

EGFR Signaling Networks in Cancer Therapy.

Haley JD, Gullick WJ, eds. Humana Press; 2009.
Hardcover, 393 pages, 52 illustrations. \$149.00 US.

It can be a daunting task for cancer researchers and biologists to keep abreast of past and growing knowledge of epidermal growth factor receptor (EGFR) signal networks, given the more than 12,000 published papers on this subject. In the book *EGFR Signal Networks in Cancer Therapy*, which is part of the *Cancer Drug Discovery and Development* series, the authors have compiled contributions from an impressive international collaboration of 59 authors to address this problem. Included are 23 independent reviews, each of which covers important aspects of EGFR signaling networks in cancer therapy. Each review is well organized and uniformly structured, including title, contents, abstract, keywords, introduction, text, discussion, conclusions, and references. This organized format endows the book with conciseness and readability for readers.

The book is divided into two sections. The first section, *EGFR Signaling Networks*, includes 15 chapters and addresses the basic biology of EGFR signaling networks. Chapters 1 to 5 characterize the structure and the molecular and cellular behavior of the EGFR family member in cancer. Chapters 6 to 11 mainly introduce the important EGFR signaling network-associated signaling pathways, including STATs, Ras, PI3K, Src, E-cadherin, and IGF signaling and their interaction with EGFR signaling in cancer. Chapters 12 and 13 emphasize the negative regulation of EGFR signaling pathway and function of its nuclear localization. A major strength of this book, in addition to presenting the basic knowledge of EGFR signaling network, is a section on proteomics-based experiments. This includes high-throughput quantitative research strategies and computational and mathematical modeling techniques, which are well described in chapters 14 and 15. These emerging approaches allow quantitative characterization and temporal dynamics of the EGFR signaling network with high accuracy and specificity and are important for investigators interested in systems biology related to EGFR.

The second section, *EGFR in Tumorigenesis and EGFR Tyrosine Kinase Inhibitors in Cancer Therapy*, includes 8 chapters dedicated to clarifying the EGFR network and its relevance to targeted cancer therapy strategies. Chapters 16 to 19 discuss how the abnormal EGFR signaling contributes to various cancer processes such as proliferation, tumor cell survival, invasion, angiogenesis, and metastasis. In our opinion, however, the most important four chapters (20 to 23) focus on the EGFR-targeted clinical therapies, with special emphasis on tyrosine kinase inhibitors. In chapter 20, the authors comprehensively examine the molecular, pathological,

and clinical correlates of therapeutic response to EGFR inhibitors and survival outcome in patient studies. These chapters carefully review the relevance of kinase inhibitor therapy to EGFR protein overexpression, gene amplification, somatic mutations, EGFR signaling pathway perturbations and change to pathway output, and posttranslational modification status. In addition, synergy of EGFR activation with other EGFR signaling network members such as KRAS, P53, and PIK3CA pathways is stressed. Chapter 21 reviews the mechanisms of COX-2 in reducing the sensitivity to EGFR inhibitors. In chapter 22, the authors summarize current various attempts to identify biomarkers of sensitive and resistance to small molecule EGFR tyrosine inhibitors. Epithelial mesenchymal transition (EMT) is specially highlighted. It is commendable that some seemingly inconsistent facts about EGFR gene amplification and protein quantitation among different assay techniques are also discussed in this book. Based on in-depth comparisons and other considerations, the authors propose guidelines for molecular testing predictive of clinical benefit for patients treated with EGFR targeting strategies. In chapter 23, the authors probe the novel combinatorial strategies of EGFR inhibitors with other pathways inhibitors, including AKT, ER, MTOR, HDAC, SRC, and COX-2 inhibitors. These important studies describe how these approaches could maintain EGFR inhibitor sensitivity and/or overcome acquired resistance. These sections summarize how our understanding of such mechanisms may lead to biomarker discovery and allow personalized therapies for cancer patients using EGFR targeting agents.

Overall, this book bridges the basic and clinical progress in EGFR network in cancer therapy over 40 years of EGFR research. Due to the contributors' basic science and clinical backgrounds, the book is "bench to bedside" and is best suited for basic scientists, translational scientists, and oncologists who engage in EGFR-associated research and clinical therapy at various levels. The book provides a comprehensive EGFR resource for researchers not only in basic biological fields but also in preclinical and clinical therapy, and it provides a concise review of this increasingly complex area of research.

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Bioinformatics in Cancer and Cancer Therapy.

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This book is part of the Cancer Drug Discovery and Development series published by Humana Press. In its preface, bioinformatics is loosely defined as the “collection, classification, storage, and analysis of biochemical and biological information using computers and mathematical algorithms.” However, the book provides little insight into the field of bioinformatics from the perspective of the initial definition and fails to deliver on the main objectives outlined by the editor. The book is composed of poorly arranged chapters that describe how genomics and proteomics technologies are used within cancer research, providing specific examples of experiments with little to no information on the bioinformatics tools and algorithms used to analyze the data. The authors of the chapters primarily rely on cited references to provide details about bioinformatics methodologies and devote the majority of text to describing the molecular techniques used in the areas of genomics and proteomics.

This book would have been more useful if it included examples of the bioinformatics tools, databases, and analytical methods applied to generate the results presented in each chapter. Many other books

on bioinformatics are available that provide a more in-depth explanation of the algorithms used for data analysis and bioinformatics methods and tools. One titled *Clinical Bioinformatics* (Trent RJA, ed. Humana Press; 2008) includes most of the techniques described in this reviewed book but has much more information about bioinformatics.

On a positive note, the book offers a detailed overview of the types of genomics, proteomics and mouse model experiments that are propelling modern cancer research, with an emphasis on personalized medicine and disease classification, which might be of interest to many readers.

Overall, if seeking a book that is a good source for learning about and understanding bioinformatics as it applies to cancer research, leave this book on the shelf and choose another.

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