

PROTEOMICS INVESTIGATION TO UNVEIL MOLECULAR DETAILS OF CELLULAR PROCESSES

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The “Omics Sciences” have revolutionized modern biology. To date, there is no scientific field, from medicine to environmental sciences, passing through biochemistry and pharmacology that does not resort to these sciences for the study of complex biological systems. Proteomics among these fields aims to study the entire set of constitutive proteins of a tissue, an organism in specific moment with the ambitious prospect of correlating this ‘molecular snapshot’ to the observed phenotype. From the conception of proteomics as a large-scale evolution of the chemistry and biochemistry of proteins, we have gradually come to the definition of a science that has revolutionized the central dogma of biology highlighting how every metabolic and functional process is the result of a complex network of nonlinear interactions between genes, transcripts and proteins. The bursting success of Proteomics and all other “Omics Sciences” has been possible in the last decade thanks to the strong technological push supported by the development of powerful bioinformatics tools that allow the qualitative and quantitative analysis of mass spectrometry data, together with functional analysis and correlation of the genes, transcripts, proteins or metabolites to reconstruct the appropriate relationship networks. In the field of Proteomics investigation, two main application areas have been taken off: functional proteomics, which aims to define the molecular mechanisms underlying biological processes of interest through to the identification of in vivo protein-protein interaction (PPI) [1]; differential proteomics, addressed to the comparison of protein expression profiles in multiple biological conditions, e. g. wild type vs mutant or vs pharmacologically treated, etc, in order to define the biological processes affected by the specific treatment or condition. Different methodologies have been developed to carry out the qualitative-quantitative analyses of the protein content in samples using both labelled and label-free approaches. [2] Among many application fields, both these approaches are also largely employed in the investigation of a biological process, both in physiological and pathological conditions such as oncological diseases [3], neurodegenerative disorders, [4], as it will be discussed in the current presentation.

[1] Iacobucci I. et al. J Proteomics. J Proteomics. 2021 Jan 6; 230: 103990. [2] Cozzolino F. et al PLoS One. 2020 Sep 4;15(9): e0238037. [3] Federico A. et al. Biochim Biophys Acta Gene Regul Mech. 2019 Apr;1 862(4):509-521. [4] Cozzolino F. et al. Hum Mol Genet. 2021 Jun 17;30(13):1175-1187.

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