PREFACE

Personalized medicine encompasses the use of biological information for each patient in order to provide customized health care tailored to the individual patient. Such an individualized approach for medical decisions, practices, and treatment became clearly necessary due to a number of observations. For instance, the course of disease differs from one person to another. The effects of drugs used for treatment of a disease also vary largely between different patients. It is now well established that individual differences between patients, such as genetic polymorphisms, have significant effect on the onset of diseases as well as on absorption of drugs and their metabolism in patient's body. Personalized medicine takes such variations into account and tries to take advantage of them. It is believed that such customized therapies will improve patients' response rates to the treatment while reducing significantly any adverse effects the drugs might have.

Personalized medicine is based on the dynamics of systems biology and uses predictive tools to evaluate health risks and to design personalized health plans to help patients to minimize risks, prevent disease, and to treat it with precision when it occurs. Some of the most contemporary and very promising tools employed in personalized treatment of patients are discussed in the first three chapters of this volume. First chapter discusses the general principles of high-performance affinity chromatography and the various approaches that have been used in this technique to examine drug–protein binding and in work related to personalized medicine. This technique is a great asset to personalized medicine because the binding of drugs with proteins and other agents in serum can affect the dosage and action of drugs. The extent of this binding may also vary with a given disease state. Second article in this thematic volume focuses on the advances in proteomic technologies that have made important contribution to the development of personalized medicine by facilitating detection of protein biomarkers, proteomics-based molecular diagnostics as well as protein biochips and pharmacoproteomics. Application of nanobiotechnology in proteomics, nanoproteomics, has further enhanced applications in personalized medicine. Proteomics has already proved to be a good bridge between diagnostics and design of therapeutics. The integration of last two processes shows to be of a great importance for advancing personalized medicine. The third chapter in this volume reviews in detail metabolomics as a tool used in personalized medicine.

Metabolomics is the newest addition to the "omics" domain and the closest to the observed phenotype. It reflects changes occurring at all molecular levels, as well as influences resulting from other internal and external factors. By comparing the metabolite profiles of two or more disease phenotypes, metabolomics can be applied to identify biomarkers related to the perturbation being investigated. These biomarkers can, in turn, be used to develop personalized prognostic, diagnostic, and treatment approaches, and can also be applied to the monitoring of disease progression, treatment efficacy, predisposition to drug-related side effects, and potential relapse.

The fourth chapter discusses the importance of a range of new approaches to developing new and reprofiled medicines to treat common and serious diseases, and rare diseases: new network pharmacology approaches, adaptive trial designs with enriched populations more likely to respond safely to treatment, as assessed by companion diagnostics for response and toxicity risk and use of "real-world" data. Case studies are described of single and multiple protein–drug targets in several important therapeutic areas. These case studies also illustrate the value and complexity in use of selective biomarkers of clinical response and risk of adverse drug effects, either singly or in combination.

Chapters 5 and 6 in this volume give in-depth analyses of applying the tools of personalized medicine in some of the most common diseases. The fifth article in this volume highlights the contributions of proteomics toward the understanding of personalized medicine in respiratory disease and its potential applications in the clinic. The sixth chapter is focused on the challenges of treating different cancer types, which behave like moving targets due to mutation and evolution, and the current state-of-the-art research in this area. A special emphasis is made on the computational approaches to accelerating novel medicine and better personalized patient care from bedside to benchtop.

Chapter 7 in this volume focuses on high-end computational methods, such as molecular dynamics (MD) simulation that has proved to be a constitutive approach for detecting the minor changes associated with single nucleotide polymorphisms (SNPs) in nucleic acids for better understanding of their role in protein structural and functional alterations. MD along with docking analysis can reveal the synergetic effect of an SNP in protein–ligand interaction and provides a foundation for designing a particular drug molecule for an individual. This compelling application of computational power and the advent of other technologies have paved a promising way toward personalized medicine. In the Eighth article of this thematic volume,

authors discuss the available clinical strategies and different methods how pharmacological chaperones can be personalized and used as a next-generation approach to address different lysosomal storage disorders.

The final two chapters in this volume exemplify the applicability of molecular modeling and simulation approaches in personalized medicine by exploring the inhibitory activity of Wortmannin toward oncogenic mutations in phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha (PIK3CA) (Chapter 9), and the importance of mutations in A1-domain of von Willebrand factor (VWD) gene for the structural and functional alterations related to thrombosis, compared to the native VWD protein (Chapter 10).

The aim of this volume is to promote further research and development in the design of new personalized therapeutics and treatments using biological information for each patient via translation of recent genomic, genetic, proteomics, and metabolomics advances into clinical context.

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