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## Mass spectrometry-based quantitative proteomics for the investigation of chromatin plasticity and epigenetic regulation

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Chromatin is a highly dynamic, well-organized and yet ill-defined protein-DNA-RNA structure that controls various DNA-dependent processes. Diverse processes are involved in the alteration of chromatin and include post-translational modifications of histone proteins, incorporation of specific histone variants, methylation of DNA and ATP-dependent chromatin remodeling. Recent achievements made Mass Spectrometry and quantitative Proteomics excellent tools within the arsenal of analytical strategies aiming at understanding how histone variants/PTMs and their specific interactors mediate the structural-functional state of chromatin. Our team has recently setup distinct quantitative MS proteomics approaches, combined with various biochemical methods of enrichment of chromatin and extra-chromatin proteins, to facilitate the investigation of the complexity and plasticity of gene expression regulation. The talk will offer an overview of the various MS-proteomics strategies developed in our group to gain novel unconventional insights into chromatin biology.

### Biography

Tiziana Bonaldi has completed her PhD from the Parco Biomedico San Raffaele (Milano) and two post-doctoral studies, first from the Ludwig Maximilians University (2003-2006) and from the Max Planck Institute of Biochemistry in Munich (2006-2008). During her post-doctoral work she became progressively expert in the field of chromatin bio-chemistry and chromatin-proteomics, using high-resolution MS to decrypt the code of histone modifications and to dissect how distinct chromatin determinants synergize to enforce specific gene expression patterns. Since 2008 she is Group Leader at the Department of Experimental Oncology of the European Institute of Oncology in Milano, where she is continuing focusing on the use of MS-proteomics to investigate chromatin-mediated gene expression regulation. She has published more than 30 papers in peer-reviewed international journals and has been serving as an editorial board member of various journals in the field of MS-Proteomics. She was awarded the EMBO Long-term fellowship in 2004 for her post-doctoral research, the Armenise-Harvard Career Development Award in 2008 and the Inner-wheel award "Women in Science" in 2010 for her scientific achievements.

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