

Post-translational Modifications: A Major Focus for the Future of Proteomics

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With 20,000 to 30,000 human genes and only 100,000 expressed proteins, the dynamic complexity of living systems is achieved, in part, through an enormous repertoire of chemical modifications of amino acids that occur during and after protein translation. There are over 400 known post-translational modifications (PTMs), and technical advances in methodology and instrumentation are permitting the discovery of new modifications, enabling the development of a global view of the role of modifications in responding to and regulating biological processes, and revealing the magnitude of complexity that is imparted to protein regulation by combinations of modifications. PTMs encode information regarding the status of the cell and synergistically modify polypeptide functions in a manner that is highly responsive to both cellular metab-

olism and external cues. In fact, it is the myriad molecular species created by multiple PTMs of a polypeptide that represent the biologically functional end point of gene expression. As analytical methods continue to improve, it will likely become a major focus of biomedical and other types of molecular research to elucidate the functions of the many different isoforms of polypeptides, which must eventually be understood first at the individual site level on polypeptides and ultimately by defining the structure/functions of individual molecular species with multiple PTMs.

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