

Functional Protein Expression Profiling: Decoding Protein Function in Biological Systems

Hui Peng*

Department of Proteomics and Metabolomics, Sun Yat-sen University, Guangzhou, China

DESCRIPTION

Protein expression profiling is a powerful technique that helps scholars identify, quantify and understand the functional role of proteins within cells, tissues or organisms. Proteins are the molecular machines responsible for most cellular processes and their expression patterns can provide valuable insights into disease mechanisms, cellular functions and the effects of treatments or environmental changes. By studying protein expression, scientists can gain a deeper understanding of biological systems and cover the way for novel therapeutic strategies.

Role of protein expression profiling

Protein expression profiling refers to the comprehensive analysis of proteins expressed in a given biological sample, typically using high-throughput techniques that enable large-scale measurement of protein levels, modifications and interactions. Unlike genomics, which focuses on transcriptomics, which measures protein expression profiling directly assesses the functional products of genes proteins. The ultimate goal of protein expression profiling is to obtain a comprehensive map of the proteome the entire set of proteins present in a cell or tissue under specific conditions.

Methodologies in protein expression profiling

Mass Spectrometry (MS): Mass spectrometry is one of the most powerful techniques for protein expression profiling. It can detect and quantify proteins with high sensitivity and specificity, even in complex biological samples. In MS-based proteomics, proteins are first digested into smaller peptides, which are then analyzed based on their mass-to-charge ratio.

Protein microarrays: Protein microarrays are another technique used for protein expression profiling. These microarrays consist of thousands of immobilized proteins on a solid surface, allowing researchers to probe protein interactions, expression levels and functional activity. Protein microarrays can be used to profile the binding affinity of antibodies, detect protein-protein

interactions and monitor changes in protein expression levels under different conditions.

Two-Dimensional Gel Electrophoresis (2D-GE): 2D-GE is a classical technique that separates proteins based on two properties Isoelectric Point (pI) and molecular weight. After separation, the proteins are visualized and their expression levels are compared under different experimental conditions. 2D-GE is especially useful for identifying changes in protein expression across different samples or conditions, such as in disease states or after drug treatment. However, this method is less sensitive than mass spectrometry and may struggle to detect low-abundance proteins or highly hydrophobic proteins.

Western blotting: Western blotting is a widely used technique to detect specific proteins within a complex sample. Proteins are first separated by size through gel electrophoresis, transferred to a membrane and probed with antibodies that recognize specific proteins of interest. Western blotting allows for the quantification of protein expression levels and the detection of PTMs.

Next-Generation Sequencing (NGS)-based approaches: Although NGS is primarily associated with genomic and transcriptomic analyses, recent advancements have enabled its use in proteomics. Techniques like sequencing combined with proteomics (proteogenomics) can provide insights into how changes at the transcript level influence protein expression and function.

CONCLUSION

Protein expression profiling is a critical tool for understanding cellular functions, disease mechanisms and therapeutic strategies. By providing insights into the proteins that effort cellular processes, it has a wide range of applications in cancer study, drug development, neurodegenerative diseases and infectious diseases. While challenges such as the complexity of the proteome and data interpretation remain, continued advancements in proteomics technologies talent to enhance our ability to profile proteins exactly and comprehensively, further our understanding of biology and improving human health.

Correspondence to: Hui Peng, Department of Proteomics and Metabolomics, Sun Yat-sen University, Guangzhou, China, Email: peng.hu@qq.in

Received: 19-Nov-2024, Manuscript No. JPB-24-36491; Editor assigned: 21-Nov-2024, PreQC No. JPB-24-36491 (PQ); Reviewed: 05-Dec-2024, QC No. JPB-24-36491; Revised: 12-Dec-2024, Manuscript No. JPB-24-36491 (R); Published: 19-Dec-2024, DOI: 10.35248/2161-0517.24.17.678

Citation: Peng H (2024). Functional Protein Expression Profiling: Decoding Protein Function in Biological Systems. J Proteomics Bioinform. 17:678.

Copyright: © 2024 Peng H. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.