seminario

Dipartimento di Biotecnologie e Bioscienze – UNIMIB

lunedì 25 marzo 2019, ore 16:00, aula U1-10, edificio U1

In-Vitro and In-Cell Cross-Linking/Mass Spectrometry: from 3D-Protein Structure Investigations to Proteome-Wide Interactome Studies

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Chemical cross-linking/mass spectrometry (XLMS) has emerged as a powerful tool for the 3D-structure analysis of proteins and protein complexes and is becoming increasingly popular in structural biology.

We have developed and successfully applied MS-cleavable cross-linkers and integrated workflows to perform XLMS at different levels, ranging from isolated protein and protein assemblies to highly complex protein mixtures, such as cell lysates and intact cells. Our protocols can be conducted within one week and are based on the commercially available MS-cleavable cross-linker disuccinimidyl dibutyric urea (DSBU). The workflows can be employed by every lab having access to a mass spectrometer with tandem MS capabilities. We provide an updated version 2.0 of the freeware software tool MeroX (www.StavroX.com) that allows a fully automated analysis to deliver insights into protein interaction networks and protein conformations on a proteome-wide scale. We demonstrate the successful application of our workflow for *Drosophila* embryo extracts as well as intact *E.coli* cells and human embryonic kidney cells. Principles of modern cross-linkers and recent applications of XLMS will be discussed.

Ospite: Rita Grandori

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