

Transcription and Chromatin

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 The content below is no longer being updated.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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HIDE ALL

Day 1 - Saturday 25 August 2018

Time	Speaker
15:00-18:00	Arrival and Registration ATC Registration Desk
16:30 - 17:30	Pre-Conference Workshop ATC Courtyard Seminar Room
18:00-18:15	Welcome and Opening Remarks ATC Auditorium
18:15–20:00	Session 1 Chair: Eileen Furlong - EMBL Heidelberg, Germany

Time	Speaker
18:15-18:35	FIREnano and ChromEMT: Visualizing the structural basis of gene activation and silencing in the nucleus Clodagh O'Shea - Salk Institute for Biological Studies, United States of America
18:35-18:55	Gene Expression Within the Context of a Topologically Associating Domain Douglas Higgs - University of Oxford, United Kingdom
18:55-19:10	RNA-mediated regulation of chromatin complexes Roberto Bonasio - <i>University of Pennsylvania, United States of America</i>
19:10-19:25	Decoding the chromatin proteome of a single genomic locus by DNA sequencing Fred van Leeuwen - Netherlands Cancer Institute, The Netherlands
19:25-19:45	Epigenetic Regulation of HIV Transcription Melanie Ott - University of California San Francisco, United States of America
19:45-20:05	A sequence anomaly of the MLL promoter imposes a transcription factor addiction in leukemia Chris Vakoc - Cold Spring Harbor Laboratory, United States of America
20:05-21:30	Dinner EMBL Canteen
21:30-23:00	Welcome Reception ATC Foyer and Roof Top Lounge

Day 2 - Sunday 26 August 2018

Time	Speaker
09:00-12:40	Session 2 Co-Chairs: Peter Verrijzer - <i>Erasmus MC, The Netherlands</i> Wendy Bickmore - <i>The University of Edinburgh, United Kingdom</i>
09:00-09:20	The Argonaut NRDE-3 and MET-2 redundantly target SET-25 to transposable elements and genes Jan Padeken - Friedrich Miescher Institute for Biomedical Research, Switzerland
09:20-09:40	Induced activation of Polycomb-repressed genes in mice Haruhiko Koseki - Laboratory for Developmental Genetics RIKEN, Japan

Time	Speaker
09:40-09:55	Independent and overlapping roles of PRC2.1 and PRC2.2 complexes in the localisation of H3K27me2 and H3K27me3 in ESCs Adrian Bracken - <i>Trinity College Dublin, Ireland</i>
09:55-10:10	Comprehensive theoretical analysis of the Polycomb – Trithorax system predicts that poised chromatin is robustly bistable and minimally bivalent Leonie Ringrose - Humboldt University, Germany
10:10-10:25	Targeting the X chromosome for dosage compensation Peter Becker - Ludwig-Maximilians-Universität München, Germany
10:25-10:45	Molecular basis of chromatin binding and modification by histone lysine methyltransferases Jürg Müller - Max Planck Institute of Biochemistry, Germany
10:45-11:15	Coffee break ATC Foyer
11:15-11:35	GPIF limits Polycomb Repressive Complex 2 activity in mammalian germ cells Raphaël Margueron - Institut Curie, France
11:35-11:50	EMBO Young Investigator Lecture Modelling the pathological long-range regulatory effects of structural variation with patient-specific hiPSC Alvaro Rada-Iglesias - University of Cologne, Germany
11:50-12:05	Telobox motifs recruit CLF/SWN-PRC2 for H3K27me3 deposition via TRB factors in Arabidopsis Franziska Turck - <i>Max Planck Institute for Plant Breeding Research,</i> <i>Germany</i>
12:05-12:20	Recruitment of Polycomb Repressive Complex 2 by MTF2 in embryonic stem cells contributes to lineage specification Gert Veenstra - <i>Radboud University, The Netherlands</i>
12:20-12:40	The Epigenetic Status of some Histone Post-Translational Modifications Danny Reinberg - Howard Hughes Medical Institute at NYU School of Medicine, United States of America
12:40-14:30	Lunch EMBL Canteen
14:30-17:00	Poster Session 1: Odd numbers ATC Helices A & B

Time	Speaker
17:00-19:20	Session 3 Chair: Michael Levine - Princeton University, United States of America
17:00-17:20	Deciphering Transcriptional Regulation of Human Core Promoters Eran Segal - Weizmann Institute of Science, Israel
17:20-17:40	Transcriptional cofactors display core promoter class-specificity Alexander Stark - IMP, Vienna, Austria
17:40-17:55	The Evolution of Long-range Gene Regulation at the HoxD locus Denis Duboule - University of Geneva and École Polytechnique Fédérale de Lausanne, Switzerland
17:55-18:10	Exploring the Molecular Basis of Cis-Regulatory Robustness uncovers a Playground for Adaptation of Gene Expression during Evolutionary Diversification of Vertebrate Limbs Rolf Zeller - University of Basel, Switzerland
18:10-18:25	Functional insights into genome topology and enhancer function during embryonic development Eileen Furlong - <i>EMBL, Heidelberg, Germany</i>
18:25-18:40	GRO-Seq data resource for identification of pri-miRNAs and keystone enhancers Minna Kaikkonen - <i>University of Eastern Finland</i>
18:40-19:00	The Remote Control of Gene Expression Wendy Bickmore - The University of Edinburgh, United Kingdom
19:00-19:15	Dynamics of X-chromosome organisation in the context of genome- wide changes during early mouse embryo development Samuel Collombet - <i>Institut Curie, France</i>
19:20-21:30	Dinner EMBL Canteen
21:30-23:00	After Dinner Drinks ATC Foyer and Rooftop Lounge

Day 3 - Monday 27 August 2018

Time	Speaker
	Session 4
	Co-Chairs:
09:00-12:40	Karen Adelman - Harvard Medical School, United States of America
	Denis Duboule - University of Geneva and Ecole polytechnique fédérale
	de Lausanne, Switzerland

Time	Speaker
09:00-09:20	Variable silencing of the repeat genome – implications for non- genetic inheritance Anne Ferguson-Smith, University of Cambridge, United Kingdom
09:20-09:40	A single ubiquitylation site in RNA Polymerase II regulates the transcriptional response to UV damage Jesper Svejstrup - The Francis Crick Institute, United Kingdom
09:40-09:55	Long-range chromatin interactions on the inactive X and at Hox clusters are regulated by the non-canonical SMC protein Smchd1 Marnie Blewitt - Walter and Eliza Hall Institute for Medical Research, Australia
09:55-10:10	Parallel assessment of enhancer activity in distinct cell types of a complex mammalian tissue Arnaud Krebs - <i>EMBL Heidelberg, Germany</i>
10:10-10:25	Beyond transcription amplification: MYC-driven oncogenic enhancer reprogramming favors the onset of tumorigenesis by inducing a stem cell-like state Alessio Zippo - <i>University of Trento, Italy</i>
10:25-10:45	Common Threads: Metabolism, Epigenetics and the Circadian Clock Paolo Sassone-Corsi - University of California Irvine, United States of America
10:45-11:15	Coffee Break ATC Foyer
11:15-11:35	To be presented onsite Xavier Darzacq - University of California Berkeley, USA
11:35-11:50	Chromatin structure shapes the diffusion dynamics of transcription factors Nacho Molina - <i>CERBM</i> – <i>Institute of Genetics and Molecular and Cellular</i> <i>Biology (IGBMC), France</i>
11:50-12:05	Mitotic chromosome association predicts genome-wide transcription factor occupancy and impact on local chromatin accessibility David Suter - École Polytechnique Fédérale de Lausanne, Switzerland
12:05-12:20	Time-Resolved Analysis Reveals Rapid Dynamics and Broad Scope of the CBP/p300 Acetylome Chunaram Choudhary - <i>University of Copenhagen, Denmark</i>

Time	Speaker
12:20-12:40	Visualization of Transcription Hubs in Living Drosophila Embryos Michael Levine - Princeton University, United States of America
12:40-14:30	Lunch ATC Foyer
14:30-17:00	Poster Session 2: Even numbers ATC Helices A & B
17.00-19:20	Session 5 Chair: Marc Timmers - University of Freiburg, Germany
17:00-17:20	SWI/SNF (BAF) chromatin remodeling complexes are frequently mutated in cancer: Mechanisms and vulnerabilities Charles Roberts - St. Jude Children's Research Hospital, United States of America
17:20-17:40	Phase-separation mechanisms in heterochromatin Geeta Narlikar - University of California, San Francisco, United States of America
17:40-17:55	Transcription and chromatin control by ubiquitin specific protease 7 (USP7) Peter Verrijzer - <i>Erasmus MC, The Netherlands</i>
17:55-18:10	Targeted degradation of BRD9 reverses oncogenic gene expression in synovial sarcoma Gerard Brien - <i>Trinity College Dublin, Ireland</i>
18:10-18:25	Click Chemistry Enables Preclinical Evaluation Of Targeted Epigenetic Therapies Paola Grandi - <i>Cellzome, Germany</i>
18:25-18:40	Implementation of the histone acetyl transferase modules in the SAGA and NuA4 co-activators Patrick Schultz - Institute of Genetics and Molecular and Cellular Biology (IGBMC), France
18:40-19:00	Deconstructing the Relationship between Chromatin and Transcription during Ultradian Metabolic Cycles Jane Mellor - University of Oxford, United Kingdom
19:00-19:20	Principles of Epigenetics and Chromatin in Development and Human Disease Ali Shilatifard - Northwestern University Feinberg School of Medicine, United States of America

Time	Speaker
19:20-21:30	Dinner EMBL Canteen
21:30-23:00	After Dinner Drinks ATC Foyer and ATC Rooftop Lounge

Day 4 - Tuesday 28 August 2018

Time	Speaker
09:00-12:40	Session 6 Co-Chairs: Tony Kouzarides - University of Cambridge, United Kingdom Katherine Jones - Salk Institute for Biological Studies, United States of America
09:00-09:20	A molecular mechanism for RNA polymerase II activation Patrick Cramer - Max Planck Institute for Biophysical Chemistry, Germany
09:20-09:40	The RNAPII CTD kinase, CDK12, cooperates with mTORC1 to regulate gene-specific translation of protein critical for mitotic genome stability Katherine Jones - Salk Institute for Biological Studies, United States of America
09:40-09:55	Making sense of non-coding transcription at enhancers Karen Adelman - Harvard Medical School, United States of America
09:55-10:10	Transcription termination and genome organisation Jean-Christophe Andrau - CNRS, France
10:10-10:25	PHF3 binds RNA polymerase II via the SPOC domain and regulates transcription of neuronal genes Dea Slade - University of Vienna, Austria
10:25-10:45	The TRiC/CCT chaperonin complex acts as a checkpoint in assembly of the basal transcription factor TFIID Marc Timmers - University of Freiburg, Germany
10:45-11:15	Coffee Break ATC Foyer

Time	Speaker
11:15-11:35	Epigenetic modulation of a preserved 3D chromatin landscape in two distinct states of pluripotency Henk Stunnenberg - Radboud Institute for Molecular Life Sciences, Radboud University Nijmegen, The Netherlands
11:35-11:50	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region Andrew Oldfield - <i>IGH, France</i>
11:50-12:05	Recruitment of chromatin remodeler Isw1b depends both on histone H3K36 methylation and DNA-binding Michaela Smolle - <i>Biomedical Center, Ludwig-Maximilians-Universität</i> <i>München, Germany</i>
12:05-12:20	Targeting nucleosomes by transcription factors in reprogramming Abdenour Soufi - University of Edinburgh, United Kingdom
12:20-12:40	Transposable elements, their controllers and the speciation of human early embryogenesis Didier Trono - École Polytechnique Fédérale de Lausanne, Switzerland
12:40-14:30	Lunch ATC Foyer
14:30-17:00	Poster Session 3: Odd and even numbers ATC Helices A & B
17:00-19:30	Session 7 Chair: Henk Stunnenberg - Radboud Institute for Molecular Life Sciences, Radboud University Nijmegen, The Netherlands
17:00-17:20	Mechanisms of reprogramming to pluripotency Kathrin Plath - University of California Los Angeles, United States of America
17:20-17:40	A GADD45a-ING1-C/EBP axis regulates energy homeostasis and organismal aging Christof Niehrs -Institute of Molecular Biology (IMB), Germany
17:40-17:55	Repression of divergent noncoding transcription by a sequence- specific transcription factor Folkert van Werven - <i>The Francis Crick Institute, United Kingdom</i>

Time	Speaker
17:55-18:10	Transcription factors activate genes through the phase separation capacity of their activation domains Ann Boija - <i>Whitehead Institute for Biomedical Research, United States of</i> <i>America</i>
18:10-18:25	Co-translation drives the assembly of mammalian transcription regulatory multi-subunit complexes Laszlo Tora - <i>Institute of Genetics and Molecular and Cellular Biology</i> <i>(IGBMC), France</i>
18:25-18:45	Probing the transcriptional consequences of Ras and Rho activation Richard Treisman - The Francis Crick Institute, United Kingdom
18:45-19:05	Modifications of RNA: their function and role in cancer Tony Kouzarides - Gurdon Institute, University of Cambridge, United Kingdom
19:05-19:15	Closing Remarks
19:30-01:00	Dinner and Party EMBL Canteen and ATC Foyer