






In collaboration with the European Commission, Directorate of Health



Conference Programme			
Wednesday 14 th April 2010			
12.00 – 14.30	Registration Session <i>Terrace of Convention Centre</i>		
14.30 – 15.15	Welcome Remarks <i>Conference Rooms 1-4 – Conference level</i> Session chairs: Francis Stewart, <i>Dresden, Germany</i> ; Mike Taussig, <i>Cambridge, UK</i> ; Lars Kristiansen, <i>ESF, France</i> ; Patrik Kolar, <i>Brussels, Belgium</i>		
15.15 – 16.00	K2: Lipid – protein interactions governing raft partitioning in membranes Kai Simons, <i>Max Planck Institute, Dresden, Germany</i>		
16.00 – 16.30	Coffee Break – <i>Hall 3</i>		
16.30 – 17.15	K3: RNA-based therapeutics reaching the clinic Gert-Jan van Ommen, <i>University of Leiden Medical Centre, Leiden, The Netherlands</i>		
17.15 – 18.00	K4: The evolution of mammalian tissue transcriptomes Hendrik Kaessmann, <i>University of Lausanne, Lausanne, Switzerland</i>		
18.00-19.30	Welcome reception – <i>Terrace</i>		
Thursday 15 th April 2010			
	Session chair: Joachim Engels, <i>Frankfurt, Germany</i> <i>(All plenary sessions from now will be held in the Great Hall)</i>		
09.00-09.45	K5: System analysis of endocytosis by functional genomics and quantitative multi-parametric image analysis Marino Zerial, <i>Max Planck Institute, Dresden, Germany</i>		
09.45 – 10.30	K6: Argonaute proteins and the mechanisms of small RNA-guided gene silencing Gunter Meister, <i>Max Planck Institute, Martinsried, Germany</i>		
10.30 – 10.40	ST1: Integrated analysis of high-dimensional endocytosis RNAi screen Angela Simeone, <i>Technical University, Dresden, Germany</i>		
10.40-10.50	ST2: Tissue-specific rewiring of signalling pathways through alternatively spliced disordered segments Marija Buljan, <i>Wellcome Trust Sanger Institute, UK</i>		
10.50-11.00	ST3: Predicting protein-RNA interactions in the pancreatic beta cell – a novel computational approach to identify regulators of rapid glucose response Christof Winter, <i>Dresden University, Dresden, Germany</i>		
11.00-11.30	Coffee break		
11.30 – 13.00	Parallel Symposia		
Symposium Title	S1: Lipid droplets as dynamic organelles of fat deposition and release: Translational research towards human disease	S2: Silencing RNAs: Small regulatory RNAs in health and disease	S3: LUPA, using the dog as a model system to decipher human disorders
Room	<i>Great Hall</i>	<i>Hall 1</i>	<i>Hall 2</i>

Organisers			
Session Chair/ Introduction 11.30-11.45	Gerd Schmitz , <i>Regensburg, Germany</i>	Gunter Meister , <i>Dresden, Germany</i>	Anne-Sophie Lequarré , <i>University of Liège, Belgium</i>
11.45-12.10	Mouse lipid storage models , Christian Wolfrum, <i>Zurich, Switzerland</i>	Function of RNA and RNA-binding factors in influenza virus replication , Thomas Meyer, <i>Berlin, Germany</i>	Dog genetics provides new insights into development and growth , Tosso Leeb, <i>Bern, Switzerland</i>
12.10-12.35	Human lipid storage and release pathology , Gerd Schmitz, <i>Regensburg, Germany</i>	Coordinated epigenetic repression of the miR-200 family and miR-205 in invasive bladder cancer , Jørgen Kjems, <i>Aarhus, Denmark</i>	Canine primary ciliary dyskinesia reveals a new gene involved in cilium structure and function , Anne-Sophie Lequarré, <i>University of Liège, Belgium</i>
12.35-13.00	Mechanisms and disturbances of endolysosomal lipid processing , Thomas Kolter, <i>Bonn, Germany</i>	The complex life of small RNA , Eric Miska, <i>Cambridge, UK</i>	Mapping genes for canine SLE-related disease and other inflammatory diseases , Göran Andersson, <i>Uppsala, Sweden</i>
13.00-14.30	Lunch, Exhibition & Poster Session 1 - Hall 3		
13.45-14.15	Transcriptome analysis and selective target enrichment: Most recent developments in NGS technology Georg Gradl, Axel Strittmatter, <i>Eurofins MWG Operon, Ebersberg, Germany</i> 		
14.30-16.00	Parallel Symposia		
Symposium Title	S4: Integrative approaches for systems biology (ENFIN)	S5: The power of many	S6: Faster, cheaper, better DNA sequencing!
Room	<i>Great Hall</i>	<i>Hall 1</i>	<i>Hall 2</i>
Organisers			
Session Chair/ Introduction 14.30-14.45	Pascal Kahlem , <i>Hinxton, UK</i>	Markus Perola , <i>Helsinki, Finland</i>	Ivo Gut , <i>Barcelona, Spain</i>
14.45-15.10	ENCORE and its ENVISION interface , Henning Hermjakob, <i>Hinxton, UK</i>	Population based biobanks are for advancement of public health Andres Metspalu, <i>Tartu, Estonia</i>	2nd generation DNA sequencing of cancer genomes , Ivo Gut, <i>Barcelona, Spain</i>
15.10-15.35	Integrating wet and dry systems biology to detect novel genes associated with the mitotic spindle , Christine Orenge, <i>London, UK</i>	Disease-orientated Biobanks - Web-based overview catalogue , Erich Wichmann, <i>Munich, Germany</i>	Diagnostics of single molecules and cells , Mats Nilsson, <i>Uppsala, Sweden</i>
15.35-16.00	The model of GSIS , John Hancock, <i>Oxford, UK</i>	The Future of European Biobank-based Research , Gert-Jan van Ommen, <i>Leiden, The Netherlands</i>	Towards DNA sequencing with a biological Nanopore , Andrew Heron, <i>Oxford, UK</i>
16.00-16.30	Coffee Break – Hall 3		
	Session chair: Andres Metspalu, <i>Tartu, Estonia</i>		

	<i>Grand Hall</i>		
16.30-16.40	ST4: TransgeneOmics: A platform for systems wide protein function analysis in metazoans Mihail Sarov, <i>Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany</i>		
16.40-16.50	ST5: Variation in transcription factor binding among humans Maya Kasowski, <i>Yale University, New Haven, USA</i>		
16.50-17.00	ST6: Genomic copy number alterations in cancer: High-resolution analysis of the NCI-60 panel Daniel Rico, <i>Spanish National Research Centre (CNIO), Madrid, Spain</i>		
17.00-17.45	K7: Next generation DNA sequencing techniques and applications Wilhelm Ansorge, <i>Ecole Polytechnique Federal Lausanne, Lausanne, Switzerland</i>		
17.45-19.15	Poster Session 1 continued – <i>Hall 3</i>		
Friday 16th April 2010			
	Session chair: Kjetil Taskén, <i>Oslo, Norway</i> (<i>Grand Hall</i>)		
09.00-09.45	K8: Epigenetic regulation of imprinting, reprogramming, and lineage commitment in mammals Wolf Reik, <i>Babraham Institute, Cambridge, UK</i>		
09.45-10.30	K9: High resolution proteomics for functional genomics Matthias Mann, <i>Max-Planck Institute, Martinsried, Germany</i>		
10.30-10.40	ST7: Functional proteomics of the human centrosome Jens Andersen, <i>University of Southern Denmark, Odense, Denmark</i>		
10.40-10.50	ST8: Meta-analysis of expression profiles of 5-aza-C treated cancer cells Ozlen Konu, <i>Bilkent University, Ankara, Turkey</i>		
10.50-11.00	ST9: The sister histone methyltransferases, Mll1 and Mll2 regulate different developmental decisions Andrea Kranz, <i>Technical University, Dresden, Germany</i>		
11.00-11.30	Coffee Break – <i>Hall 3</i>		
11.30-13.00	Parallel Symposia		
Symposium Title:	S8: Systems biology of T cell activation	S9: Proteomics and epigenetics for mammalian systems biology (HEROIC)	S12: Probing the Proteome with Binders
Room	<i>Great Hall</i>	<i>Hall 1</i>	<i>Hall 2</i>
Organisers			
Session Chair/ Introduction: 11.30-11.45	Wolfgang Schamel, <i>Freiberg, Germany</i>	Francis Stewart, Dresden, Germany	Mike Taussig, <i>Cambridge, UK</i>
11.45-12.10	Ligand discrimination by the TCR, Thomas Höfer, <i>Heidelberg, Germany</i>	Interaction analysis of SNPs discovered in genome-wide association studies (GWAS), Falk Butter, <i>Martinsried, Germany</i>	Stable binding proteins by design and evolution: towards a modular recognition code, Andreas Plückthun, <i>Zurich, Switzerland</i>
12.10-12.35	Quantitative proteomics to decipher early T cell signalling, Mogjiborahman Salek, <i>Oxford, UK</i>	Recombineering and protein tagging for systems biology, Francis Stewart, Dresden, Germany	Functional Genomics and Proteomics in Cancer Research, Jörg Hoheisel, Heidelberg, Germany
12.35-13.00	T cell differentiation in humans, Riitta Lahesmaa, <i>Turku, Finland</i>	From RNAi Screens to Molecular Function: A Systematic Pipeline for Gene Function in Mammalian Cells, Frank Bucholz, Dresden, Germany	Interaction-based protein biomarkers Mats Gullberg, <i>Uppsala, Sweden</i>
13.00-14.30	Lunch, Exhibition, Poster Session 2 – <i>Hall 3</i>		
14.30-16.00	Parallel Symposia		

Symposium Title:	S10: The PROSPECTS of proteomics	S11: Targeting high risk atherosclerotic plaques	S7: ELIXIR: Towards a sustainable infrastructure for bioinformatics research
Room	<i>Great Hall</i>	<i>Hall 1</i>	<i>Hall 2</i>
Organisers			
Session Chair:	Matthias Mann, Munich, Germany	Reijo Laaksonen, Helsinki, Finland	Andrew Lyall, Hinxton, UK
14.45-15.10	An efficient method to map the human interactome by quantitative proteomics , Nina Hubner, <i>Martinsried, Germany</i>	A disintegrin and metalloproteinases (ADAMs): Role in atherosclerosis, coronary artery disease and sudden cardiac death , Terho Lehtimäki, <i>Tampere, Finland</i>	Discovery and annotation human variation , Paul Flicek, <i>Hinxton, UK</i>
15.10-15.35	2nd Generation Proteomics: the quantitative analysis of protein properties in cell biology , Belinda Westman, <i>Dundee, UK</i>	Low density lipoprotein metabolism, hepatic lipase and coronary disease: Intriguing findings from genome wide association studies , Winfried März, <i>Augsburg, Germany</i>	The European Biomolecular Information Landscape - present and future , Graham Cameron, <i>Hinxton, UK</i>
15.35-16.00	The Antibody-based subcellular localization atlas , Emma Lundberg, <i>KTH, Sweden</i>	Lipidomics as a tool for atherosclerosis research , Reijo Laaksonen, <i>Helsinki, Finland</i>	Integrating life science related data and tools – from the molecular level to the phenotype , Søren Brunak, <i>Lyngby, Denmark</i>
16.00-16.30	Refreshment break – <i>Hall 3</i>		
	Session chair: Alfonso Valencia, <i>Madrid, Spain</i> <i>Great Hall</i>		
16.30-16.40	ST10: Mitochondrial tRNA mutations - Which can be inherited and why? Joanna Elson, <i>Newcastle University, Newcastle Upon Tyne, UK</i>		
16.40-16.50	ST11: Genome-wide expression profiling identifies a deregulated cellular network associated with human papillomavirus infection Judith Boer, <i>Leiden University Medical Center, Leiden, The Netherlands</i>		
16.50-17.00	ST12: Human host cell factors crucial for influenza virus replication identified by genome-wide RNAi screen Nikolaus Machuy, <i>Max Planck Institute, Berlin, Germany</i>		
17.00-17.45	K10: Somatic mutations in human cancer – moving towards large scale resequencing of whole cancer genomes Andy Futreal, <i>Wellcome Trust Sanger Institute, Hinxton, UK</i>		
17.45-19.15	Poster Session 2 continued – <i>Hall 3</i>		
20.00-late	Conference party (optional) – <i>Halls 4 & 5</i>		
Saturday 17th April 2010			
	Session chair: Mike Taussig, <i>Cambridge, UK</i> <i>Great Hall</i>		
10.00-10.45	K11: The Evolution of Mammalian Transcription Factor Binding Paul Flicek, <i>Wellcome Trust Sanger Institute, Hinxton, UK</i>		
10.45-11.30	K12: Time matters: Resolving dynamics in live cells on a single molecule scale Petra Schwille, <i>Technical University Dresden, Dresden, Germany</i>		
11.30-12.15	K13: Population sequencing of genomic intervals to identify variants underlying complex traits Kelly Frazer, <i>University of California, San Diego, USA</i>		
12.15-13.30	Lunch & End of Conference		