
Preface

Amino and carboxy-termini of proteins are subject to a variety of enzymatically catalyzed, post-translational modifications with diverse biological functions. Generally, protein terminal sequences may determine protein function, localization, and turnover. Endoproteases generate stable cleavage products with novel N- or C-termini while exoproteases yield step-wise truncations. In addition, there are modifications such as N-terminal acetylation and pyroglutamate formation, which contribute to protein functionality and stability. Over the last years, a number of techniques for N- and C-terminal profiling have been developed. To a large extent, these encompass proteomic techniques that are based on liquid chromatography–tandem mass spectrometry. This book presents detailed protocols for several of these novel strategies together with approaches for their annotation in order to enable an improved functional understanding of protein N- and C-terminal biology. Protein termini are often generated by proteolytic truncations thus placing proteases and (limited) proteolysis in a central position when studying N- and C-terminal biology and biochemistry. Accordingly, a large proportion of this book addresses topics of proteolysis research. Its topics include protease specificity profiling, N-terminal acetylation, assays to probe protease activity (and its possible inhibition) in cellular systems, proteomic techniques to explore protein N- and C-termini on a proteome-wide scale, computational approaches to correlate cleavage sequences with candidate proteases, design of activity-based probes for proteolytic enzymes, and biochemical approaches to deconvolute extracellular protease activities. The book targets researchers who focus on biochemistry and cell biology and who share a broad interest in protein functionality and protein modifications.

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