

SEMINAR

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Biomedical Applications of Proteomics, Glycoproteomics, and Glycomics

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There has been a revolution in biology since the introduction of the Polymerase chain reaction in the mid 1980s. This revolution has until recently focused on the sequencing of genes, and has led to the large-scale genome sequencing projects which are in progress. This emphasis on straight sequencing has, in turn, given rise to a second focus on functional genomics, epitomized by the use of cDNA microarray technology, in an attempt to understand how the information contained in the genomic sequence of an organism is used, and to bridge the gap between raw sequence data and the state of the proteins within an organism. Unfortunately, there is an increasing realization that often very poor correlations exist between the level of any particular mRNA and the protein it is encoding. This may be due to a number of reasons, including post-translational processing, and widely varying turnover rates.

One response to this problem by the biochemical community has been the development of the field of proteomics. Proteome was defined in 1996 as the “total protein complement of the genome”. Proteomics has become an area of study centering on the identification and characterization of the total expression of proteins in cells, tissues, and organisms and the factors causing this to change. Understanding complex biological systems, their interactions with and reactions to various stimuli is the ultimate goal of many researchers. Mass spectrometry (MS) has emerged as the most common method for unequivocally identifying proteins. Identification, however, is only the first step in understanding the biological role of a protein. Increasingly protein modifications, which occur both during and after its expression, are implicated in its function. The type and number of post-translational modifications cannot be easily predicted from the DNA sequence alone and requires analysis at the protein level. The identification and characterization of post-translational modifications is clearly where the field of proteomics is headed, and will keep scientists in this area busy for year to come.

This presentation will also include a basic discussion on proteomic techniques including approaches to provide more complete protein coverage, issues related to dynamic range, as well as methods to evaluate the confidence in protein identification. Attention will also be given to the application of glycomics and glycoproteomics to obtain information on this important post-translational modification.