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Editorial

A Brief Note on the Study of Proteomics: A Simple Protein

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EDITORIAL NOTE

Proteomics is the study of proteins in a wide scale. Proteins serve a variety of tasks in living organisms. Proteomics allows an ever-increasing number of proteins to be identified. It is an important component of functional genomics and involves the study of proteomes from the overall level of protein composition, structure, and activity. Proteomics refers to the large-scale experimental investigation of proteins and proteomes in general, but it is frequently used to refer to protein purification and mass spectrometry in particular. After the development of the two-dimensional gel and mapping of proteins from the bacterium Escherichia coli in 1975, the first studies of proteins was called as proteomics.

The term "proteome" is a combination of the words "protein" and "genome." It was coined in 1994 by Macquarie University's then-Ph.D student Marc Wilkins, who established the first specialised proteomics laboratory in 1995. Proteomics is the next stage in the study of biological systems after genomes and transcriptomics. Because an organism's genome is more or less constant, whereas proteomes change from cell to cell and over time, it is more complicated than genomics. Various cell types express different genes; therefore even the most basic set of proteins produced by a cell must be identified. RNA analysis was initially used to analyse this phenomena, but it was determined to have no link with protein content. It is now well understood that mRNA is not always translated into protein, and that the amount of protein produced for a given amount of mRNA is dependent on the gene from which it is transcribed as well as the physiological condition of the cell. Proteomics confirms the presence of a protein and offers a quantitative estimate of its amount.

Phosphorylation is one such change, which occurs in the process of cell function to various enzymes and structural proteins. The addition of a phosphate to specific amino acids-most commonly serine and threonine mediated by serine-threonine kinases, or more rarely tyrosine mediated by tyrosine kinase receptors a protein a target for binding or interacting with a specific set of other proteins that identify the phosphorylated domain. Because protein phosphorylation is one of the most researched protein modifications, many "proteomic" activities focus on identifying the set of phosphorylated proteins in a specific cell or tissue type under specific conditions. Ubiquitin is a small protein that enzymes called e3 ubiquitin ligases can bind to specific protein substrates. Determining how protein pathways are regulated requires determining whether proteins are poly-ubiquitinated. As a result, this is another legitimate "proteomic" study. Similarly, determining the set of ligases expressed in a given cell type is useful once a researcher has determined which substrates each ligase ubiquitinates. During development, cellular differentiation, cell cycle, or carcinogenesis, a cell may produce different sets of proteins at different times or under different situations. Most proteins can undergo a wide spectrum of post-translational changes, which adds to the complexity of the proteome. As a result, even if the research topic is limited, a "proteomics" study can soon become complex. When looking for a biomarker for a certain cancer subtype, a proteomics scientist may choose to look at several blood serum samples from multiple cancer patients to reduce confounding factors and account for experimental noise.

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