



From Functional Genomics to Systems Biology

EMBL CONFERENCE

We have moved our website to embl.org/events. The content below is no longer being updated.

EMBL Courses and Conferences during the Coronavirus pandemic

With the onsite programme paused, many of our events are now being offered in virtual formats.

Registration is open as usual for many events, with back-up plans in place to move further courses and conferences online as necessary. Registration fees for any events affected by the COVID-19 disruption are fully refundable.

More information for participants of events at EMBL Heidelberg can be found [here](#).

Programme

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Day 1 - Saturday 10 November

Time	Speaker
13:00-15:00	Registration and Lunch
15:00-15:05	Welcome remarks
15:05-18:50	Session I Chair: Eileen Furlong - EMBL Heidelberg, Germany
15:05-15:35	Nascent transcription profiling in single cells by intron seqFISH Long Cai - California Institute of Technology, USA
15:35-16:05	Proteome dynamics Matthias Selbach - Max Delbrück Center for Molecular Medicine, Germany

Time	Speaker
16:05-16:20	Determining protein structures using genetics Joern Schmiedel - Centre for Genomic Regulation (CRG), Spain
16:20-16:50	High throughput yeast library generation for comparative cell analyses Michael Knop - ZMBH, University of Heidelberg, Germany
16:50-17:20	Coffee Break
17:20-17:50	Integration of local and regional cis-regulatory information Barak Cohen - Washington University in St. Louis, USA
17:50-18:05	Perturbing shape readout in vitro and in vivo provides mechanistic insight into adaptive DNA recognition by a multi-homeodomain complex Judith Kribelbauer
18:05-18:20	Using single-cell transcriptomics and planarians to study stem cells, their differentiation and their evolution Jordi Solana - Oxford Brookes University, UK
18:20-18:50	Reconstructing axolotl limb regeneration using single-cell transcriptomics Barbara Treutlein - Max Planck Institute for Evolutionary Anthropology, Germany
19:00-21:00	Dinner in the Canteen
21:00-23:00	Drinks in ATC Roof Top Lounge

Day 2 - Sunday 11 November

Time	Speaker
09:00-12:45	Session II Chair: Barbara Treutlein - Max Planck Institute for Evolutionary Anthropology, Germany
09:00-09:30	Thermal stability and solubility in molecular biology Mikhail Savitski - EMBL Heidelberg, Germany
09:30-10:00	Using Machine Learning to Detect Enhancer Variation and Evolutionary Conservation Michael Beer - Johns Hopkins University, USA

Time	Speaker
10:00-10:15	A rare codon-based translational program drives cell proliferation Joao Guimaraes - University of Basel, Switzerland
10:15-10:45	Understanding cell-fate decisions to non-lethal dose of chemotherapy Lani Wu - University of California San Francisco, USA
10:45-11:15	Coffee Break
11:15-11:45	The functional relevance of eukaryotic protein phosphorylation Pedro Beltrao - EMBL-EBI Hinxton, UK
11:45-12:00	The Single Cell Landscape of Breast Cancer Hartland Jackson - University of Zurich, Switzerland
12:00-12:15	Engineered chromatin readers reveal the proteome composition at key chromatin states in living cells Baubec Tuncay - University of Zurich, Switzerland
12:15-12:45	DNA binding bispecificity by forkhead transcription factors Martha Bulyk - Harvard Medical School, USA
12:45-14:00	Lunch
14:00-16:30	Poster Session I: Odd numbers
16:30-19:30	Session III - Chair: Joshua Coon - University of Wisconsin, USA
16:30-17:00	New technology for rapid and comprehensive proteome analysis Joshua Coon - University of Wisconsin, USA
17:00-17:15	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline Natalie Romanov - EMBL Heidelberg, Germany
17:15-17:45	Mapping cellular memory at single cell resolution Amos Tanay - Weizmann Institute, Israel
17:45-18:15	Coffee Break
18:15-18:45	Understanding enhancer usage during embryonic development at a single cell level Eileen Furlong - EMBL Heidelberg, Germany
18:45-19:00	Decoding Chromatin Modification States Using Chemical Biology and Computational Proteomics Till Bartke

Time	Speaker
19:00-19:30	Big data and health Mike Snyder - Stanford University, USA
19:30-21:00	Dinner in the Canteen
21:00-23:00	Drinks in ATC Roof Top Lounge

Day 3 - Monday 12 November

Time	Speaker
09:00-12:45	Session IV - Chair: Arnaud Krebs - EMBL Heidelberg, Germany
09:00-09:30	Probing protein structural changes on a proteome-wide scale Paola Picotti - ETH Zurich, Switzerland
09:30-09:45	Meiotic Sex Chromosome Inactivation in the <i>Drosophila melanogaster</i> male germline Brian Oliver - NIH, USA
09:45-10:00	Comprehensive characterization of protein abundance, stability and aggregation during vertebrate brain aging Alessandro Ori - Leibniz Institute on Aging - Fritz Lipmann Institute, Germany
10:00-10:15	Single cell expression analysis uncouples transdifferentiation and reprogramming Mirko Francesconi - CRG, Spain
10:15-10:45	Lineage estimation from single-cell RNA-seq time-series Fabian Theis - Helmholtz Zentrum München, Germany
10:45-11:15	Coffee Break
11:15-11:30	Transcription factor activity and nucleosome organisation in mitosis <i>Nick Owens, Institut Pasteur</i>
11:30 - 11:45	Stress response dynamics that span different signaling pathways Rati Sharma, <i>Harvard University</i>
11:45-12:00	Predicting complex genetic phenotypes using error propagation in weighted networks Andrei Kucharavy - Johns Hopkins University, USA
12:00-12:15	Mutations in disordered regions can cause disease by creating dileucine motifs Katrina Meyer - Max Delbrück Center for Molecular Medicine in the Helmholtz Association, German

Time	Speaker
12:15-12:45	Proximity-dependent biotinylation as a tool to understand cellular signaling: revisiting Target of Rapamycin signaling Anne-Claude Gingras - Lunenfeld-Tanenbaum Research Institute, Canada
12:45-14:00	Lunch, ATC Foyer
14:00-16:30	Poster Session II: Even numbers
16:30-19:30	Session V - Chair: Paola Picotti , ETH Zurich, Switzerland
16:30-17:00	The tool of revelation: ionbot uncovers an exciting new view on the proteome Lennart Martens - Ghent University, Belgium
17:00-17:15	Decoding SOX10 gene regulatory programs using time-series, single-cell, and cross-species chromatin profiling Liesbeth Minnoye - VIB - KU Leuven, Belgium
17:15-17:45	Understanding principles of transcription regulation at the resolution of single DNA molecules Arnaud Krebs - EMBL Heidelberg, Germany
17:45-18:15	Coffee Break
18:15-18:45	Genome-wide analysis of protein-DNA interactions Jussi Taipale - Karolinska Institutet, Sweden
18:45-19:00	Identifying protein interactions relevant in cancer development Marija Buljan - ETH Zurich, Institute of Molecular Systems Biology, Switzerland
19:00-19:30	The Ups and Downs of Protein Expression Regulation in Response to Misfolding Stress Christine Vogel - New York University, USA
19:30-24:00	Gala Dinner and party in the ATC

Day 4 - Tuesday 13 November

Time	Speaker
09:00-12:45	Session VI - Chair: Mikhail Savitski , EMBL Heidelberg, Germany
09:00-09:30	Functional characterization and therapeutic targeting of gene regulatory elements Nadav Ahituv - University of California, San Francisco, USA

Time	Speaker
09:30-09:45	Mechanisms of neurogenic gene expression – Specific enhancer-regulator interactions with spatiotemporal resolution Ana Luisa Guimarães - BIMS-BMDC, Germany
09:45-10:00	In vivo phosphoproteomics reveals pathogenic signaling changes in diabetic islets Francesca Sacco - University of Rome Tor Vergata, Italy
10:00-10:15	Divergent enhancers underlying rapid adaptation in natural stickleback populations Stanley Neufeld - MPI for Developmental Biology, Germany
10:15-10:45	Identifying deleterious mutations across the proteome by limited mistranslation mutagenesis Judith Villen - University of Washington, USA
10:45-11:15	Coffee Break
11:15-11:45	Proteomics for translational research Matthias Mann - Max Planck Institute of Biochemistry, Germany
11:45-12:00	Leveraging transcription factor cooperativity for the discovery of protein-phenotype interactions Ignacio Ibarra - EMBL Heidelberg, Germany
12:00-12:15	Clock-dependent chromatin topology modulates circadian transcription and behaviour Jake Yeung - École Polytechnique Fédérale de Lausanne, Switzerland
12:15-12:45	Multiplexed protein maps link subcellular organization to cellular states Lucas Pelkmans - University of Zurich, Switzerland
12:45-13:00	Closing Remarks
13:00	Packed lunch
13:15	Buses downtown and Frankfurt Airport