
Wednesday 11 September 2019

- 11:00 - 13:00 **Arrival and Registration**
ATC Registration Desk
- 13:00 - 13:10 **Opening remarks**
ATC Auditorium
- 13:10 - 17:10 **Session 1 Chair: Nevan Krogan**
University of California, San Francisco, USA
ATC Auditorium
- 13:10 - 13:40 **Genome Architecture Mapping: Exploring state specific 3D** 1
Ana Pombo
Max Delbrück Center for Molecular Medicine, Germany
- 13:40 - 14:10 **From genomic data to molecular insights: statistical models to learn about gene regulation 2**
Nicholas Luscombe
The Francis Crick Institute and UCL Genetics Institute, UK
- 14:10 - 14:25 **Dissecting the mechanisms of molecular and cellular variation in human adipogenesis** 3
Daniel Alpern
EPFL, Switzerland
- 14:25 - 14:40 **Rewiring of energy metabolism drives resistance to the proteasome inhibitor bortezomib** 4
Celia Berkers
Utrecht University, The Netherlands
- 14:40 - 15:10 **Biphasic input-output relationships—there might be no such thing as too much of a good thing** 5
Hana El-Samad
University of California, San Francisco, United States of America
- 15:10 - 15:40 **Coffee Break & Meet the Speakers**
ATC Auditorium Foyer
- 15:40 - 16:10 **The power of ONE: Immunology in the age of single cell genomics** 6
Ido Amit
Weizmann Institute of Science, Israel

- 16:10 - 16:25 **Integration of single cell DNA and RNA sequencing data to unravel tumor subclones** 7
Nicola Andrea Casiraghi
German Cancer Research Center (DKFZ), EMBL Heidelberg, Germany
- 16:25 - 16:40 **Linking the tRNA epitranscriptome to cellular protein homeostasis using a novel comprehensive multi-omics approach** 8
Johannes Leufken
University of Bern, Switzerland
- 16:40 - 16:55 **The pause-initiation limit restricts transcription activation in human cells** 9
Saskia Gressel
Max Planck Institute for Biophysical Chemistry, Germany
- 16:55 - 17:10 **Multi-state synaptic phosphorylation barcodes in health and disease** 10
Marcelo Coba
University of Southern California, United States of America
- 17:10 - 17:50 **Flash talks I - selected from abstracts # 69, 73, 75, 87, 99, 129, 131, 145, 163, 183**
(1 slide / 2 min each) in ATC Auditorium
- 17:50 - 19:00 **Poster Session I and digital presentations (odd numbers)**
ATC Helix A
- 19:00 - 21:00 **Dinner**
EMBL Canteen
- 21:00 - 22:30 **After dinner drinks**
ATC Rooftop Lounge

Thursday 12 September 2019

09:00 - 12:45	Session 2 Chair: Judit Villén ATC Auditorium	
09:00 - 09:30	Single cell proteome variability in human cells Emma Lundberg <i>Science for Life Laboratory (KTH), Sweden</i>	11
09:30 - 09:45	Integrated multiomics unravels metabolic diet-microbiota-host interactions Maria Zimmermann-Kogadeeva <i>EMBL Heidelberg, Germany</i>	12
09:45 - 10:00	Contextualizing signalling pathways with genomic and transcriptomic data to dissect drug efficacy and gene essentiality in cancer Julio Saez-Rodriguez <i>Heidelberg University, Germany</i>	13
10:00 - 10:30	Title to be announced onsite Edward Marcotte <i>The University of Texas at Austin, United States of America</i>	14
10:30 - 11:00	Coffee Break & Meet the Speakers ATC Auditorium Foyer	
11:00 - 11:30	Understanding RNA binding protein function through Christopher Burge <i>Massachusetts Institute of Technology, United States of America</i>	
11:30 - 11:45	Prediction of drug-target interactions through drug and overexpression metabolome profiling Duncan Holbrook-Smith <i>ETH Zurich, Switzerland</i>	16
11:45 - 12:00	Towards improved biophysical models of protein folding to identify disease-causing mutations Amelie Stein <i>University of Copenhagen, Denmark</i>	17

- 12:00 - 12:15 **A Functional Map of HIV-Host Interactions in Primary Human T cells** 18
Joe Hiatt
University of California, San Francisco, United States of America
- 12:15 - 12:45 **Splicing kinetics and coordination revealed by direct nascent RNA sequencing through nanopores** 19
L. Stirling Churchman
Harvard Medical School, United States of America
- 12:45 - 14:15 **Lunch**
ATC Auditorium Foyer
- 14:15 - 17:15 **Session 3 Chair: Patrick Cramer**
Max Planck Institute for Biophysical Chemistry, Germany
ATC Auditorium
- 14:15 - 14:45 **Towards predicting gene expression from DNA sequence** 20
Jussi Taipale
University of Cambridge, United Kingdom
- 14:45 - 15:00 **Deciphering the Signaling Network Landscape of Breast Cancer Supports Personalized Medicine** 21
Marco Tognetti
University of Zurich, ETH Zurich, Switzerland
- 15:00 - 15:15 **A reference map of the human protein interactome reveals tissue-specific biological mechanisms** 22
Katja Luck
Dana-Farber Cancer Institute, United States of America
- 15:15 - 15:45 **Encoding of cellular multi-specificity by a model molecular switch** 23
Tanja Kortemme
University of California, San Francisco, United States of America
- 15:45 - 16:15 **Coffee Break and Meet the Speakers**
ATC Auditorium Foyer

- 16:15 - 16:45 **From Proteomes to metabolomes - how a new generation of high-throughput analytics enables the prediction of the cellular metabolome** 24
Markus Ralser
The Francis Crick Institute, United Kingdom and Charité University Medicine, Germany
- 16:45 - 17:15 **Epigenetic variation across individuals reveal insights into disease mechanisms** 25
Judith Zaugg
EMBL Heidelberg, Germany
- 17:15 - 17:50 **Flash talks II - selected from abstracts # 38, 40, 42, 56, 64, 68, 102, 128, 133, 134, 146, 148, 154, 160, 170, 176, 184**
(1 slide / 2 min each) in ATC Auditorium
- 17:50 - 19:00 **Poster Session II and digital presentations (even numbers)**
ATC Helix A
- 19:00 - 21:30 **Banquet Dinner**
EMBL Canteen
- 21:30 - 00:00 **Conference Party with DJ**
ATC Auditorium Foyer

Friday 13 September 2019

09:00 - 12:30	Session 4 Chair: Judith Zaugg ATC Auditorium	
09:00 - 09:30	Reconstructing development and regeneration using single-cell genomics Barbara Treutlein <i>ETH Zurich, Switzerland</i>	26
09:30 - 09:45	A multiomics driven approach for industrial-scale modeling of neurological disease using human induced pluripotent stem cells Robert Altshuler <i>Novartis Institutes for Biomedical Research, United States of America</i>	27
09:45 - 10:00	Native molecule sequencing by nano-ID reveals synthesis and stability of RNA isoforms Björn Schwalb <i>Max Planck Institute for Biophysical Chemistry, Germany</i>	28
10:00 - 10:30	Cell signaling as a cognitive process? Philippe Bastiaens <i>Max Planck Institute of Molecular Physiology, Germany</i>	29
10:30 - 11:00	Coffee Break & Meet the Speakers ATC Auditorium	
11:00 - 11:30	Systematic investigation of the regulation and function of alternative splicing networks Benjamin Blencowe <i>University of Toronto, Canada</i>	30
11:30 - 12:00	Systems integration of metabolomics and in vivo metabolic flux analysis reveals complex regulatory networks in diabetic complications Subramaniam Pennathur <i>University of Michigan, United States of America</i>	31

12:00 - 12:30	Proteomes in 3D Paola Picotti <i>ETH Zurich, Switzerland</i>	32
12:30 - 14:00	Lunch ATC Auditorium Foyer	
14:00 - 16:30	Session 5 Chair: Uwe Sauer <i>ETH Zurich, Switzerland</i> ATC Auditorium	
14:00 - 14:30	Integrative modeling of biomolecular assembly structures Andrej Sali <i>University of California, San Francisco, United States of America</i>	33
14:30 - 15:00	Measuring the impact of amino acid substitutions on protein function proteome-wide Judit Villén <i>University of Washington, United States of America</i>	34
15:00 - 15:30	Multiplexed probing of chromatin effects on DNA double-strand break repair. Bas van Steensel <i>The Netherlands Cancer Institute, The Netherlands</i>	35
15:30 - 16:00	Coffee Break and Meet the speakers ATC Auditorium Foyer	
16:00 - 16:15	Multi-omics define divergent gene expression regulation and drivers of esophageal squamous cell carcinoma Wei Wu <i>University of California, San Francisco, United States of America</i>	36
16:15 - 16:30	The wild metabolism of domesticated tomato – multi-omic analysis of a <i>Solanum lycopersicum-pennellii</i> introgression population Jedrzej Szymanski <i>Leibniz Institute of Plant Genetics and Crop Plant Research, Germany</i>	37

16:30 - 17:00 **Closing remarks**
ATC Auditorium

17:00 **Departure**