

Bronchial asthma (asthma for short) is a heterogeneous disease characterized by chronic airway inflammation, airway remodeling, and airway hyperresponsiveness, with reduced lung function and reversible airflow restriction. At present, nearly 400 million people suffer from asthma worldwide, and the prevalence and mortality rates are increasing year by year. Most patients with asthma can benefit from the combined treatment of inhaled corticosteroids and bronchodilators, but 5–10% of patients experience refractory asthma, which does not achieve satisfactory control after the “optimal treatment”. Notably, a breakthrough has not been made in the treatment of moderate and severe asthma, which continues to present great challenges to patients, their family members, and society, and has attracted the attention of the academic community. In this context, “Asthma Research in the Context of Modern Biotechnology” focuses on relevant issues and hopes to be helpful to clinicians and researchers.

As a complex disease caused by the interaction of many exogenous and endogenous factors, various environmental exposures and individual genetic composition all play an important role in asthma. This book describes in detail the important role of genomics technologies such as genome-wide association study (GWAS) and whole genome sequencing (WGS) sequencing in the discovery and identification of asthma susceptibility genes and the screening of genetic variations associated with drug responses. Moreover, the progress of epigenetics in asthma research including DNA methylation, histone modification, and regulation of non-coding RNA (long non-coding RNA [lncRNA] and circular RNA [circRNA]) is also described to help readers quickly understand the field of asthma epigenetics research. This book describes the importance of high-throughput analysis techniques in asthma research, including DNA methylation chips, chromatin immunoprecipitation sequencing, microRNA (miRNA) sequencing, full transcriptome sequencing, co-expression networks, and competitive endogenous RNA (ceRNA) analysis. In particular, the combination of high-throughput epigenetic analysis technology with traditional biological function and clinical research will improve the genetic interpretation of diseases, which is expected to bring new breakthroughs for the pathogenesis of asthma research, and expand the possibilities for precision medicine treatment of asthma. The book also introduces the progress of proteomic research on different tissue types of asthma, such as blood (serum), alveolar lavage fluid, sputum, and saliva, as well as the application of proteomic techniques in the study of asthma, such as capillary electrophoresis, chromatography, and protein chip. The development of proteomic techniques facilitates rapid identification of a large number of target molecules with diagnostic and therapeutic significance to improve the prevention and treatment of related diseases. Airway remodeling is closely related to refractory asthma. In this book, molecular markers and cell sources of airway smooth muscle cells, the critical cells in airway remodeling and the core pathological features of asthma, are discussed, which can provide reference for drug development of subsequent targeted therapy. In addition, the book also discusses the emerging treatment of asthma, such as the action mechanism, efficacy, and safety of mesenchymal stem cells (MSCs) and the future prospects of clinical treatment of asthma. The advantages of targeted delivery of drugs or genes, low toxicity, and high bioavailability of nanomaterials, have allowed nano modification of drugs and novel nano genes to become a new direction of asthma research.

Every medical advancement is closely related to the support of research technology at that time, and the ultimate cure of asthma is inevitably related to modern science and technology. The authors of “Asthma Research in the Context of Modern Biotechnology” are all scholars active in clinical and basic scientific research. By compiling papers published in this field, the pathogenesis, research progress, and research results of asthma are discussed from different dimensions of genomics, transcriptomics, epigenetics, and proteomics. It is published with the hope to deepen the understanding of respiratory doctors, graduate students, and scientific researchers on the progress of asthma research, promote the organic combination of clinical practice and topical research, and foster further innovation.

This book contains a raft of results of previous research. The publishing house has provided very specific guidance in the planning, organization, and compilation of this book. Hereby, we would like to express our most sincere thanks.

In the process of compiling this work, although our best attempts were made to keep track of the latest development

of the subject and to explain it clearly, there are inevitably inadequacies, and even mistakes, in the book due to the rapid development of the field and the limitations of the editors. We sincerely hope that experts and fellow scholars can provide critique and corrections of any such discrepancies.



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