
Preface

The addition of chemical tags to proteins has long been recognized as one important mechanism to regulate different functions of the target protein. Of particular interest is the enzymatic addition of one acetyl group to proteins, a reversible process that has been discovered more than 40 years ago, and which can occur co- and posttranslationally. Highly specific acetyltransferases catalyze the addition of an acetyl group to target sequences in proteins, and deacetylases specifically remove these chemical tags if necessary.

Since the initial discovery, many thousands of proteins have been identified to be acetylated, and immense research power has been attributed worldwide into experiments to solve the biological implications of each and every protein acetylation.

Two particular sites of protein acetylation have been described intensively: the N-terminal methionine residue of a nascent protein and lysine residues within a protein.

In this book a comprehensive collection of methods describing several different topics of protein acetylation is assembled. Starting with different methods used for initial identification of protein acetylation, such as mass spectrometry, column- and gel electrophoresis-based approaches, and ending with methods to computationally predict and to functionally study the biological response to protein acetylation, this book covers most technical aspects involved in the studies of protein acetylation.

We hope that the readers will be satisfied with this large collection of methods and will succeed in their own research on protein acetylation.

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