Multi-layer regulation of the adaptive response to chemotherapy in ovarian cancer by protein-methylation: a proteomic perspective

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The seminars are open to the public.

Abstract: Methylation on histones and non-histone proteins plays a critical role in regulating gene expression and adaptive responses in cancer. Protein methyltransferases and demethylases are attractive targets for cancer therapy, with ongoing development and testing of inhibitors. Thus, innovative analytical platforms are essential for comprehensively analyzing cancer cell methyl-proteomes during tumor progression and in response to external stimuli.

Our research has been at the forefront of this field, developing distinct MS-proteomics strategies for mapping the epigenome of cancer patient samples and exploring the methyl-proteome beyond chromatin. These approaches have enabled the identification of novel PTM signatures with potential as biomarkers and the discovery of new cellular mechanisms underlying cancer plasticity, heterogeneity, and response to therapy.

In this talk, I will discuss this journey, detailing the development and optimization of these new analytical platforms and showing their application in the context of the investigation of adaptive chemoresistance in ovarian cancer.

Biography: Tiziana Bonaldi is a Tenured Group Leader at the European Institute of Oncology (IEO) in Milan, overseeing the “Cancer epigenetics and gene expression regulation” Group since 2008. After earning a PhD in Molecular and Cellular Biology at the Dibit, San Raffaele Institute in Milan, she conducted post-doctoral research at LMU in Munich, focusing on MS methods for studying the histone code, and at the MPI of Biochemistry in Martinsried, refining expertise in quantitative MS-based proteomics. Recognized with the “Armenise-Harvard Career Development Award” in 2007, she progressed to Associate Professor at IEO in 2014 and was appointed Assistant Professor (researcher RTD-B) at the University of Milan in 2021. In 2023 she has been elected EMBO member.

Research-wise, TB applies MS-based proteomics to investigate molecular mechanisms in cancer adaptive responses, particularly in epigenetic gene expression regulation. Her work spans technological innovations and original findings in MS-analysis of chromatin composition, histone modifications, and protein methylation in cancer, including primary samples. TB explores novel roles of epigenetic enzymes in cancer onset, progression, and therapy response, pioneering epi-proteomics analyses of primary samples.

TB actively promotes gender balance initiatives at IEO and coordinates the EU-funded LIBRA project of the EU-LIFE consortium. Additionally, she holds various institutional roles at IEO, including Chair of the Scientific Council of the Dept. of Experimental Oncology and membership in educational committees. TB contributes to the EU-funded EPIC-XS consortium, developing analytical strategies for clinical epi-proteomics studies and providing proteomics services for external EU users.

With over 110 peer-reviewed scientific papers and an h-index of 44 on Google Scholar, TB is recognized for her significant contributions in chromatin proteomics and cancer epigenetics filed.