

Epichrom 2025 program

12th of June 2025

Albano Campus – Hus 1, Hörsal 1, Albanovägen 32

<https://maps.app.goo.gl/w8zVeu4EqAk58qh27>

Registration 8:30 – 9:00

Block 1 – Epigenetic regulation in the brain

9:00-9:10 Welcome and organization – Mattias Mannervik

Chair: Mattias Mannervik

9:10-9:30 **Fereshteh Dorazehi (Lund University):** MORC2 directs transcription-dependent CpG methylation of the repetitive human genome in early neurodevelopment.

9:30-9:50 **José Ramón Bárcenas Walls (Stockholm University):** Epigenomic atlas of the human forebrain at single-cell resolution

9:50-10:10 **Silvia Remeseiro (Wallenberg Centre for Molecular Medicine, Umeå University):** Deciphering neuron-to-glioma synapses through 3D genomics and epigenetics data

10:10-10:30 **Vivien Horvath (Lund University):** Age-associated DNA methylation alterations as a potential causal mechanism of a transposon-mediated brain disorder

10:30-11:00 Coffee break

Block 2 – Chromatin modifiers and epigenetic control

Chair: Anki Östlund Farrants

11:00-11:20 **Astradeni Efthymiadou (Karolinska Institute):** Non-redundant roles of the HDAC3 corepressor complex subunits SMRT and NCOR in controlling inflammatory and metabolic macrophage pathways *Before 2pm

11:20-11:40 **Berta Garrido Zabala (Uppsala University):** Dual targeting of G9a and DNMTs effectively induces tumour cell death in multiple myeloma

11:40-12:00 **Vladislav Kuzin (Karolinska Institute):** Unraveling the Role of TOP2A and Repetitive Elements in Chromosomal Translocation

12:00-12:20 **Yuri Schwartz (Umeå University):** Polycomb repression works without Siesta

12:20-14:00 Lunch and poster session

Block 3 – Emerging technologies and their applications

Chair: Marek Bartosovic

- 14:00-14:20 **Serhat Aktay (KTH):** Mapping the functional genomic landscape using divergent transcription analysis of PRO-seq data
- 14:20-14:40 **Mikhail Panfilov (Uppsala University):** Mechanistic insights into DNA movement during chromatin remodeling
- 14:40-15:00 **Maria Needhamsen (Karolinska Institute):** Long-read Sequencing: Virus Characterization, HLA haplotyping and Hydroxymethylation Profiling of Human Neurons
- 15:00-15:20 **Bastien Herve (Karolinska Institute):** – Deciphering multiple sclerosis lesions via multiomics and DBiT sequencing
- 15:20-15:50 Coffee break

Block 4 – Chromatin and epigenetic regulation of development

Chair: Mattias Mannervik

- 15:50-16:10 **Yorick van de Grift (Linköping University):** Intestinal Cell Identity Decisions: a WNT-WNT situation
- 16:10-16:30 **Alek Erickson (Stockholm University):** Atlas of human facial development reveals enhancers of mesenchymal patterning genes
- 16:30-16:50 **Alessandro Gozzo (Linköping University):** Paternal Argonaute proteins control sperm-borne mitochondrial small RNA and embryonic metabolism
- 16:50-17:10 **Violeta de Anca Prado (Uppsala University):** Genetic and germ line methylomic consequences following a multigenerational exposure related to metabolic diseases in mouse.
- 17:10-17:30 **Artemy Zhigulev (KTH):** Rare gain-of-function regulatory mutations explain the missing heritability of bicuspid aortic valve
- 17:30-17:35 Conclusion
- 17:35 - onwards Mingle with food and drinks

Sponsors:

