
Sunday 12 November 2017

- 11:00 - 13:00 **Arrival / Registration with light refreshments**
ATC Reception and Foyer
- 13:00 - 13:10 **Opening remarks**
ATC Auditorium
- 13:10 - 17:20 **Session 1: Recent advances in genomics, proteomics,
and metabolomics**
Chair: Nevan Krogan, University of California, San Francisco

ATC Auditorium
- 13:10 - 13:40 **Data integration to predict complex phenotypes** 1
Ruedi Aebersold
ETH Zurich, Switzerland
- 13:40 - 13:55 **An Approach to Spatiotemporally Resolve Protein
Interaction Networks in Living Cells** 2
Ruth Huttenhain
*University of California, San Francisco, United States of
America*
- 13:55 - 14:10 **Visualizing genome transcription at nucleotide resolution** 3
Andreas Mayer
Max Planck Institute for Molecular Genetics, Germany
- 14:10 - 14:40 **Single-cell epigenomics maps the continuous regulatory
landscape of human hematopoietic differentiation** 4
William Greenleaf
Stanford University, United States of America
- 14:40 - 15:20 **Coffee Break & Meet the Speakers**
ATC Foyer
- 15:20 - 15:35 **Quantitative analysis of lipidome and proteome dynamics
reveals circadian regulation of whole-body lipid
metabolism** 5
Christer Ejsing
EMBL Heidelberg, Germany

- 15:35 - 15:50 **Charting the cross-functional map of transcription factors and metabolism in human cells** 6
Karin Ortmayr
ETH Zurich, Switzerland
- 15:50 - 16:20 **Spatial single-cell metabolomics by correlative imaging** 7
Theodore Alexandrov
EMBL Heidelberg, Germany
- 16:20 - 16:50 **Coffee Break**
ATC Foyer
- 16:50 - 17:20 **CRISPRi/a for systematic interrogation of functional genomics** 8
Stanley Qi
Stanford University, United States of America
- 17:20 - 17:50 **Flash talks (1 slide / 2 min each):**
39 Kwee, # 60 Calura, #68 Da Silva Liberio, #70 Diether,
#73 Eckhardt, #79 Flynn, #97 Kelberman, #135 Perino, #155 Velten
- 17:50 - 19:20 **Poster Session I (odd numbers plus #60, #68, #70)**
ATC Helix A
- 19:20 - 21:00 **Dinner**
EMBL Canteen
- 21:00 - 22:30 **After-dinner drinks**
ATC Rooftop Lounge

Monday 13 November 2017

09:00 - 12:45	Session 2: Integrating different 'omics data Chair: Uwe Sauer, ETH Zurich ATC Auditorium	
09:00 - 09:30	The constraints of metabolism Matthias Heinemann <i>University of Groningen, The Netherlands</i>	9
09:30 - 09:45	Gene expression dynamics in dividing cells Katharina Baum <i>MDC Berlin, Germany</i>	10
09:45 - 10:00	Comprehensive characterization of protein abundance, stability and aggregation during vertebrate brain aging Alessandro Ori <i>Leibniz Institute on Aging – Fritz Lipmann Institute (FLI), Germany</i>	11
10:00 - 10:30	Integrative modeling of biomolecular assembly structures and pathways Andrej Sali <i>University of California, San Francisco, USA</i>	12
10:30 - 11:00	Coffee Break ATC Foyer	
11:00 - 11:30	Joint genetic analysis using poly-omic iPS cell models Oliver Stegle <i>EMBL-EBI, United Kingdom</i>	13
11:30 - 11:45	Integrative omics profiling within the Swedish SCAPIS SciLifeLab (S3) Wellness Profiling program Linn Fagerberg <i>Royal Institute of Technology, Sweden</i>	14
11:45 - 12:00	Molecular signatures that can be transferred across different omics platforms Michael Altenbuchinger <i>University of Regensburg, Germany</i>	15

12:00 - 12:15	Dynamic metabolomics reveals that insulin primes the adipocyte for glucose metabolism Katsuyuki Yugi <i>RIKEN, Japan</i>	16
12:15 - 12:45	From epigenetic variation across individuals to insights into disease Judith Zaugg <i>EMBL Heidelberg, Germany</i>	17
12:45 - 14:15	Lunch ATC Foyer	
14:15 - 17:25	Session 3: Post-translational modification: expanding proteome diversity beyond amino acid sequences data Chair: Vera van Noort, KU Leuven ATC Auditorium	
14:15 - 14:45	Copy number variations associated with changes in post-translational regulation in cancer Pedro Beltrao <i>EMBL-EBI, United Kingdom</i>	18
14:45 - 15:00	Deciphering Heterochromatin Proteome with Next Generation Proteomics Tania Auchynnikava <i>The University of Edinburgh, United Kingdom</i>	19
15:00 - 15:15	A kinome-scale proteome predicts and interprets the metabolome of a cell by means of artificial intelligence Aleksiej Zelezniak <i>Chalmers University of Technology, Sweden</i>	20
15:15 - 15:45	Understanding post-translational modifications Vera van Noort <i>KU Leuven, Belgium</i>	21
15:45 - 16:25	Coffee Break & Meet the Speakers ATC Foyer	

16:25 - 16:55	Proteomics for signaling and clinical studies Matthias Mann <i>Max Planck Institute of Biochemistry, Germany</i>	22
16:55 - 17:25	The functional phosphoproteome Judith Villen <i>University of Washington, United States of America</i>	23
17:25 - 17:55	Flash talks (1 slide / 2 min each): #52 Billmann, #72 Do, #76 Erola, #80 Foroutan, #112 Lindeboom, #118 Martini, #146 Siarheyev, #154 Varela Coelho	
17:55 - 19:25	Poster Session II (even numbers) ATC Helix A	
19:25 - 21:15	Banquet Dinner EMBL Canteen	
21:15 - 00:00	Conference Party with DJ ATC Foyer	

Tuesday 14 November 2017

09:00 - 12:15	Session 4: Novel 'omics technologies (including Omics and structural biology) Chair: Judith Zaugg, EMBL Heidelberg ATC Auditorium	
09:00 - 09:30	Landscape of nuclear transport receptor cargo specificity Martin Beck <i>EMBL Heidelberg, Germany</i>	24
09:30 - 09:45	Mapping epigenomic regulatory networks via coupled single cell ATAC-seq and CRISPR screens Adam Rubin <i>Stanford University, United States of America</i>	25
09:45 - 10:00	Joint profiling of chromatin accessibility, DNA methylation and transcription in single cells Ricard Argelaguet <i>EMBL-EBI, United Kingdom</i>	26
10:00 - 10:30	Multiomics approaches to study transcription regulation Patrick Cramer <i>Max Planck Institute for Biophysical Chemistry, Germany</i>	27
10:30 - 11:00	Coffee Break ATC Foyer	
11:00 - 11:30	Probing protein structural changes on a proteome-wide scale Paola Picotti <i>ETH Zurich, Switzerland</i>	28
11:30 - 11:45	A CRISPR-Cas9 Functional Genomics Platform for the Interrogation of Host-Pathogen Interactions in Primary Cell Types Judd F. Hultquist <i>J. David Gladstone Institutes, United States of America</i>	29

11:45 - 12:15	Towards a structure / function simulation of a cancer cell	30
	Trey Ideker <i>University of California, San Diego, United States of America</i>	
12:15 - 14:00	Lunch ATC Foyer	
14:00 - 17:40	Session 5: Clinical applications of multi-omics Chair: Mónica Campillos, Helmholtz Zentrum Munich ATC Auditorium	
14:00 - 14:30	Learning tumor phylogenies from single-cell data	31
	Niko Beerenwinkel <i>ETH Zurich, Switzerland</i>	
14:30 - 14:45	Identification of novel pathways linked to Bardet-Biedl Syndrome using integrated RNA-sequencing and deep proteomic profiling	32
	Rosalind Davies <i>UCL Great Ormond Street Institute of Child Health, United Kingdom</i>	
14:45 - 15:00	Predicting the cumulative output of biomedical research	33
	Thomas Stoeger <i>Northwestern University, United States of America</i>	
15:00 - 15:30	Integrative analysis of chemical high-throughput screens uncovers novel biological information	34
	Monica Campillos <i>Helmholtz Zentrum Munich, Germany</i>	
15:30 - 16:10	Coffee Break & Meet the Speakers ATC Foyer	
16:10 - 16:40	Genomics of drug sensitivity in primary blood cancers	35
	Wolfgang Huber <i>EMBL Heidelberg, Germany</i>	

16:40 - 16:55	Genetic diagnosis of rare disorders by multi-omics analysis	36
	Julien Gagneur <i>Technical University of Munich, Germany</i>	
16:55 - 17:10	Biomarker discovery and target identification through a multi-omics knowledge platform	37
	Krol Aram <i>Euretos, The Netherlands</i>	
17:10 - 17:40	The path from sugar to CO₂	38
	Joshua Rabinowitz <i>Princeton University, United States of America</i>	
17:40 - 17:50	Closing remarks	
	ATC Auditorium	

Please remember to collect your poster. Posters that have not been collected will be disposed of after the meeting.

Check your inbox when the meeting ends! You will find an email with the link to the online feedback questionnaire. Please take time to complete it!