

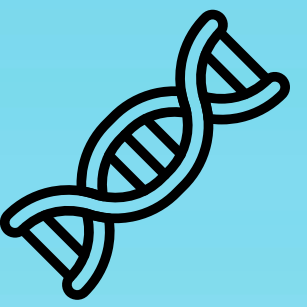


UNIVERSITÀ
DI TRENTO

Dipartimento di
Biologia Cellulare,
Computazionale e Integrata - CIBIO

NEURO & CANCER
epigenetic

mini symposium



Giuseppe Diaferia

*Botton-Champalimaud
Pancreatic Cancer Centre*

14

September
at 2.30 pm

Room B108
POVO 2



EPIGENETIC DRIVERS OF TRANSCRIPTIONAL PLASTICITY AND NEURAL INVASION IN PANCREATIC CANCER

Pancreatic ductal adenocarcinoma (PDAC) is characterized by high cellular heterogeneity and plasticity, which drive therapy resistance and disease progression. Using spatial profiling, preclinical models, and transcriptional analyses, this study identifies novel cellular states and the gene programs that regulate tumor cell plasticity and perineural invasion. It also demonstrates how combining molecular biology with AI-based imaging can improve tumor characterization and support precision oncology in PDAC.



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Simone Tamburri

European Institute of Oncology, Milano

14

**September
at 3.30 pm**

**Room B108
POVO 2**



SCAFFOLD-DRIVEN MODULAR ASSEMBLY OF POLYCOMB PRC1 COMPLEXES CONTROLS GENOME- WIDE CHROMATIN TARGETING

Polycomb group proteins (PcG) sono regolatori fondamentali dello sviluppo e dell'organizzazione dei tessuti, ma alterazioni nella loro attività sono associate a tumori e malattie dello sviluppo. In questo studio, attraverso un approccio integrato che combina proteomica, modellistica strutturale e genomica, viene ricostruita l'architettura del complesso PRC1, identificandone i moduli funzionali, le modalità di assemblaggio e le interazioni tra le diverse componenti. Il lavoro mostra inoltre come mutazioni associate a cancro e disturbi del neurosviluppo alterino specifiche interfacce strutturali del complesso, offrendo una nuova chiave di lettura dei meccanismi molecolari alla base di queste patologie.



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Andreas Mayer

Innsbruck University

15

**September
at 9 am**

**Room B108
POVO 2**



FROM MULTI-OMICS TO MECHANISMS: UNDERSTANDING GENE EXPRESSION REGULATION AND DYSREGULATION BY BET FAMILY PROTEINS

Gene expression is regulated by promoters and enhancers, but how transcription at enhancers is coordinated with their target genes remains poorly understood. Using the high-resolution HiS-NET-seq approach, researchers identified thousands of previously unannotated transcribed enhancers in human cells. Their findings show that the BET protein BRD4 is a key regulator of transcription at both enhancers and target genes, helping maintain their long-range interactions. Current research focuses on understanding the distinct roles of BRD4, BRD2 and BRD3 in gene regulation, particularly in leukemia.



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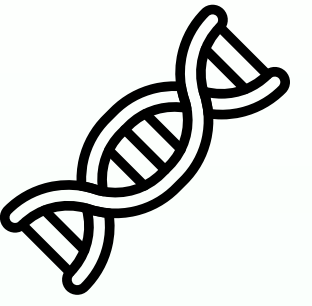


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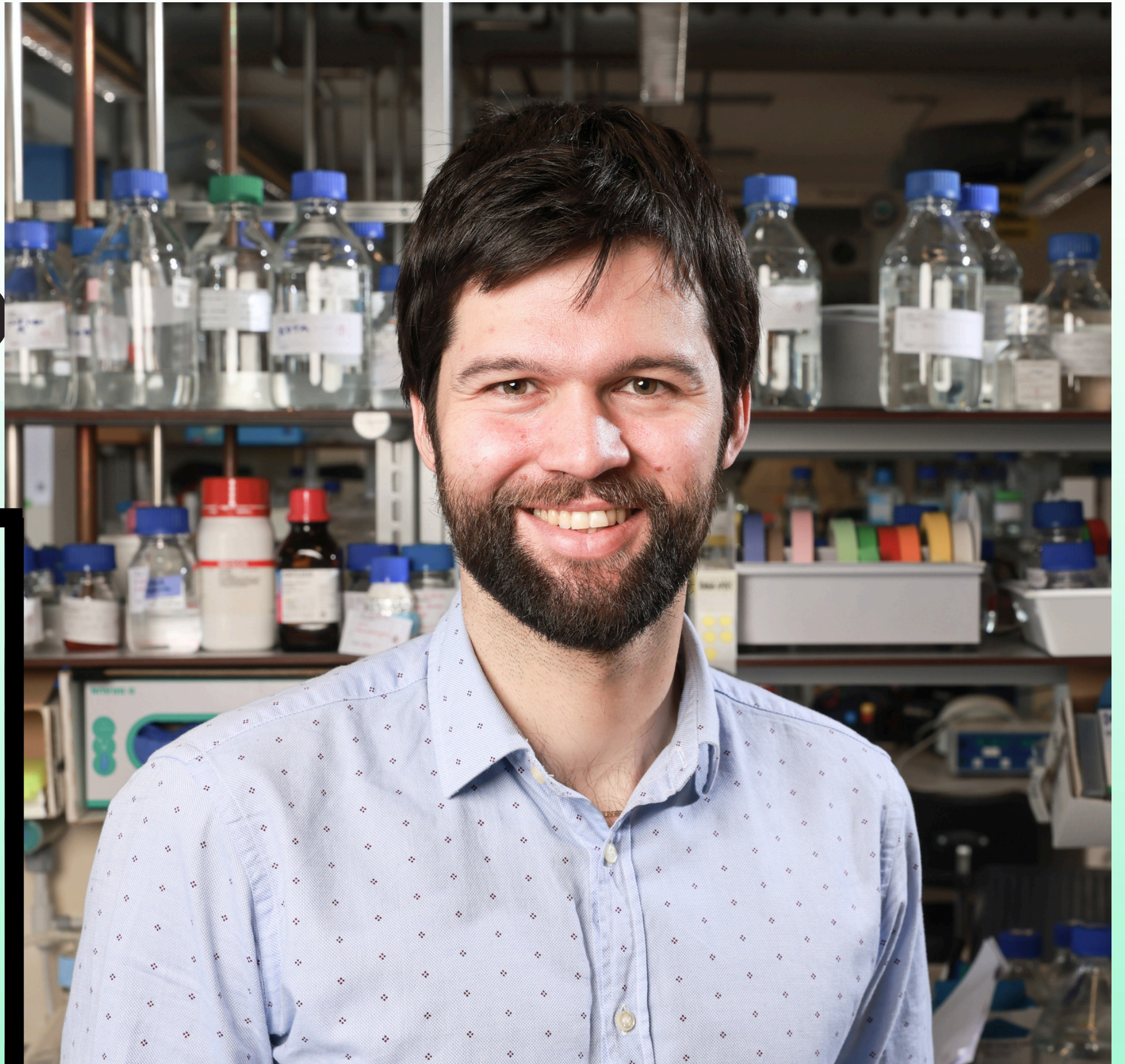
Davide Martino Coda

*Neuroepigenetics lab, École
Polytechnique Fédérale de Lausanne*

15

**September
at 10 pm**

**Room B108
POVO 2**



EPIGENETIC CONTROL OF MEMORIES

Epigenetic modifications are known to be involved in memory, but whether changes at a single genomic site can directly influence learned behavior has remained unclear. Here, researchers developed a CRISPR-based epigenetic editing system that can target specific loci in specific neuronal populations at precise times in the adult mouse brain. Focusing on memory-associated engram cells, they showed that the epigenetic state of a single locus can causally and reversibly regulate memory expression. This approach provides a powerful tool to investigate how cell- and locus-specific epigenetic regulation shapes memory and other long-lasting cellular behaviors.

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