MAY 20th 2025 | 4:00PM CET VIRTUAL

iPSZÜRICH

A Lecture Series Focused on Induced Pluripotent Stem Cells

MAX DELBRÜCK CENTER

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FROM MULTI-OMICS TO MECHANISMS OF CHROMATIN REGULATION IN CELL DIFFERENTIATION AND DISEASES

The epigenetic landscape is a crucial factor in defining cell types and their developmental stages, where the precise positioning of chromatin modifications controls the activity of regulatory regions and gene expression during cell differentiation. Increasing number of studies in recent years report *de novo* point mutations in chromatin-modifying proteins that cause neurodevelopmental and cardiovascular disorders, but the underlying mechanisms of these pathological mutations remain unclear. One of the main focuses of our lab is on dissecting the molecular consequences of pathological mutations in chromatin-modifying proteins (in particular, in histone demethylase LSD1/KDM1A) using CRISPR-engineered human iPSCs. Using induced neurons, endothelial cells, and cardiomyocytes, and 2D and 3D model systems—including neuron-microglia co-cultures, cortical organoids, and vessels-on-chip—we study the impact of chromatin dysfunction across tissues. Through integrated omics and chromatin-aware gene regulatory network inference, we identify molecular pathways and cell type–resolved gene networks perturbed by epigenetic mutations. Our work bridges systems biology, state-of-the-art computational approaches and stem cell technologies to dissect diesease mechanisms from large omics data, emphasizing the importance of chromatin regulation in orchestrating cell fate decisions.