

Program

EPICHROM 2020

Swedish Epigenetics and Chromatin Meeting

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UMEÅ UNIVERSITY

FEB 27-28, 2020



<https://icelab.se/event/epichrom-2020/>

Detailed schedule

Thursday, February 27th

8:00	Registration opens
8:50	Welcome
9:00 – 10:00	Session 1 Chair: Ludvig Lizana, Umeå University, Sweden
9:00	Keynote: Martin Howard, John Innes Centre, UK <i>Dissecting the mechanistic basis of Polycomb epigenetic memory: fusing mathematical modelling with experiments</i>
9:40	Marcel Tarbier, SciLifeLab, Stockholm University, Sweden <i>Dissecting gene regulation at the single-cell level</i>
10:00 – 10:30	Coffee break
10:30 – 11:55	Session 2 Chair: Francesca Aguilo, Umeå University, Sweden
10:30	Plenary: Cristian Bellodi, Lund University, Sweden <i>Selective translation control by pseudouridine-modified tRNA fragments in stem and cancer cells</i>
11:00	Cyrinne Achour, Umeå University, Sweden <i>Investigation of a Non-Canonical Role for METTL3 in Breast Cancer</i>
11:20	Simon Elsässer, SciLifeLab, Karolinska Institutet, Sweden <i>High resolution mapping of native G-quadruplexes in the mammalian genome</i>
11:40	Angela Garding, Covaris (sponsored) <i>Standardizing chromatin sample preparation for epigenomics applications</i>
11:55 – 13:30	Lunch at Universum
13:30 – 15:20	Session 3 Chair: Yuri Schwartz, Umeå University, Sweden
13:30	Keynote: Lluís Morey, University of Miami, USA <i>Epigenetic mechanisms in breast cancer</i>
14:10	Juan Ignacio Barrasa López, Umeå University, Sweden <i>Human Polycomb Complexes: Aiming the target</i>
14:30	Patrick Nylund, Uppsala University, Sweden <i>A distinct metabolic response defines sensitivity to EZH2 inhibition in multiple myeloma</i>
14:50	Plenary: Francisca Lottersberger, Linköping University, Sweden <i>Nuclear architecture influences chromatin mobility and DNA damage repair</i>
15:20 – 15:50	Coffee break
15:50 – 17:15	Session 4 Chair: Åsa Strand, Umeå University, Sweden
15:50	Plenary: Claudia Köhler, Swedish University of Agricultural Sciences, Sweden <i>Domesticated transposable elements regulate imprinted genes in plants</i>

- 16:20 Marti Quevedo Calero, Umeå University, Sweden
Interplay between epigenetics and cellular metabolic state during the establishment of photosynthesis
- 16:40 Roshan Vaid, Stockholm University, Sweden
Release of promoter-proximal paused Pol II in response to histone deacetylase inhibition
- 17:00 – 17:20 **Pitch your poster**
- Pamela Akuwudike, Stockholm University, Sweden
Long term effects of fractionated radiation exposure on cancer induction in normal cells
 - Alba Atienza-Párraga, Uppsala University, Sweden
The rewiring of the multiple myeloma epigenome underlies its sensitivity to DNMT and EZH2 inhibition.
 - Nidal Ghosheh, University of Skövde, Sweden
DNA hypermethylation underlies the suppression of important ADME genes in human pluripotent stem cells derived hepatocytes
 - Thomas Grundström, Umeå University, Sweden
Regulation of differential DNA damage and repair in diversification and affinity maturation of antibodies
 - Lucas Hedström, Umeå University, Sweden
Zooming in Hi-C maps with Convolutional Neural Networks
 - Johan Henriksson, Umeå University, Sweden
Predicting regulators of T helper cell gene expression
 - Shujing Liu, Swedish University of Agricultural Sciences, Sweden
*Histone H2A ubiquitination is not required for PRC1-mediated H3K27 trimethylation in the liverwort *Marchantia polymorpha**
 - Lovisa Örkenby, Linköping University, Sweden
*Early embryonic heat shock results in rapid changes of small non-coding RNA and long-term epigenetic memories in *Drosophila**
 - Denise Rawcliffe, Umeå University, Sweden
*Binding partners of autosome-specific POF protein in *Drosophila melanogaster**
 - Kanwal Tariq, Stockholm University, Sweden
*Non-coding transcripts, *IGS32as* and *IGS38s*, regulate rDNA and upstream spacer promoter*
- 18:00 – 19:00 **Private visit at Bildmuseet**
- 19:00 – 21:00 **Poster Session** (Bildmuseet)
Dinner and drinks will be served

Friday, February 28th

- 8:30-10:05 **Session 5**
Chair: Silvia Remeseiro, Umeå University, Sweden
- 8:30 **Keynote:** Ana Losada, CNIO, Spain
Two distinct cohesin complexes with specialized functions in genome folding
- 9:10 Andreas Hörnblad, Umeå University, Sweden
PAN-AMPK activator O304 reverts gene expression changes and remobilisation of histone marks in diet-induced obese mice
- 9:30 Peter Svensson, Karolinska Institutet, Sweden
HIV-1 and chromatin: hiding from the cells defense systems by impersonating an enhancer
- 9:50 Sarantis Chlamydas, Active Motif (sponsored)
Epigenetics in the era of Omics
- 10:05-10:30 **Coffee break**
- 10:30 – 11:55 **Session 6**
Chair: Jan Larsson, Umeå University, Sweden
- 10:30 **Plenary:** Claudia Kutter, Karolinska Institutet, Sweden
Slimming down liver cancer cells with lincRNAs
- 11:00 Klaus Tangsgaard, New England Biolabs (sponsored)
Enzymatic Methyl-Seq: Next Generation Methylomes
- 11:15 Galina Zheleznyakova, Karolinska Institutet, Sweden
Genome-wide small non-coding RNA analysis in patients with Multiple Sclerosis
- 11:35 Jingwen Wang, SciLifeLab, Karolinska Institutet, Sweden
Improved transcriptome annotation and read-through transcript identification with TIF-Seq2
- 11:55 – 13:00 **Lunch at KBC**
- 13:00 – 14:40 **Session 7**
Chair: Yuri Schwartz, Umeå University, Sweden
- 13:00 **Keynote:** Xin Chen, Johns Hopkins University, Sweden
Breaking symmetry: asymmetric histone inheritance
- 13:40 Sandhya Malla, Umeå University, Sweden
Interplay between Histone regulation and DNA methylation
- 14:00 Malin Ueberschår, Stockholm University, Sweden
BEN-solo factors partition active chromatin to ensure proper gene activation in Drosophila
- 14:20 **Concluding Remarks**