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Epigenetic Mechanisms in Cancer Epigenetics Territory and Cancer Cancer Epigenetics Drug Discovery in Cancer Epigenetics Cancer Epigenetics Epigenetic Cancer Therapy Epigenetics and Cancer Cancer Epigenetics for Precision Medicine Epigenetic Advancements in Cancer Cancer Epigenetics Epigenetics of Cancer Prevention Cancer Epigenetics Epigenetic Alterations in Oncogenesis Alterations of Epigenetics and MicroRNAs in Cancer and Cancer Stem Cell Epigenetics in Cancer: Mechanisms and Drug Development Metabolism and Epigenetic Regulation: Implications in Cancer Epigenetics in Cancer The Role of Epigenetic Modifications in Cancer Progression Epigenetic Cancer Therapy Epigenetic Regulation of Cancer in Response to Chemotherapy Epigenetics in Cancer Prevention DNA Methylation, Epigenetics and Metastasis Epigenetic Alterations in Oncogenesis Computational Epigenetics and Diseases Epigenetics in Cancer Epigenetics and Gene Expression in Cancer, Inflammatory and Immune Diseases Genetics and Epigenetics of Breast Cancer Genetic and Epigenetic Control on Immune Responses Regulating Molecules in Cancer Development, Progression, and Treatment Epigenetics and Cancer Epigenetics in Cancer Epigenetics for Drug Discovery Epigenetics in Biology and Medicine Cancer For researchers Introduction to Epigenetics Systems Analysis of Chromatin-Related Protein Complexes in Cancer DNA and Histone Methylation as Cancer Targets Epigenetics in Cancer and Tumor Progression Patho-Epigenetics of Disease The Epigenetics Revolution Medical Epigenetics

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 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. This open access textbook leads the reader from basic concepts of chromatin structure and function and RNA mechanisms to the understanding of epigenetics, imprinting, regeneration and reprogramming. The textbook treats epigenetic phenomena in animals, as well as plants. Written by four internationally known experts and senior lecturers in this field, it provides a valuable tool for Master- and PhD- students who need to comprehend the principles of epigenetics, or wish to gain a deeper knowledge in this field. After reading

this book, the student will: Have an understanding of the basic toolbox of epigenetic regulation Know how genetic and epigenetic information layers are interconnected Be able to explain complex epigenetic phenomena by understanding the structures and principles of the underlying molecular mechanisms Understand how misregulated epigenetic mechanisms can lead to disease The epigenetic regulation plays an important role in normal development and maintenance of tissue specific genes expression in humans and the disturbance of these patterns lead to changes involved in tumor formation. More recently, epigenetic changes have been observed in early stages of tumor development and together with the genetic alterations have been defined as abnormalities, necessary for cancer initiation and progression. In, Cancer Epigenetics: Methods and Protocols, expert researchers reviewed these epigenetics changes in different tumor types and described several technologies that are currently available to detect epigenetic changes. These technologies have lead to a better understanding of the processes in normal and cancerous cells. Written in the highly successful Methods in Molecular BiologyTM series format, the chapters include the kind of detailed description and implementation advice that is crucial for getting optimal results in the laboratory. Thorough and intuitive, Cancer Epigenetics: Methods and Protocols aids scientists in continuing to study epigenetic alterations used in clinical practice as biomarkers of early cancerous lesions or markers of progression and prognosis. Epigenetic Cancer Therapy, Second Edition provides a comprehensive discussion of healthy and aberrant epigenetic biology, along with new discoveries to improve our understanding of cancer epigenetics and therapeutics. The book encompasses 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. Since the publication of the first edition of this book, the field of epigenetics has undergone significant change. New epigenetic therapies have been designed and approved for clinical use. Our knowledge of the plasticity of the epigenome in cancer and disease has expanded dramatically, with increasing evidence linking pollution to epigenetic changes in cancer development. This second edition has been fully updated to address these changes, along with promising therapeutic programs such as CRISPR/Cas9 mediated approaches, CAR-T based therapies, epigenetic priming, histone modifications, and similar, transformative advances across synthetic biology and cellular engineering. 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. 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 This volume discusses certain epigenetic changes recognized in early carcinogenic lesions and different tumors, as well as factors that alter the epigenome and epigenetic profile such as diet, alcohol, immunity, circadian rhythm, and more. The chapters in this book further delve into this field and cover topics such as epigenome-based precision medicine in lung cancer; interplay between genetic and epigenetic changes in breast cancer subtypes; genetic regulation of PDCD1 gene in cancer immunology; and pyrosequencing methylation analysis. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Cutting-edge and authoritative, Cancer Epigenetics for Precision Medicine: Methods and Protocols is a valuable resource to help researchers and scientists identify these specific biomarkers and work towards the prevention, diagnosis, and prognosis of different cancers in the future. The purpose of this book is to provide an up to date review of the nature and consequences of epigenetic changes in cancer. Epigenetics literally means “ above ” genetics, and consists of heritable gene expression or other phenotypic states not accounted for by DNA base sequence. Epigenetic changes are now known to make a large contribution to various aspects of tumorigenesis. These changes include alterations in global and promoter specific DNA methylation, activating and repressive histone modifications, and changes in higher order chromatin structures. Each of these topics will be covered in this book. 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. This volume shares technologies that detect common epigenetic changes which are very important in the early detection, progression, and prognosis of cancer as well as the design of new therapeutic tools against cancer cells. Beginning with a bit of background on epigenetic mechanisms, Cancer Epigenetics: Risk Assessment, Diagnosis, Treatment, and Prognosis continues with cancer specific type epigenetic change, methods and technologies used for detecting epigenetic changes, factors that influence epigenetic changes in cancer, as well as a final section on future directions in the field. Written for the highly successful Methods in Molecular Biology series, chapters in this volume include the kind of detailed implementation advice that guarantees easily reproducible results. Comprehensive and practical, Cancer Epigenetics: Risk Assessment, Diagnosis, Treatment, and Prognosis provides the most up-to-date knowledge of epigenetics and its implication in cancer prevention by risk assessment and screening and cancer control by treatment. In multicellular organisms the establishment, maintenance, and programmed alterations of cell-type specific gene expression patterns are regulated by epigenetic mechanisms. Thus, epigenetic alterations (DNA methylation, DNA associated Polycomb-Trithorax protein complexes, histone modifications) ensure the unique transcriptional activity and phenotypic diversity of diploid cells that carry identical or nearly identical DNA sequences. Because DNA methyltransferase I (DNMT1) associates with replication foci during S phase and prefers hemimethylated DNA as a substrate, DNMT1 ensures the clonal propagation of cytosine methylation patterns (maintenance methylation). Thus, DNA methylation may provide a memory function by helping progeny cells to “ remember ” their proper cellular identity. An alternative system of epigenetic memory, the Polycomb and Trithorax groups of protein complexes, that may operate both independently from and in concert with DNA methylation, ensures the heritable regulation of gene expression via modification of histone tails. The complex interplay of epigenetic regulatory mechanisms permits both the dynamic modulation of gene expression and the faithful transmission of gene expression patterns to each progeny cell upon division. These carefully orchestrated processes can go wrong, however, resulting in epigenetic reprogramming of the cells that may manifest in pathological changes, as it was first realized during the studies of epigenetic alterations in malignant tumors. By now it became a well established fact that not only genetic changes, but also the disruption of epigenetic regulation can result in carcinogenesis and tumor progression. Scientists working in other fields soon followed the pioneering work of cancer researchers, and revealed that epigenetic dysregulation forms the basis of a wide spectrum of human diseases. Epigenetics is the study of heritable changes in gene expression or cellular phenotype, caused by mechanisms other than changes in the DNA sequence. Examples include DNA methylation and histone modification. These changes may remain through cell divisions and multiple generations. Epigenetic differences among individuals may account for some of the differences between monozygotic (identical) twins. Aberrant DNA methylation is also frequently associated with human aging and diseases, such as cancer. This collection of overviews and laboratory protocols provides crucial, distilled information about the roles of epigenetics in cancer development. The overviews are geared for research scientists who need to learn more about the current understanding of epigenetic variation in humans and how the processes of DNA methylation and histone modification are regulated. The protocols give step-by-step instructions on how to detect DNA methylation using various methods such as MAPit, CHARM (arrays) and methylation-specific PCR. This e-book — a curated collection from eLS, WIREs, and Current Protocols — offers a fantastic introduction to

the fields of genetics, genomics, and oncogenesis for students or interdisciplinary collaborators. Table of Contents: Introduction Epigenetic Variation in Humans eLS Jon F. Wilkins Genetic and Epigenetic Heterogeneity in Cancer eLS Joshua B. Stevens, Batoul Y. Abdallah, Steven D. Horne, Guo Liu, Steven W. Bremer and Henry H. Heng Techniques & Applications Mediators and Dynamics of DNA Methylation WIREs Systems Biology and Medicine Robert Shoemaker, Wei Wang and Kun Zhang DNA Methylation Alterations in Multiple Myeloma as a Model for Epigenetic Changes in Cancer WIREs Systems Biology and Medicine Amy Sharma, Christoph J. Heuck, Melissa J. Fazzari, Jayesh Mehta, Seema Singhal, John M. Greally and Amit Verma Ink4?-Arf Locus in Cancer and Aging WIREs Developmental Biology Charles J. Sherr Protocols Simultaneous Single-Molecule Mapping of Protein-DNA Interactions and DNA Methylation by MAPit Current Protocols in Molecular Biology Carolina E. Pardo, Russell P. Darst, Nancy H. Nabilsi, Amber L. Delmas and Michael P. Kladde Comprehensive High-Throughput Arrays for Relative Methylation (CHARM) Current Protocols in Human Genetics Christine Ladd-Acosta, Martin J. Aryee, Jared M. Ordway and Andrew P. Feinberg Methylation-specific PCR Current Protocols in Human Genetics Bradford Coffee This thesis investigates epigenetics in cancer with particular emphasis on breast cancer. There are two major themes, see Figure above. The first theme relates to the potential for assessing and developing more efficient epigenetic drugs while the second theme investigates mechanism of downregulation of ANKRD11, a putative tumour suppressor gene, in human breast cancer. This thesis is in the publication format with Chapters 1 and 3 as published articles, Chapter 2 submitted for publication and Chapter 4 as a manuscript in preparation. Theme 1: To improve the epigenetic-based therapeutic approach (Chapter 1 and 2). One of the roles that epigenetics plays in cancer development is the inhibition of transcription of tumour suppressor genes. Chapter 1, published as a review in Biodrugs, examines the knowledge of currently available therapeutic approaches related to epigenetic mechanisms such as DNA methylation for cancer treatment. Drug-related issues that could influence the application of therapeutics for clinical use are reviewed and possible developments to improve the clinical use of the drugs explored. Epigenetic-based drugs are emerging as anti-cancer therapies in the clinic. Existing demethylating agents have poor pharmacological properties that limit their clinical use, and the application of nano-based encapsulation to resolve these issues is discussed. Chapter 2, submitted as an original research article to Biodrugs, presents the development and assessment of an assay to allow comparison of epigenetic-related drugs in a high throughput format. Decitabine is encapsulated in a liposomal formulation and the potency of this newly formulated decitabine and existing drugs are effectively compared using the developed assay system. Further development and validation of the assay system and the liposomal formulated decitabine, not included in the submitted manuscript are included as supplementary data. Theme 2: Investigation of gene silencing mechanism of tumour suppressor ANKRD11 (Chapter 3 and 4). ANKRD11 is novel gene that was previously characterised in our laboratory, and found to be a putative tumour suppressor gene and a p53-coactivator (Neilsen et al. 2008). Chapter 3, published in European Journal of Cancer, investigates the mechanism of downregulation of ANKRD11 in human breast cancer. This chapter identifies the promoter sequence of ANKRD11, demonstrates the critical region of the ANKRD11 promoter subjected to DNA methylation, and associates the DNA methylation levels of ANKRD11 with its gene expression and clinical data. Further analysis of the DNA methylation pattern of this gene revealed a putative GLI1 transcription-factor binding site within the localised region of the promoter that is methylated. Chapter 4, presented as a manuscript in preparation, further explores the relationship between ANKRD11 and GLI1 in breast cancer. GLI1 is a Hedgehog signalling transcription factor, which has been shown to be involved in breast cancer development. This study analyses the transcriptional activity of ANKRD11 in the cells overexpressed with GLI1 and quantifies differential expression of these two genes in different stages of breast cancer. Future experiments to confirm and extend these exciting preliminary findings are discussed. The final chapter of this thesis summarises the findings of these studies and possible future research directions. The impact of these

findings for the development of anti-cancer drugs, and the possible role of expression of ANKRD11 and GLI1 in breast cancer are highlighted. This volume explores the epigenetic alterations and their association with various human cancers. Considering one of human cancer as an example, individual chapters are focused on defining the role of epigenetic regulators and underlying mechanisms in cancer growth and progression. Epigenetic alteration including DNA methylation, histone modification, nucleosome positioning and non-coding RNAs expression are involved in a complex network of regulating expression of oncogenes and tumor suppressor genes and constitute an important event of the multistep process of carcinogenesis. Recent advances in the understanding of the epigenetic regulation and detailed information of these epigenetic changes in various cancers provide new avenues of advancements in diagnostics, prognostics, and therapies of this highly fatal disease. Cancer is a class of diseases in which a group of cells display the traits of uncontrolled growth, invasion, and sometimes metastasis. These three malignant properties of cancers differentiate them from benign tumors, which are self-limited, do not invade or metastasize. Most cancers form a tumor but not all cancer e.g. leukemia.Cancer may affect people at all ages, even fetuses, but risk for the more common varieties tends to increase with age. Nearly all cancers are caused by abnormalities in the genetic material of the transformed cells. These abnormalities may be due to the effects of carcinogens, such as tobacco smoke, radiation, chemicals, or infectious agents. Other cancer-promoting genetic abnormalities may be randomly acquired through errors in DNA replication or are inherited and thus present in all cells from birth. Complex interactions between carcinogens and the host genome can explain mechanism of cancers develop after exposure to a known carcinogen.This book addresses the biomolecular mechanisms of new aspects of genetics in the initiation of Cancer and progression of Tumor. Epigenetics of Cancer Prevention, Volume Ten is the first to look at epigenetics and chemoprevention together. Although there is numerous scientific data available on how epigenetics can lead to cancer and how chemoprevention can be beneficial in the treatment of, or improvement of quality of life, together they will set an advanced understanding for the reader in this upcoming field of chemoprevention influencing epigenetics. This book discusses molecular epigenetic targets of natural products, such as green tea polyphenols, curcumin and resveratrol, and organ specific epigenetic targets related to diverse types of cancer, for example prostate, colorectal, breast, lung and skin cancers. Additionally, it encompasses a discussion on research methods and limitations to study epigenetics and epigenomics of chemopreventive drugs and personalized cancer treatment with phytochemicals. The book is ideal for cancer researchers, health care professionals and all individuals who are interested in cancer prevention research and its clinical applications, especially in natural remedies. Lists natural agents, including nutraceuticals, and their effects on normal or tumor genome Addresses various epigenetic systems and mechanisms in the regulation and support of the mammalian genome Discusses how various parts of dietary phytochemicals can influence or modify epigenetic mechanisms in several types of cancer The purpose of this book is to provide an up to date review of the nature and consequences of epigenetic changes in cancer. Epigenetics literally means “ above ” genetics, and consists of heritable gene expression or other phenotypic states not accounted for by DNA base sequence. Epigenetic changes are now known to make a large contribution to various aspects of tumorigenesis. These changes include alterations in global and promoter specific DNA methylation, activating and repressive histone modifications, and changes in higher order chromatin structures. Each of these topics will be covered in this book. Chapter 1: History Chapter 2: Cancer biology 2.1 cellular and molecular 2.2 Genetics 2.3 Epigenetics 2.4 Metastasis 2.5 Metabolism Chapter 3: Causes 3.1 Chemicals 3.2 Diet and exercise 3.3 Infection 3.4 Radiation 3.5 Heredity 3.6 Physical agents 3.7 Hormones 3.8 Autoimmune diseases Chapter 4: Classification 4.1 Carcinoma 4.2 Sarcoma 4.3 Blastoma 4.4 Lymphoma and leukemia Chapter 5: Treatment 5.1 Chemotherapy 5.2 Radiotherapy 5.3 Surgery 5.4 Immunotherapy Chapter 6: Vaccine Medical Epigenetics, Second Edition provides a comprehensive analysis of epigenetics in health management, across a broad spectrum of disease categories and specialties, and with a focus on human

systems, epigenetic diseases that affect these systems, and evolving modes of epigenetic-based treatment. Here, more than 40 leading researchers examine how each human system is affected by epigenetic maladies, offering an all-in-one resource on medical epigenetics not only for those directly involved with health care, but investigators in life sciences, biotech companies, graduate students, and others who are interested in applied aspects of epigenetics. Incorporating both diagnostic and prognostic epigenetic approaches, this volume also fully supports the application of epigenetics in precision medicine. This second edition of Medical Epigenetics, a volume in the Translational Epigenetics series, has been fully revised to address recent advances in disease epigenetics and role of epigenetics in precision medicine, with all-new chapters on skin cancer epigenetics, network analysis in medical epigenetics, machine learning in epigenetic diseases, and clinical trials of epigenetics drugs. Features chapters from leading researchers and clinicians dedicated to the burgeoning role of epigenetics in medical practice Covers emerging topics, including twin epigenetics, as well as epigenetics of gastrointestinal disease, muscle disorders, endocrine disorders, ocular medicine, pediatric diseases, sports medicine, noncoding RNA therapeutics, pain management and regenerative medicine Organized from system disorders to multi-system disorders that involve epigenetic aberrations Examines the role of epigenetics in precision medicine Addresses the importance of fighting cancers with an epigenetics approach. The book also includes a chapter that provides short but practical protocols widely used in epigenetics research. Finally, it provides insight into future directions in cancer epigenetics research. Metabolic programs of individuals are key determinants for disease susceptibility and immune response. This book, edited by experts in the field, summarizes epigenetic signaling pathways that regulate metabolic programs associated with cancer and cancer-related secondary diseases. The first part of the book highlights key metabolic pathways that are implicated in cancer and provides a comprehensive overview on the carbohydrate, protein, lipid, amino- and nucleic acid metabolic pathways that are deregulated in cancer. Special attention is paid to the altered tumor micro-environment that is influenced by the metabolic milieu. Furthermore, the fundamental relationship between the cellular metabolic environment and cell death-mediated autophagy is discussed. The second part of the book covers our understanding of the fundamental epigenetic regulations that are implicated in controlling the metabolic programs in cancer cells. Many aspects of epigenetic regulation of non-coding RNAs as well as DNA/RNA methylation, which influencing metabolic homeostasis in cancer, are discussed in detail. Special emphasis is placed on the epigenetic regulation of the amino acid, glucose/carbohydrate metabolism and epigenetic regulation during hypoxia and its connection to cancer. Last but not least, the third part of the book covers small molecule modulators of histone modifying enzymes, which can be used as therapeutic tools. The readers learn about the cross-talk between epigenetics and immunometabolims, as well as the epigenetic regulation of oncometabolites to combat cancer. Given its scope, the book will appeal to a broad readership interested in epigenetic, cancer and metabolic research. This book provides a broad and rich outline of the epigenetic mechanisms involved in cancer progression and the generation of metastasis. It describes the tumor suppressor genes undergoing transcriptional silencing by CpG island promoter hypermethylation in the different tumor types of the human anatomy and their association with tumoral behaviour. It also provides a comprehensive insightful look at the molecular players involved in DNA methylation, histone modification and chromatin remodelling complexes causing epigenetic lesions linked to the metastasic phenotypes. Finally, it explains how epigenetic lesions associated with cancer spreading can be targeted using new and potent chemotherapy drugs. The book is a state-of-the-art reference to all scientific researchers and clinicians interested in the understanding of the biological processes leading to tumor dissemination and to those that are keen to translate this knowledge to a better management of cancer patients. Each contributor is a specialist in their epigenetic area and their joint effort has created a unique view of the DNA methylation, histone and chromatin changes that define cancer metastasis. This book discusses the contribution of genetics and epigenetics alterations in the initiation, development, and recurrence of breast cancer. It also reviews the

potential of translating the epigenetic alterations into diagnosis, prognosis, and breast cancer therapy. The initial chapters explore the epigenetics, etiology, and conventional treatment strategies for breast cancer. The subsequent chapters discuss the genetic landscape and cover three main epigenetic modulation mechanisms; histone modification, DNA methylation, and miRNA silencing. Further, the book explores the potential of epigenetic drugs in treating breast cancer. Lastly, it covers the phytochemicals targeting epigenetic modulators in breast cancer treatment. This book is an essential source for researchers and practitioners interested in exploring the potential of epigenetics modulators in breast cancer treatment. Drug Discovery in Cancer Epigenetics is a practical resource for scientists involved in the discovery, testing, and development of epigenetic cancer drugs. Epigenetic modifications can have significant implications for translational science as biomarkers for diagnosis, prognosis or therapy prediction. Most importantly, epigenetic modifications are reversible and epigenetic players are found mutated in different cancers; therefore, they provide attractive therapeutic targets. There has been great interest in developing and testing epigenetic drugs, which inhibit DNA methyltransferases, histone modifying enzymes or chromatin reader proteins. The first few drugs are already FDA approved and have made their way into clinical settings. This book provides a comprehensive summary of the epigenetic drugs currently available and aims to increase awareness in this area to foster more rapid translation of epigenetic drugs into the clinic. Highlights the potential of epigenetic alterations in cancer for drug development Covers the tools and methods for epigenetic drug discovery, preclinical and clinical testing, and clinical implications of epigenetic therapy Provides important information regarding putative epigenetic targets, epigenetic technologies, networks and consortia for epigenetic drug discovery and routes for translation 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 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. Genes interact with the environment, experience, and biology of the brain to shape an animal ' s behavior. This latest volume in Advances in Genetics, organized according to the most widely used model organisms, describes the latest genetic discoveries in relation to neural circuit development and activity. Explores the latest topics in neural circuits and behavior research in zebrafish, drosophila, C.elegans, and mouse models Includes methods for testing with ethical, legal, and social implications Critically analyzes future prospects Epigenetics can potentially revolutionize our understanding of the structure and behavior of biological life on Earth. It explains why mapping an organism's genetic code is not enough to determine how it develops or acts and shows how nurture combines with nature to engineer biological diversity. Surveying the twenty-year history of the field

while also highlighting its latest findings and innovations, this volume provides a readily understandable introduction to the foundations of epigenetics. Nessa Carey, a leading epigenetics researcher, connects the field's arguments to such diverse phenomena as how ants and queen bees control their colonies; why tortoiseshell cats are always female; why some plants need cold weather before they can flower; and how our bodies age and develop disease. Reaching beyond biology, epigenetics now informs work on drug addiction, the long-term effects of famine, and the physical and psychological consequences of childhood trauma. Carey concludes with a discussion of the future directions for this research and its ability to improve human health and well-being. This volume addresses the question of how knowledge of epigenetic phenomena like DNA methylation and acetylation can be applied to early cancer detection and risk assessment. The objectives of the papers include defining the terminology used in epigenetics. Epigenetic Regulation of Cancer in Response to Chemotherapy, Volume 158 of the Advances in Cancer Research series, highlights new advances in the field, with this new volume presenting chapters on timely topics, including Epigenetically Programmed Resistance to Chemotherapy and Promotion of Immune Evasion in Cancer, A Role for the Epigenome in Cancer Cell Drug Tolerance, Histone Methylation and X Chromosomal Genes in Metastasis of Breast Cancer, Targeting Epigenetic Regulation Using Small Molecule Inhibitors, Histone Deacetylase Inhibitors as Sanguine Epigenetic Therapeutics against Pugnacious Lung Cancer, From ecology to oncology: To understand cancer stem cell dormancy, ask a Brine shrimp (Artemia), and more. Additional chapters cover Predictive Models of Chemoresistance Generated by Crunching the Public Drug Screen, Epigenomic and Genomic Profiling Datasets via Regression-, Machine Learning, and Knowledge-Based Methods, Probing on the Mechanisms of lncRNAs on Cancer Drug Resistance, Drug Tolerant Persister Cells in Cancer: Current Knowledge and Therapeutic Perspectives, and much more. Provides the authority and expertise of leading contributors from an international board of authors Presents the latest release in the Advances in Cancer Research series Includes the latest information on the Epigenetic Regulation of Cancer in Response to Chemotherapy This book will provide an invaluable guide to epigenetics, one of the fastest moving fields in drug discovery, for medicinal chemists working in academia and in the pharmaceutical industry. 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. This practical collection examines methodologies originating from the benefits of genome-wide approaches to studying epigenetics, which has opened the emerging field of epigenomics. Focusing on the areas of cancer, inflammatory and autoimmune disorders, chapters discuss three main components of the epigenome and their role in the regulation of gene expression and present a detailed method section specific

to studying each component, including data analyses, troubleshooting, and feasibility in different experimental settings. The main topics are high-throughput and targeted methods for DNA methylation analysis, nucleosome position mapping, studying epigenetic effects of gut microbiota, optical imaging for detection of epigenetic aberrations in living cells, methods for microRNA, and histone code profiling. Written for the Methods in Pharmacology and Toxicology series, the book includes the kind of detail and implementation advice to encourage success in the lab. Authoritative and easily applicable, Epigenetics and Gene Expression in Cancer, Inflammatory and Immune Diseases aims to provide pharmacologists, molecular biologists, bioinformaticians, and toxicologists with a vital background on epigenetics and state-of-the-art techniques in epigenomics. 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.

Epigenetic modifications underlie all aspects of human physiology, including stem cell renewal, formation of cell types and tissues. They also underlie environmental impacts on human health, including aging and diseases like cancer. Consequently, cracking the epigenetic "code" is considered a key challenge in biomedical research. Chromatin structure and function are modified by protein complexes, causing genes to be turned “ on ” or “ off ” and controlling other aspects of DNA function. Yet while there has been explosive growth in the epigenetics field, human chromatin-modifying machines have only recently started to be characterized. To meet this challenge, our book explores complementary experimental tracks, pursued by expert international research groups, aimed at the physical and functional characterization of the diverse repertoire of chromatin protein machines - namely, the "readers, writers and erasers" of epigenomic marks. These studies include the identification of RNA molecules and drugs that interact selectively with components of the chromatin machinery. What makes this book distinctive is its emphasis on the systematic exploration of chromatin protein complexes in the context of human development and disease networks. Computational Epigenetics and Diseases, written by leading scientists in this evolving field, provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases. In particular, the major computational tools, databases, and strategies for computational epigenetics analysis, for example, DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA, are summarized, in the context of human diseases. This book discusses bioinformatics methods for epigenetic analysis specifically applied to human conditions such as aging, atherosclerosis, diabetes mellitus, schizophrenia, bipolar disorder, Alzheimer disease, Parkinson disease, liver and autoimmune disorders, and reproductive and respiratory diseases. Additionally, different organ cancers, such as breast, lung, and colon, are discussed. This book is a valuable source for graduate students and researchers in genetics and bioinformatics, and several biomedical field members interested in applying computational epigenetics in their research. Provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases Summarizes the major computational tools, databases, and strategies for computational epigenetics analysis, such as DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA Covers the major milestones and future directions of computational epigenetics in various kinds of human diseases such as aging, atherosclerosis, diabetes, heart disease, neurological disorders, cancers, blood disorders, liver diseases, reproductive diseases, respiratory diseases, autoimmune diseases, human imprinting disorders, and infectious diseases

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