MPI-NAT SEMINAR SERIES

Anniina Vihervaara

KTH Royal Institute of Technology, Stockholm, Sweden

Tracking mechanisms of transcription and molecular modifications of engaged Pol II at nucleotide resolution

Dynamic regulation of RNA polymerases at promoters and enhancers defines transcriptional programs in health and disease. In human cells, 3 billion nucleotide pairs encode the instructions for RNA and protein synthesis, a code that is read by thousands of transcription factors and their co-regulators. How distinct cells utilise the genetic code is coordinated by dynamic DNA-protein interactions at promoters and distal regulatory elements, ultimately orchestrating RNA polymerase (Pol I-III) molecules across the genome. Crucial to mechanistic understanding of transcription and its regulation is uncovering the detailed promoter and enhancer architecture and tracking engaged Pol I-III machineries through the rate-limiting steps of transcription. To investigate transcription and its regulation, my lab uses and develops techniques that uncover detailed positions of transcription regulators at promoters and enhancers, identify interactions between distant elements, and monitor the process of transcription at nucleotide-resolution. Here, I will describe our recent biochemical and computational advances in tracking the molecular composition of engaged RNA Polymerases at nucleotide-resolution genome-wide. I will then set the molecular mechanisms into biological context by discussing how cells can rapidly reprogram transcription upon acute stress, precisely restore the cell type-specific gene expression program upon recovery, and encode a memory of the encountered stress. The stress-induced transcription is contrasted to mechanisms that reprogram transcription in differentiating cells, showing slow but persistent changes, and using master regulators of both differentiation and stress.

Thursday, 07.12.2023, 01:00 pm

Host: Kristina Zumer
Department of Molecular Biology

Seminar Room, 2nd floor, T4
Fassberg Campus

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