Dna Methylation And Cancer Therapy Reprint

DNA methyltransferases are important enzymes in a broad range of organisms. Dysfunction of DNA methyltransferases in humans leads to many severe diseases, including cancer. This book focuses on the biochemical properties of these enzymes, describing their structures and mechanisms in bacteria, humans and other species, including plants, and also explains the biological processes of reading of DNA methylation and DNA demethylation. It covers many emerging aspects of the biological roles of DNA methylation functioning as an essential epigenetic mark and describes the role of DNA methylation in diseases. Moreover, the book explains modern technologies, like targeted rewriting of DNA methylation by designed DNA methyltransferases, as well as technological applications of DNA methyltransferases in DNA labelling. Finally, the book summarizes recent methods for the analysis of DNA methylation in human DNA. Overall, this book represents a comprehensive state-of-the-art- work and is a must-have for advanced researchers in the field of DNA methylation and epigenetics.

Breast Cancer - From Biology to Medicine thoroughly examines breast cancer from basic definitions, to cellular and molecular biology, to diagnosis and treatment. This book also has some additional focus on preclinical and clinical results in diagnosis and treatment of breast cancer. The book begins with introduction on epidemiology and pathophysiology of breast cancer in Section 1. In Section 2, the subsequent chapters introduce molecular and cellular biology of breast cancer with some particular signaling pathways, the gene expression, as well as the gene methylation and genomic imprinting, especially the existence of breast cancer stem cells. In Section 3, some new diagnostic methods and updated therapies from surgery, chemotherapy, hormone therapy, immunotherapy, radiotherapy, and some complementary therapies are discussed. This book provides a succinct yet comprehensive overview of breast cancer for advanced students, graduate students, and researchers as well as those working with breast cancer in a clinical setting.

Methylation of DNA at cytosine residues as well as post-translational modifications of histones, including phosphorylation, acetylation, methylation and ubiquitylation, contribute to the epigenetic information carried by chromatin. These changes play an important role in the regulation of gene expression by modulating the access of regulatory factors to the DNA. The use of a combination of biochemical, genetic and structural approaches has allowed demonstration of the role of chromatin structure in transcriptional control. The structure of nucleosomes has been elucidated and enzymes involved in DNA or histone modifications have been extensively characterized. Since deregulation of epigenetic marks has been reported in many cancers, a better understanding of the underlying molecular mechanisms bears the promise that new drug targets may soon be found. The newest developments in this quickly developing field are presented in this book.

Anomalous epigenetic patterns touch many areas of study including biomedical, scientific, and industrial. With perspectives from international experts, this resource offers an all-inclusive overview of epigenetics, which bridge DNA information and function by regulating gene expression without modifying the DNA sequence itself. Epigenetics, in its

DNA Methylation and Cancer TherapySpringer Science & Business Media

Candidate gene based studies have identified a handful of aberrant CpG DNA methylation events in prostate cancer (Brooks et al. 1998; Yegnasubramanian et al. 2004). However, large scale DNA methylation profiles have not been examined for normal prostates or prostate tumors. Additionally, the mechanisms behind these DNA methylation alterations are unknown. In this thesis, I describe the results of my efforts to better understand these previously unexplored areas of biology. For the study presented in this thesis, I quantitatively profiled 95 primary prostate tumors and 86 healthy prostate tissue samples for their DNA methylation levels at 26,333 CpGs representing 14,104 gene promoters by using the Illumina HumanMethylation27 platform. When the profiles of the prostate tissue samples were compared, I observed a substantial number of tumor-specific DNA methylation alterations. A 2-class Significance Analysis of this dataset revealed 5,912 CpG sites with increased DNA methylation and 2,151 CpG sites with decreased DNA methylation in tumors (FDR

DNA Methylation: Approaches, Methods and Applications describes the relation DNA methylation has to gene silencing in disease, and explores its promising role in treating cancer. Written by leaders in the field, this exceptional compilation of articles outlines the best techniques to use when addressing questions concerning the cytosine methylation

This book explores epigenetic strategies, bridging fundamental cancer epigenetics, different paradigms in tumor genetics and translational understanding for both the clinic and improved lifestyles. The work provides target-based insights for treating different types of cancers and presents research on evolutionary epigenetics, introducing ‘Medical Epi- Anthropology’ and ‘Cancer Epi-Anthropology’. Translating multi-disciplinary research into therapeutic design is at the core of this book. Readers may explore how cancer management involves unmasking the involved networks and the interactive status of different genes to achieve the appropriate methylome based therapy. Early chapters explore fundamental aspects and brain tumours, whilst later chapters investigate breast cancer and various other cancers, and the final chapter presents an evolutionary insight in cancer epigenetics, considering that the epigene is beyond DNA methylation, RNA interference and histone modification in cancer development. This book will be of interest to researchers in different medical and scientific fields, including clinical management (diagnosis, prognosis, prediction, prevention, and guidelines), genetic education, nutrition and nutrigenomics, industrial chemistry, and drug innovation. Because of the unique bridging between science and medicine this book will also be useful as an educational and translational research package.

This book will focus on DNA and histone methylation in epigenetics and describe how it is involved in the molecular mechanisms responsible for the development of cancer. Chapters will summarize the current knowledge of the molecular basis of DNA and histone methylation and explain how it is involved in cancer, describe the features of DNA and histone methylation associated with particular types of cancer, diagnostic/therapeutic applications, and future directions of DNA and histone methylation as cancer targets.

Epigenetic Mechanisms in Cancer provides a comprehensive analysis of epigenetic signatures that govern disease development, progression and metastasis. Epigenetic signatures dictating tumor etiologies present an opportunity for biomarker identification which has broad potential for improving diagnosis, prognosis, prediction, and risk assessment. This volumes offers a unique evaluation of signature differences in childhood, sex-specific and race-specific cancers, and in doing so broadly illuminates the scope of epigenetic biomarkers in clinical environments. Chapters detail the major epigenetic process in humans consisting of DNA methylation, histone modifications and microRNAs (miRNAs) involved in the initiation, progression and metastasis of tumors. Also delineated are recent technologies such as next generation sequencing that are used to identify epigenetic profiles (primarily methylation analysis) in samples (normal, benign and cancerous) and which are highly important to the analysis of epigenetic outcomes. Offers broad coverage that is applicable to audiences in various area of cancer research - population studies, diagnostics, prognosis, prediction, therapy, risk, etc. Provides critical review analysis

of the topics that will clarify and delineate the potential roles of epigenetic signatures in cancer management Covers basic, as well as, clinical areas of epigenetic mechanisms in tumorigenesis Features contributions by leading experts in the field Provides comprehensive coverage of current epigenetic signatures involved in the etiology of various cancers and miRNAs

“Gynaecological Malignancies - Updates and Advances” aims to present a review of the significant advances in the understanding and management of gynaecological malignancies. Major areas of importance in this field will be covered, incorporating new knowledge that has arisen due to the advancements in molecular techniques and the ability to correlate these molecular changes with clinical behaviour of gynaecologic tumours. The therapeutic implications of molecular subtyping to match appropriate therapies and the appreciation of the use of up to date radiotherapy techniques will be explored.

Cell Press Reviews: Cancer Therapeutics informs, inspires, and connects cancer researchers at all stages in their careers with timely, comprehensive reviews written by leaders in the field and curated by Cell Press editors. The publicatio offers a broad view of some of the most compelling topics in cancer therapeutics including: Genetic approaches for personal oncology Targeting epigenetic dysregulation and protein interaction networks Vaccines and antibodies in cancer immunotherapy Tumor heterogeneity and chemotherapy resistance Tumor associated macrophages in anticancer treatment Contributions come from leading voices in the field, including: - Daniel A. Haber, Director of Massachusetts General Hospital Cancer Center and Professor at Harvard Medical School - Tony Kouzarides, Professor at the University of Cambridge, Deputy Director of the Wellcome Trust/Cancer Research UK Gurdon Institute, and a founder of the cancer drug discovery company Chroma Therapeutics - Charles L. Sawyers, Chair of the Human Oncology and Pathogenesis Program at Memorial Sloan Kettering Cancer Center, President of the American Association for Cancer Research, member of the presidentially appointed National Cancer Advisory Board, and recipient of the 2013 Breakthrough Prize in Life Sciences Cell Press Reviews: Cancer Therapeutics is part of the Cell Press Reviews series, which features reviews published in Cell Press primary research and Trends reviews journals. Provides timely, comprehensive articles on a wide range of topics in cancer therapeutics Offers insight from experts on genetic, molecular, and cellular aspects of cancer therapy Features reviews on basic science advances translated into drug discovery and therapeutic approaches Includes articles originally published in Cell, Cancer Cell, Trends in Genetics, Trends in Molecular Medicine, and Trends in Pharmacological Sciences

"The regulation of the genome by the epigenetic modifications of DNA methylation and histone modification is increasingly recognized as a vital factor in the development, physiology and pathology of vertebrates. There is mounting evidence suggesting that both aberrant DNA methylation and histone modifications are common events in cancer. This has lead to the establishment of both DNMTs and HDACs as important targets in cancer therapy. There are currently several clinical trials that are testing inhibitors of both DNMTs and HDACs as anticancer agents. This thesis attempts to understand the roles that DNMT1 and HDAC1 play in the regulation of gene expression and epigenomic inheritance. In the first chapter, we examined the effects of DNMT1 inhibitors on gene expression and found that DNMT1 can regulate gene expression independent of its DNA methyltransferase activity. This novel role of DNMT1 has challenged a widely accepted theory that the mechanism of DNMT1 inhibitors involves inhibition of the catalytic activity of DNMT1, thus leading to demethylation and reexpression of tumor suppressors previously silenced by methylation. In chapter 2, we further examined different roles of DNMT1. We showed that different DNMT1 inhibitors inhibit different DNMT1 functions and produce different effects on gene expression. Our data suggests that inhibition of DNMT1 enzymatic activity can produce serious long-term effects as a result of massive non-selective demethylation of the genome. In contrast, reduction of DNMT1 levels was shown to result in a rapid arrest of cell growth, limited demethylation and induction of stress-response genes. We hypothesize that these effects are a result of the activation of an epigenetic check point that has evolved to protect the cell from undergoing replication in the absence of DNMT1. In chapter 3, we further explore the roles of DNMT1 in methylation independent regulation of gene expression, which has been suggested to in" --

Studies have shown that alterations of epigenetics and microRNAs (miRNAs) play critical roles in the initiation and progression of human cancer. Epigenetic silencing of tumor suppressor genes in cancer cells is generally mediated by DNA hypermethylation of CpG island promoter and histone modification such as methylation of histone H3 lysine 9 (H3K9) and tri-methylation of H3K27. MiRNAs are small non-coding RNAs that regulate expression of various target genes. Specific miRNAs are aberrantly expressed and play roles as tumor suppressors or oncogenes during carcinogenesis. Important tumor suppressor miRNAs are silenced by epigenetic alterations, resulting in activation of target oncogenes in human malignancies. Stem cells have the ability to perpetuate themselves through self-renewal and to generate mature cells of various tissues through differentiation. Accumulating evidence suggests that a subpopulation of cancer cells with distinct stem-like properties is responsible for tumor initiation, invasive growth, and metastasis formation, which is defined as cancer stem cells. Cancer stem cells are considered to be resistant to conventional chemotherapy and radiation therapy, suggesting that these cells are important targets of cancer therapy. DNA methylation, histone modification and miRNAs may be deeply involved in stem-like properties in cancer cells. Restoring the expression of tumor suppressor genes and miRNAs by chromatin modifying drugs may be a promising therapeutic approach for cancer stem cells. In this Research Topic, we discuss about alterations of epigenetics and miRNAs in cancer and cancer stem cell and understand the molecular mechanism underlying the formation of cancer stem cell, which may provide a novel insight for treatment of refractory cancer.

"Cancer cells have aberrant DNA methylation patterns which are characterized by hypomethylation of a large set of promoters and hypermethylation of tumor suppressor genes. The dynamic nature of the epigenome makes it a valuable target for therapeutic interventions. This thesis focuses on understanding the use of various inhibitors towards DNA methylation-related proteins and their respective anti-cancer activities at both global and gene-specific levels. The widely used demethylating agent 5-azacytidine and 5-aza-2'-deoxycytidine (5-azaCdR) are FDA-approved drugs for the treatment of myelodysplastic syndrome. However, these nucleoside analogs which trap the DNA methyltransferases (DNMTs) are non-specific. Studies have shown that 5-azaCdR induced pro-metastatic genes and caused long distance metastasis. This raises serious safety concerns for their clinical use. On the contrary, targeting the DNMTs individually or in combination did not result in dramatic induction of pro-metastatic genes as with 5-azaCdR treatment. In particular, single DNMT1-specific inhibition resulted in maximum growth suppression when compared to inhibition of all three major DNMTs, while not increasing cell invasiveness. DNMT1 has been shown to be important for cancer growth. Our study supports the idea that DNMT1 has a major role in cancer over the other DNMTs and that DNMT1 inhibitors could be effective anti-cancer drugs. 5-azaCdR has nevertheless been proven to be a potent suppressor of cancer growth. We tested the idea of a combinatorial treatment that may minimize its side-effects on cell invasion while maintaining its growth suppressor effects. The methyl-CpG binding protein 2 (MBD2) protein has been shown to demethylate pro-metastatic genes. Its inhibition in concurrent with 5-azaCdR treatment synergistically suppressed cancer growth, while reversed the 5-azaCdR-induced invasion. In order to have a deeper understanding of the impact of the treatments, microarrays studies on the methylome and transcriptome of the treated cells were carried out. Bioinformatics analysis indicated that the combined treatment suppressed gene networks that were involved in cell mobility, while synergistically enhanced gene networks that were involved in cell death. This data indicate that combining 5-azaCdR treatment with MBD2 inhibition results in more potent anti-cancer effects than either treatment alone. In order to explore the currently available drugs that inhibit MBD2, we tested the combination of S-adenosylmethionine (SAM) with 5-azaCdR on the same cancer cell lines. SAM remethylated gene promoters of pro-metastatic genes and repressed 5-azaCdR-induced invasion similarly to MBD2 inhibition. We then investigated the relationship between SAM and MBD2

downregulation and observed hypermethylation on both CpG and non-CpG sites in the MBD2 promoter upon SAM treatment. Interestingly, inhibition of MBD2 using short interference RNA also resulted in hypermethylation of its own promoter. This observation suggested that SAM treatment could directly downregulate MBD2 expression, which is further downregulated through a feedback loop. These results also suggested that SAM treatment could have a direct effect on MBD2 promoter, which in turn affects multiple MBD2 targets that are involved in invasion. Together, the data from this thesis support the idea that targeting the epigenome could be a highly efficacious anti-cancer therapy and that combining drugs that target DNA methylation could increase the potency over individual treatments." --

Sixty years after the "central dogma," great achievements have been developed in molecular biology. We have also learned the important functions of noncoding RNAs and epigenetic regulations. More importantly, whole genome sequencing and transcriptome analyses enabled us to diagnose specific diseases. This book is not only intended for students and researchers working in laboratory but also physicians and pharmacists. This volume consists of 14 chapters, divided into 4 parts. Each chapter is written by experts investigating biological stresses, epigenetic regulation, and functions of transcription factors in human diseases. All articles presented in this volume by excellent investigators provide new insights into the studies in transcriptional control in mammalian cells and will inspire us to develop or establish novel therapeutics against human diseases.

Cancer is one of the leading causes of death in most countries and its consequences result in huge economic, social and psychological burden. Breast cancer is the most frequently diagnosed cancer type and the leading cause of cancer death among females. In this book, we discussed gene expression and DNA abnormalities including methylation in breast cancer. A recent important topic, roles of miRNAs and their potential use in cancer therapy have been discussed in this cancer type as well. Bioinformatics is very important part of recent human genome developments and data mining and thus this topic has also been added for the readers. It is hoped that this book will contribute to development of novel diagnostic as well as therapeutic approaches, which lead to cure of breast cancer.

Cancer is a broad group of diseases involving unregulated cell growth with elevated death rates as more people live in old age with mass lifestyle changes occurring in the world. The causes of cancer are diverse, complex, and still only partially understood. The chances of surviving the disease vary remarkably by the type and location of the malignancy and the extent of disease at the start of treatment. Early cancer detection is proving to be a valid approach. Cancer can be detected in a number of ways, including the presence of certain signs and symptoms, screening tests, or medical imaging. Cancer therapy is dynamically changing and revision and change in patient management is constant as our knowledge increases. Cancer is routinely treated with chemotherapy, radiation therapy and surgery. Tailored cancer targeted therapy is becoming an emerging objective of today. In this book, a constructive group of cancer research experts bring the reader their shared vision, to give an extensive and realistic view of individual tumors such as breast, oral, prostate, gastric, and neuroendocrine tumors. New and contemporary terms and concepts in genetics and epigenetics, diet, anticancer treatments, and anticancer drug delivery systems are introduced in this volume. This reference highlights present experimental strategies and key findings that enhance our understanding of cancer and of future therapies. This eBook is aimed at a broad audience of undergraduates, medical students, PhDs, cancer researchers, and also cancer patient families with the goal to conceive a curiosity about the subjects presented that will hopefully lead to further studies.

Among the deadliest type of cancers, lung cancer faces several challenges in diagnosis and treatment: late diagnosis and misdiagnosis, inadequate tumor sampling, and resistance development to current therapies, among others. Together with advances in the understanding of molecular features, factors, and mechanisms involved in initiation and tumor progression, important improvements have occurred in diagnostics and therapeutics in the shape of advances in molecular genotyping, procedures for sampling, new potential, and less invasive sources of samples for the diagnosis and development of new targeted therapies. The aim of this book is to provide an exciting read on strategies in the diagnosis and therapy of lung cancer.

Overall, this book illustrates the complexities of the regulation and deregulation of genes mediated through epigenetics in the development and progression of human malignancies. All the articles have been carefully chosen to represent several cancer systems with state of our knowledge on the role of epigenetic deregulation of microRNAs (miRNAs) and their target mRNAs along with epigenetic deregulation of mRNAs. This book also illustrates the role of several dietary agents, collectively called nutraceuticals or natural agents in modulating the epigenetic reprogramming of miRNAs and mRNAs for the prevention and/or treatment of human malignancies. It is well known that genetic aberrations, especially inherited through parents (somatic genetic alterations) contribute to the development of less than 10% of all cancer yet epigenetic alterations in genes especially through selective methylation and acetylation appears to be responsible for the development and progression of the vast majority of all cancers. Therefore, understanding the role of epigenetics in the regulation of genes especially through deregulated expression of miRNAs as presented in this book will allow scientists to devise targeted therapeutic strategies for re-expression of the lost genes or down-regulate the genes that are over-expressed in order to eradicate cancer. It is hoped that targeting epigenetics will not only target cancer cells but it will also target the tumor microenvironment (more like the entire tumor environment such as the entire host) for achieving better treatment outcomes for patients diagnosed with cancer which will lead to achieve the long-term objective for complete eradication of cancer. This book contains fifteen chapters which begins with the concept of systems and network biology for investigating the epigenetics of cancer followed by a series of articles on the role of miRNAs and their target genes in the biology of pancreatic cancer and other cancers such as breast, kidney, prostate and and colon. Since it is becoming increasingly clear that cancer stem cells (CSCs) are important in the development and progression of cancer, and CSCs are important in therapeutic resistance, treatment failure and tumor recurrence, thus the importance of CSCs and epigenetics has been highlighted by a very timely article on epigenetic variations of stem cell markers in cancer including miRNAs. Moreover, just targeting heterogeneous cancer cell populations may not be optimal to eradicate tumors and for which one must take a holistic approach for developing drugs that could also target the tumor microenvironment and tumor dormancy that are regulated through epigenetics. Keeping abreast with this thought process the concluding chapter provides a concept towards curative cancer therapy with maspin, which could be a unique window of opportunity to target tumor dormancy. Therefore, it suggest that targeting the tumor dormancy and the tumor microenvironment using novel therapeutics specifically by targeting epigenetics would become the future of medicine.

Recent studies have indicated that epigenetic processes may play a major role in both cellular and organismal aging. These epigenetic processes include not only DNA methylation and

histone modifications, but also extend to many other epigenetic mediators such as the polycomb group proteins, chromosomal position effects, and noncoding RNA. The topics of this book range from fundamental changes in DNA methylation in aging to the most recent research on intervention into epigenetic modifications to modulate the aging process. The major topics of epigenetics and aging covered in this book are: 1) DNA methylation and histone modifications in aging; 2) Other epigenetic processes and aging; 3) Impact of epigenetics on aging; 4) Epigenetics of age-related diseases; 5) Epigenetic interventions and aging: and 6) Future directions in epigenetic aging research. The most studied of epigenetic processes, DNA methylation, has been associated with cellular aging and aging of organisms for many years. It is now apparent that both global and gene-specific alterations occur not only in DNA methylation during aging, but also in several histone alterations. Many epigenetic alterations can have an impact on aging processes such as stem cell aging, control of telomerase, modifications of telomeres, and epigenetic drift can impact the aging process as evident in the recent studies of aging monozygotic twins. Numerous age-related diseases are affected by epigenetic mechanisms. For example, recent studies have shown that DNA methylation is altered in Alzheimer's disease and autoimmunity. Other prevalent diseases that have been associated with age-related epigenetic changes include cancer and diabetes. Paternal age and epigenetic changes appear to have an effect on schizophrenia and epigenetic silencing has been associated with several of the progeroid syndromes of premature aging. Moreover, the impact of dietary or drug intervention into epigenetic processes as they affect normal aging or age-related diseases is becoming increasingly feasible.

Due in part to the selective nature of telomerase inhibition as an anticancer approach, the field has expanded considerably in the past decade. The recent advances in methods of telomerase inhibition encompass many different areas of research including molecular biology, cell biology, biochemistry, oncology and gerontology. Telomerase Inhibition provides methods and protocols for those researchers. The techniques described in this book should provide the researcher with a diverse and comprehensive set of tools with which to study telomerase inhibition. Leaders in the field provide recently developed methods that have widespread application such as targeting the telomerase holoenzyme, its RNA template and other elements associated with telomerase activity. Additional methods involving the screening of telomerase inhibitors and telomerase inhibition combined with other chemotherapeutic agents are presented. This text, on the cutting edge of the field, will provide investigators with the most recent methods applied to the expanding field of telomerase inhibition.

Cancer Epigenetics: Biomolecular Therapeutics in Human Cancer is the only resource to focus on biomolecular approaches to cancer therapy. Its presentation of the latest research in cancer biology reflects the interdisciplinary nature of the field and aims to facilitate collaboration between the basic, translational, and clinical sciences.

The growing knowledge about disturbances of epigenetic gene regulation in hematopoietic stem cell disorders is now being translated into treatment approaches that target the epigenetic defects pharmacologically. This book first presents the latest evidence regarding the epigenetic regulation of hematopoietic stem cell differentiation and hemoglobin production. The significance of DNA methylation abnormalities in hematopoietic disorders and of epigenetic disturbances in lung cancer and other solid tumors is then discussed. A major part of the book, however, relates specifically to the translation of basic research and drug development to clinical applications, and in this context both present and future clinical strategies are considered. Individual chapters are devoted to the use of DNA hypomethylating agents and chromatin-modifying agents, and the treatment of hematologic malignancies and solid tumors by means of epigenetic agents is discussed in detail.

The book helps the reader to better understand cytogenetics and the intricacies of the methodology. The different methods of fluorescence in situ hybridization are discussed and the results achieved are presented. The book provides a comprehensive review of basic and applied aspects of cytogenetics and thus is of intense interest to all those interested in chromosomes and their alterations by different types of mutagens, including chemical mutagens and ionizing and nonionizing radiation, with special reference to electromagnetic fields.

Nuts and bolts of biomarker research / Sharmistha Ghosh and Sudhir Srivastava -- Cancer genome methylation : biology, biomarker and therapeutic opportunities / Shashwat Sharad, Taduru Sreenath, Shiv Srivastava, and Albert Dobi -- Microrna biomarkers for early detection of cancer / Wendy Wang, Matthew R. Young, and Sudhir Srivastava -- Inflammation and cancer / Pamela L. Beatty, Sandra Cascio, and Olivera J Finn -- Exosomes : a valuable biomedical tool in biomarker discovery and development / Jocelyn Lee, Sharmistha Ghosh, and Sudhir Srivastava -- Epithelial-to-mesenchymal transition (EMT) : clinical implications / Elisa CWoodhouse and Suresh Mohla -- Breast cancer / Benjamin A. Katchman, Christos Patriotis, and Karen S Anderson -- Ovarian cancer / Christos Patriotis, Archana Simmons, Karen H. Lu, Robert C. Bast, Jr, and Steven J. Skates -- Esophageal cancer biomarkers / Yanxin Luo, Kishore Guda, Sanford Markowitz, Amitabh Chak, Andrew M Kaz, and William M Grady -- Predictive biomarkers for therapy in adenocarcinoma of the upper digestive tract / Heath D Skinner, Qiongrong Chen, Elena Elimova, Roopma Wadhwa, Shumei Song, and Jaffer A Ajani -- Pancreatic cancer / Sam CWang and Peter J Allen -- Colon cancer / Paul DWagner -- Prognosis and predictive biomarkers for colorectal cancer / Upender Manne, Balananda-Dhurjati Kumar Putcha, Temesgen Samuel, and Sudhir Srivastava -- Early detection of lung cancer / Mohamed Hassanein, Melinda C. Aldrich, Stephen A. Deppen, Karl E. Krueger, Eric L. Grogan, and Pierre P. Massion -- Commonalities in lung cancer and COPD / Malgorzata Wojtowicz and Eva Szabo -- Prostate cancer / Jacob Kagan, Ian M. Thompson, and Daniel W. Chan -- Improving the clinical validity of biomarker research in cancer detection / David F. Ransohoff -- Cancer overdiagnosis, ramifications and research strategies / Barbara K. Dunn and Barnett S. Kramer -- Predictive markers and driver genes from treatment trials : potential utility for early diagnosis / Brian S. Sorg, Sarfraz Memon, Kelly Y. Kim, Aniruddha Ganguly, Tracy Lively, James Tricoli, Magdalena Thurin, Lokesh Agrawal, Tawnya C. McKee, Barbara A. Conley, and J. Milburn Jessup -- Statistical consideration in predictive and prognostic markers / Fei Ye and Yu Shyr -- Clinical validation of molecular biomarkers in translational medicine / Harry B. Burke and William E. Grizzle -- Cancer biomarker assays : performance standards / Anna K Fuzery and Daniel W. Chan -- Bioethics and cancer biomarker research / Nathan Nobis, William Grizzle, and Stephen Sodeke -- Colon cancer screening / Molly Perencevich, Jennifer Inra, and Sapna Syngal

During the past few decades, it has become increasingly apparent that heredity is not the sole determining factor in disease development, such as cancer. This landmark work covers a wide array of aspects in the relatively new area of epigenetics, ranging from its role in the basic mechanisms of tumorigenesis, to the newest epigenetic drugs being developed and used for cancer therapy. Cancer Epigenetics presents in-depth discussions of DNA methylation alterations, histone and RNA modifications, and nucleosome remodeling, which are all intimately involved in the

formation of tumors. It also analyzes metabolic influences on cancer epigenetics and advances in epigenetic cancer gene therapy. Discusses the Latest Advances in the Role of Epigenetics in Tumor Initiation, Progression, and Metastasis With stand-alone chapters written by research pioneers in the field, this definitive resource covers— DNA methylation and cancer Histone modifications in cancer Emerging areas of cancer epigenetics Epigenetics in the diagnosis, prognosis, and therapy of cancer Future directions in epigenetic cancer research Bringing together different topics into a single compilation, this text is a prime resource for those with interests ranging from the basic mechanisms of tumor biology to cancer therapy. It also serves as a core textbook for advanced courses with a focus on genetic diseases, molecular biology, and/or cancer. This seminal work answers the call for a thorough and authoritative reference that covers the critical and contemporary aspects of this revolutionary field.

DNA methylation is an epigenetic process that occurs when a methyl group binds to one of DNA's four bases, cytosine. These changes are responsible for controlling the activity of genes by turning them off. This book contains ten articles that explore the details and challenges of cancer epigenetics.

NA methylation has bewildered molecular biologists since Hotchkiss discovered it almost six decades ago (Hotchkiss RDJ. Biol Cem 1948; 175:315-332). The fact that the chemical structure of our D genome consists of two components that are covalently bound, the genetic information that is replicated by the DNA replication machinery ana DNA methylation that is maintainea by independent enzymatic machinery, has redictably stimulated the imagination and curiosity of generations of mo Edular biologists. An obvious question was whether DNA methylation was a bearer of additional information to the genetic information and what was the nature of this information? It was tempting to speculate that DNA me thylation applied some form of control over programming of the genome s expression profile. Once techniques to probe the methylation profile of whole genomes as well as specific genes became available, it became clear that DNA methylation patterns are gene and tissue specific and that patterns of gene expression correlate with patterns of methylation. DNA methylation pat terns emerged as the only component of the chemical structure of DNA that exhibited tissue and cell specificity. This data seemingly provided an attrac tively simple explanation for the longstanding dilemma of how could one identical genome manifest itself in so many different forms in multicellular organisms? The DNA methylation pattern has thus become the only known factor to confer upon DNA a unique cellular identity.

Epigenetic Cancer Therapy unites issues central to a translational audience actively seeking to understand the topic. It is ideal for cancer specialists, including oncologists and clinicians, but also provides valuable information for researchers, academics, students, governments, and decision-makers in the healthcare sector. The text covers the basic background of the epigenome, aberrant epigenetics, and its potential as a target for cancer therapy, and includes individual chapters on the state of epigenome knowledge in specific cancers (including lung, breast, prostate, liver). The book encompasses both large-scale intergovernmental initiatives as well as recent findings across cancer stem cells, rational drug design, clinical trials, and chemopreventative strategies. As a whole, the work articulates and raises the profile of epigenetics as a therapeutic option in the future management of cancer. Concisely summarizes the therapeutic implications of recent, large-scale epigenome studies, including the cancer epigenome atlas Discusses targeted isoform specific versus pan-specific inhibitors, a rational drug design approach to epigenetics relevant to pharmacoepigenetic clinical applications Covers new findings in the interplay between cancer stem cells (CSCs) and drug resistance, demonstrating that epigenetic machinery is a candidate target for the eradication of these CSCs

Epigenetics is one of the fastest growing fields of sciences, illuminating studies of human diseases by looking beyond genetic make-up and acknowledging that outside factors play a role in gene expression. The goal of this volume is to highlight those diseases or conditions for which we have advanced knowledge of epigenetic factors such as cancer, autoimmune disorders and aging as well as those that are yielding exciting breakthroughs in epigenetics such as diabetes, neurobiological disorders and cardiovascular disease. Where applicable, attempts are made to not only detail the role of epigenetics in the etiology, progression, diagnosis and prognosis of these diseases, but also novel epigenetic approaches to the treatment of these diseases. Chapters are also presented on human imprinting disorders, respiratory diseases, infectious diseases and gynecological and reproductive diseases. Since epigenetics plays a major role in the aging process, advances in the epigenetics of aging are highly relevant to many age-related human diseases. Therefore, this volume closes with chapters on aging epigenetics and breakthroughs that have been made to delay the aging process through epigenetic approaches. With its translational focus, this book will serve as valuable reference for both basic scientists and clinicians alike. Comprehensive coverage of fundamental and emergent science and clinical usage Side-by-side coverage of the basis of epigenetic diseases and their treatments Evaluation of recent epigenetic clinical breakthroughs

Restriction Landmark Genomic Scanning (RLGS) is a new multiplex method for simultaneous analysis of over 3,000 genome loci. Written by the inventor of RLGS, Yoshihide Hayashizaki, and his co-workers, this is the first manual on this method. RLGS is a powerful technique with enormous potential for biological (animal and plant sciences), and biomedical research. Yielding results much faster than conventional techniques, RLGS is particularly suited to the identification of the chromosomal location of the genes implicated in inherited diseases, and for the genetic disturbances present in cancerous tissue.

Alterations in the normal DNA methylation processes are known to have major consequences for embryonic development and are associated with congenital defects, autoimmunity, aging and malignant transformation. The main purpose of this book is to provide information about the importance of methylation mechanisms in human health and disease. The book, covers the basic mechanism of DNA and protein methylation, aiming at the advanced undergraduate and graduate biomedical students and researchers working in the epigenetic area. The textbook chapters provide background as well as advanced information in the methylation area. On the other hand, it provide readers with both classical and relevant recent discoveries that have been made in the field, pointing out pathways where questions remain.

Recent advances in the fields of genomics and bioinformatics have made it increasingly clear that genetic sequence alone cannot explain how the genome regulates the development and function of complex multicellular organisms both in health and disease. This inference has led to the expansion of epigenetics as a discipline. Epigenetics refers to the way in which the environment in the wide sense participates in the regulation of gene expression. Several studies show that the well-known beneficial role of a healthy lifestyle over a number of pathologies or as a pre-emptive therapy is at least in part exerted through epigenetic mechanisms, thus giving rise to a new paradigm of preventive medicine based on the concept of genetic plasticity. In Epigenetics of Lifestyle, several contributors provide a comprehensive view of how various facets of lifestyle, including nutrition, exercise, stress, addiction or social interactions, affect chromatin (the combination of DNA and proteins that make up the contents of a cell nucleus) - resulting in profound and long-lasting changes in gene function. In summary, Epigenetics of Lifestyle is a fresh approach towards epigenetics and presents the reader with significant research findings in epigenetics and lifestyle studies. This volume is a simplified source of information for both undergraduate and working professionals interested in lifestyle medicine and life sciences in general.

Handbook of Epigenetics: The New Molecular and Medical Genetics, Second Edition, provides a comprehensive analysis of epigenetics, from basic biology, to clinical application. Epigenetics is considered by many to be the new genetics in that many biological phenomena are controlled, not through gene mutations, but rather through reversible and heritable epigenetic processes. These epigenetic processes range from DNA methylation to prions. The biological processes impacted by epigenetics are vast and encompass effects in lower organisms and humans that include tissue and organ regeneration, X-

chromosome inactivation, stem cell differentiation, genomic imprinting, and aging. The first edition of this important work received excellent reviews; the second edition continues its comprehensive coverage adding more current research and new topics based on customer and reader reviews, including new discoveries, approved therapeutics, and clinical trials. From molecular mechanisms and epigenetic technology, to discoveries in human disease and clinical epigenetics, the nature and applications of the science is presented for those with interests ranging from the fundamental basis of epigenetics, to therapeutic interventions for epigenetic-based disorders. Timely and comprehensive collection of fully up-to-date reviews on epigenetics that are organized into one volume and written by leading figures in the field Covers the latest advances in many different areas of epigenetics, ranging from basic aspects, to technologies, to clinical medicine Written at a verbal and technical level that can be understood by scientists and college students Updated to include new epigenetic discoveries, newly approved therapeutics, and clinical trials