
Thursday 7 March 2019

- 11:00 - 12:30 **Arrival and Registration**
ATC Registration Desk
- 12:30 - 12:45 **Opening remarks**
ATC Auditorium
- 12:45 - 13:30 **Keynote Lecture 1** 1
Ubiquitin mediated regulation of transcription factor stability
Vishva Dixit
Genentech, United States of America
ATC Auditorium
- 13:30 – 16:30 **Session 1: Cell Biology**
Chair: Michal Sharon, Weizmann Institute of Science
ATC Auditorium
- 13:30 - 14:00 **MAPPING the degradation landscape via proteasomal profiling** 2
Yifat Merbl
Weizmann Institute of Science, Israel
- 14:00 - 14:30 **Dissecting oncogenic EGF receptor signaling in-vivo by quantitative interaction proteomics and phosphoproteomics** 3
Jesper Olsen
University of Copenhagen, Denmark
- 14:30 - 15:00 **Coffee Break and Meet the Speakers**
ATC Auditorium Foyer
- 15:00 - 15:30 **Exploring proteome and organelle homeostasis mechanisms using quantitative proteomics** 4
Wade Harper
Harvard Medical School, United States of America

EMBL–Wellcome Genome Campus Conference: Proteomics in Cell Biology and Disease Mechanisms

- 15:30 - 15:45 **Decoding Chromatin Modification States Using Chemical Biology and Computational Proteomics** 5
Till Bartke
Helmholtz Zentrum München, Germany
- 15:45 - 16:00 **Quantitative analysis of murine T lymphocyte proteomes** 6
Alejandro Brenes
University of Dundee, United Kingdom
- 16:00 - 16:15 **Decoding Proteostasis: Understanding how proteome foldedness changes under proteostasis stress** 7
Dezerae Cox
Bio21 Institute, University of Melbourne, Australia
- 16:15 - 16:30 **The Solute Carrier Transporters Interactome** 8
Alvaro Ingles-Prieto
CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria
- 16:30 - 17:15 **Flash talks (odd numbers – 1 slide /1 minute each)**
ATC Auditorium
- 17:15 - 19:00 **Poster Session 1 (odd numbers)**
ATC Helix A
- 19:00 - 21:00 **Dinner**
EMBL Canteen
- 21:00 - 23:00 **After Dinner Drinks**
ATC Rooftop Lounge

Friday 8 March 2019

09:00 - 12:00	Session 2: Structural Proteomics Chair: Wade Harper, Harvard Medical School ATC Auditorium	
09:00 - 09:30	Regulation of the 20S proteasome by a novel family of inhibitory proteins Michal Sharon <i>Weizmann Institute of Science, Israel</i>	9
09:30 - 10:00	Proteomic variation across individuals Martin Beck <i>EMBL Heidelberg, Germany</i>	10
10:00 - 10:45	Coffee Break and Meet the Speakers ATC Auditorium Foyer	
10:45 - 11:15	To be presented onsite Paola Picotti <i>ETH Zürich, Switzerland</i>	11
11:15 - 11:30	Enumerating the site-occupancy, complexity, and diversity of mucin type O-glycosylation on CD43 using electron transfer dissociation (ETD) mass spectrometry Vandita Dwivedi <i>National Institute of Immunology, India</i>	12
11:30 - 11:45	Cell Cycle Dependent Localization of Protocadherins Nazli Ezgi Özkan Küçük <i>Koç University, Turkey</i>	13
11:45 - 12:00	Multilayered proteomic interaction analysis identifies cancer mutations that affect the composition and function of kinase complexes Martin Mehnert <i>ETH Zürich, Switzerland</i>	14
12:00 - 13:30	Lunch ATC Auditorium Foyer	

EMBL–Wellcome Genome Campus Conference: Proteomics in Cell Biology and Disease Mechanisms

- 13:30 - 16:30 **Session 3: Proteomics from lab to the clinic**
Chair: Vishva Dixit, Genentech
ATC Auditorium
- 13:30 - 14:00 **Microscaled methods for proteogenomic analysis of patient-derived tumors** 15
Steven Carr
Broad Institute of MIT and Harvard, United States of America
- 14:00 - 14:30 **Peroxisome remodeling en route to virus replication** 16
Ileana Cristea
Princeton University, United States of America
- 14:30 - 15:00 **Novel MS scan modes applied to translational research** 17
Matthias Mann
Max Planck Institute of Biochemistry, Germany
- 15:00 - 15:30 **Coffee Break and Meet the Speakers**
ATC Auditorium Foyer
- 15:30 - 15:45 **Using Tandem Mass Tag Proteomics for the Detection of Changes in Phosphorylation State After Treatment with a Tyrosine Kinase Inhibitor, Dasatinib** 18
David Galbraith
Bristol-Myers Squibb, United States of America
- 15:45 - 16:00 **Plasma proteome profiling to detect and avoid sample-related biases in biomarker studies** 19
Philipp Geyer
Max Planck Institute of Biochemistry, Germany
- 16:00 - 16:15 **Deep Phosphoproteomics Profiling of 20 Breast Cancer Cell Lines Reveals Distinct Molecular Signaling of Triple-negative Breast Cancer** 20
Alexander Hogrebe
University of Copenhagen, Denmark

- 16:15 - 16:30 **Opposing effects of cancer-type-specific SPOP mutants** 21
Namrata Udeshi
Broad Institute of MIT and Harvard, United States of America
- 16:30 - 17:15 **Flash talks (even numbers – 1 slide /1 minute each)**
ATC Auditorium
- 17:15 - 19:00 **Poster Session 2 (even numbers)**
ATC Helix A
- 19:00 - 21:00 **Conference Dinner**
EMBL Canteen
- 21:00 - 00:00 **Conference Party**
ATC Rooftop Lounge

Saturday 9 March 2019

09:00 - 12:00	Session 4: Cell signaling Chair: Steven Carr, Broad Institute of MIT and Harvard, USA ATC Auditorium	
09:00 - 09:30	Measurements of protein motions by proteomics: The allosteric activation of ERK2 by phosphorylation Natalie Ahn <i>University of Colorado, Boulder, United States of America</i>	22
09:30 - 10:00	Unconventional Serine Ubiquitination: finding substrates, ligases and deubiquitinases Ivan Dikic <i>Goethe University Frankfurt, Germany</i>	23
10:00 - 10:30	New technologies to interrogate the dynamics and function of the phosphoproteome Judit Villen <i>University of Washington, United States of America</i>	24
10:30 - 11:00	Coffee Break and Meet the Speakers ATC Auditorium Foyer	
11:00 - 11:15	Deep proteome profiling of breast cancer cells unraveled subtype-specific pathway dysregulations Asfa Alli Shaik <i>Institute of Molecular and Cell Biology, Singapore</i>	25
11:15 - 11:30	Proteome-wide profiling of lysine deacetylase complexes with chemical probes Iris Finkemeier <i>University of Münster, Germany</i>	26
11:30 - 11:45	A Precise and Sensitive LRRK2 Kinase Activity Assay by Targeted LC-MS/MS Analysis of its Substrate Phosphorylation Stoichiometry Ozge Karayel <i>Max Planck Institute of Biochemistry, Germany</i>	27

11:45 - 12:00	Targeting the evolution of persistent clones in Jak2-mutated neoplasms Dr.Ashok Kumar Jayavelu <i>Max-Planck-Institute of Biochemistry, Germany</i>	28
12:00 - 12:15	Mining and integration of multi-species proteomics data with the Biological Knowledge Graph Rita Colaço <i>University of Copenhagen, Denmark</i>	29
12:15 - 13:30	Lunch EMBL Canteen	
13:30 - 14:30	Session 5: Integrated proteomics Chair: Judit Villen, University of Washington ATC Auditorium	
13:30 - 14:00	Deep Proteomes, iPS cells & Data Mountains Angus Lamond <i>University of Dundee, United Kingdom</i>	30
14:00 - 14:30	Functional relevance of eukaryotic protein phosphorylation Pedro Beltrao <i>EMBL-EBI, United Kingdom</i>	31
14:30 - 14:40	Poster prize ATC Auditorium	
14:40 - 15:25	Keynote Lecture 2 Integrative studies of Ubiquitin Signaling Brenda Schulman <i>Max Planck Institute of Biochemistry, Germany</i> ATC Auditorium	32
15:25 - 15:30	Closing remarks ATC Auditorium	
15:45	Departure (buses to Frankfurt Airport and Downtown)	

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!