
Preface

Proteomics techniques have constantly been developed further through the last decade and have been applied successfully for all kinds of samples and biological or medical questions. Nowadays, they are established methods in many research labs, and proteomic studies can be accomplished with good reliability and coverage on a routine basis. Therefore, proteomics can be used as a powerful tool in functional genomics and systems biology studies. Current challenges are thus the implementation of proteomic analyses in these comprehensive studies. This applies for both sample generation and preparation to ensure consistency over several levels of analyses like genomics, transcriptomics, and metabolomics and integration of the multilevel data to generate biological knowledge. This book gives an overview of contemporary quantitative proteomics methods and data interpretation approaches and also gives examples of how to implement proteomics into systems biology.

Regensburg, Germany

Jörg Reinders

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