriminated. Both techniques can be applied to gene expression analysis, genotyping, and other applications, and can be conveniently carried out on a single platform: the Rotor-Gene Q, a unique rotary cycler which delivers high thermal and optical uniformity from tube to tube to ensure highly precise results.</p> <p>Dr Thorsten Traeger, Project Manager, R&D, Qiagen</p> 	<p>The 1000 Genomes Project, a Large Data Problem</p> <p>Laura Clarke, Scientific Programmer, EBI</p>
15.10	<p>Afternoon Refreshments – Exhibition Room – Palm Court</p>	

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15.35	High Throughput Design and Application to PCR based Methylation Biomarker Detection Dr Andreas Weinhäusel, Senior Scientist, Molecular Diagnostics, Austrian Research Centers ARC	ChIP-Seq: How to Analyze Epigenetic Profiles to Address Fundamental Biological Questions <ul style="list-style-type: none">• The experimental and bioinformatic workflow of ChIP-Seq• Publicly available software tools for ChIP-Seq applications• Studying X inactivation in mouse embryonic stem cells using ChIP-Seq Dr Hendrik Marks, Post Doctoral Researcher, Radboud University
16.00	CLOSE OF CONFERENCE	

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18th November, Post Conference Workshop – qPCR Congress



Venue: Westminster Suite

Workshop Schedule – Biostatistics Conducted by Dr Neven Zoric, CEO at TATAA biocenter

This course explains statistics applicable to qPCR and teaches how to use statistics to interpret real-time PCR gene expression data, and classify samples based on real-time PCR expression profiling. Course is based on seminars and computer-based demonstrations. During the course you will learn:

- How to calculate mean, standard deviation (of sample and population), coefficient of variation, confidence interval, P-value.
- How to compare a group of samples with a mean (simple t-test), to compare two groups of samples (unpaired t-test), and group of samples before and after treatment (paired t-test)
- How to compare three or more groups (one way ANOVA), and groups of samples measured before, during and after treatment (repeated measures ANOVA)
- How to study the effect of treatment (linear regression)
- How to compare samples that are not from a Gaussian population (Wilcoxon test, Mann-Whitney test)
- How to visualize and interpret real-time PCR expression data of many genes in many samples (principal component analysis)
- How to identify related samples based on real-time PCR expression profiling (Hierarchical clustering)
- How to find response profiles describing samples studied by real-time PCR expression profiling (self-organizing maps)

How to design real-time PCR expression studies (experimental design).

Registration & Coffee 8.30 - 9.00 a.m.

09.00-10.00	Basic principles of statistics: Trueness and precision, concepts of mean, median, percentiles, boxplot, standard deviation, coefficient of variation, standard error of the mean, confidence intervals
10.00-10.45	Advanced principles of statistics: <ul style="list-style-type: none">- the Gaussian distribution- the Central Limit theorem- p values and statistical hypothesis testing- z-scores- distribution-free (rank based methods, re-sampling methods) vs. normal (Gaussian) distribution dependent tests.
10.45-11.00	Morning Coffee
11.00-12.00	Overview of statistical tests <ul style="list-style-type: none">- when to use which test- comparison between 2 (paired/unpaired) groups: (paired) t-test, Mann-Whitney test, Wilcoxon rank sum test, ratio t-test
12.00-12.30	Statistical testing for significant differences <ul style="list-style-type: none">- use of InStat software (www.graphpad.com/demos)
12.30-13.30	Lunch
13.30-14.30	Pattern recognition: Hierarchical Clustering <ul style="list-style-type: none">- Scaling (mean centering, autoscaling)- Self organizing maps
14.30-15.15	Scatter plot, Principal Component Analysis, Potential Curves, Procrustes Rotation
15.15-15.30	Afternoon Coffee
15.30-17.00	Gene expression profiling <ul style="list-style-type: none">- Lymphoma diagnostics- Embryonic development of <i>Xenopus laevis</i>- Yeast metabolism- Stem cell differentiation- Use of GenEx software (www.multid.se) Coordination
17.00-17.15	Questions and answers
17.15	End of biostatistics course day