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Post-translation modifications
Editorial overview
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The development of proteomics has been one of the great achievements in analytical chemical biology in the past 10 years. The determination of the total protein constituents in biological samples has allowed new and unprecedented insights into cellular processes and diseases. To make proteomics routine and ubiquitous, significant improvements in mass spectrometry, bioinformatics, and separation science were realized through unprecedented international collaborative and competitive efforts. The next stage of this evolution is even more difficult as we face the issue of post-translational modifications (PTMs). Proteomics approaches have often neglected PTMs not purposely but out of necessity. PTMs introduce a whole new level of analytical challenge due to the complexity presented. For example, a protein that is glycosylated at 3 sites with 10 different glycans at each sight can result in 1000 different glycoforms of that protein. Glycosylation is only one form among of scores of different types of PTMs (Figure 1). In this issue we focus on emerging methods for the studies and analyses of specific PTMs ranging from glycosylation to lipidation. The analytical challenge of PTMs has inspired a wide variety of approaches to their study; These include incorporating new chemistry, such as in the mechanistic probes presented by Dr Amy Barrios for profiling tyrosine phosphatases and the metabolic labels discussed by Dr Howard Hang for protein lipidation. Creating new methods for *in vivo* tracking of PTMs, such as the fluorescent biosensors presented by Dr Jin Zhang. The utilization of new methodologies for understanding the functions and signaling properties of PTMs and their binding proteins, such as the protein microarrays discussed by Dr Gavin MacBeath and the glycan microarrays presented by Dr Jeff Gildersleeve, and the development of new methods for comprehensive analysis, presented in reviews on phosphorylation by Dr Albert Hect, and glycosylation analysis at both the site-specific and global levels (reviews by Dr Carlito Lebrilla on mass spectrometry techniques and Dr Lara Mahal on lectin microarray techniques, respectively). Clearly, there will be no single method for the analysis of all PTMs, but several methods each specific for the type of PTM. The reviews presented here illustrate not only the challenges of PTM analysis but also the significant progress in these areas.

Figure 1
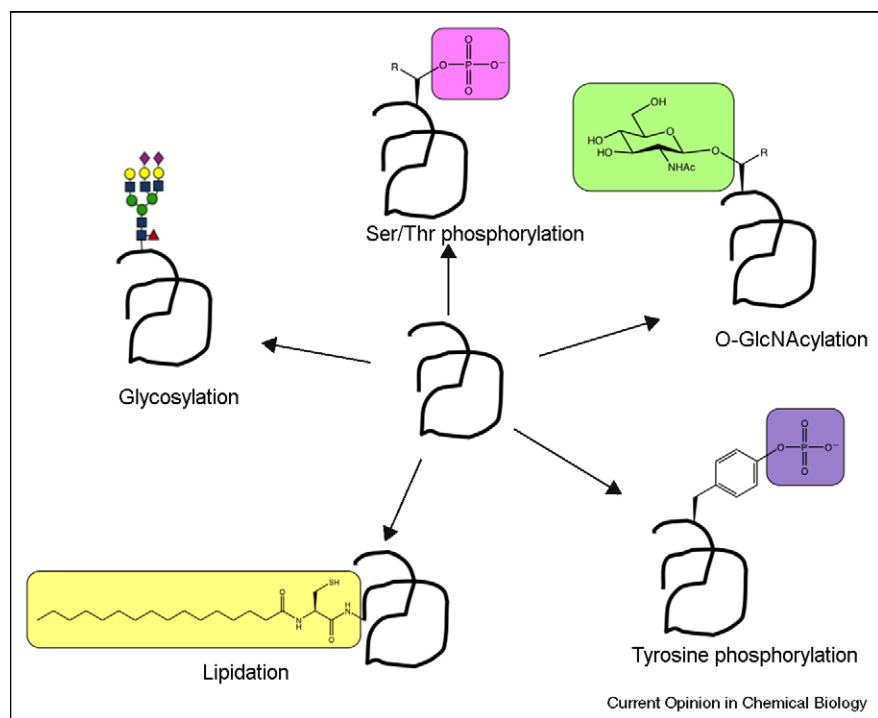
Post-translational modifications for which analytical techniques are highlighted within this issue.