



**UNIVERSITÀ
DI TRENTO**

Department of
Cellular, Computational
and Integrative Biology - CIBIO

Organizers:

Marta Biagioli
Fulvio Chiacchiera

Epigenetics Mondays Seminars

Every Monday from May 9th till May 30th

May 23rd @ 2:30PM

Room A109 – Polo Ferrari 1

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A proteomic view of the role of protein post-translational modifications, on histone and beyond, in cancer onset, and plasticity and therapy escape

Chromatin is a dynamic nucleoprotein complex controlling various DNA-dependent processes. A large number of site-specific post-translational modifications of histones (hPTMs) contribute to the maintenance and modulation of chromatin plasticity, gene activation, DNA replication and repair, and a variety of other biological processes. The observation of the diversity, frequency and co-occurrence of hPTMs at distinct genomic loci led to the notion that these marks create a molecular barcode, read by effector proteins that translate it into specific functional outcomes. This language is often altered in disease, especially cancer, as a consequence of the aberrant expression or mutation of enzymatic epigenetic modifiers and with a direct impact of transcriptional patterns and maintenance of cell identity.

The molecular details of this epigenetic code are only partially characterized and new approaches are needed to dissect them in physiological conditions and to understand how they are distorted during tumorigenesis. Recent achievements have made Mass Spectrometry (MS) and quantitative proteomics excellent tools to help understanding how histone PTMs modulate gene expression in health and how they are altered in disease. Moreover, the unbiased view offered by MS-proteomics allowed gaining a broader perspective on extent and function of epigenetic modifications beyond histones.

My team contributed to the field by setting-up distinct MS-proteomics strategies to investigate the chromatin plasticity and nuclear dynamics governed by post-translational modifications, on and beyond histones.

By walking through to these strategies in my talk, I will give special emphasis on the description of MS-based approaches for epigenome mapping of cancer patient samples to identify novel PTMs signature with potential as biomarker and the exploration of the methyl-proteome beyond chromatin, its plasticity upon pharmacological modulation of methyl-transferases and its functional implication in adaptive response to stress, in cancer cell.