



## EDITORIAL

### PROTEOMICS

A proteome is a set of proteins produced in an organism, system, or biological context. Proteomics is the large-scale study of proteomes. We may refer to the proteome of a specific species (*Humans, Monkeys*) or a specific organ (liver, kidney). The proteome is not constant; it differs from cell to cell and changes over time. To some degree, the proteome reflects the underlying transcriptome. However, protein activity is also modulated by many factors in addition to the expression level of the relevant gene.

Proteomics is usually explored to investigate:

- When and where proteins are expressed;
- How proteins interact with one another.
- Rates of protein production and degradation;
- How proteins are modified;
- The movement of proteins between sub cellular compartments;
- The involvement of proteins in metabolic pathways;

Several high-throughput technologies have been developed to investigate proteomes in depth. The most commonly applied are Mass Spectroscopy (MS)-based techniques such as Tandem-MS and gel-based techniques such as differential in-gel electrophoresis (DIGE). These high-throughput technologies generate huge amounts of data. Databases are critical for recording and carefully storing this data, allowing the researcher to make connections between their results and existing knowledge.

Happy Reading,

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