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Altri autori (Persone)	RippeKarsten
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Nota di contenuto	Genome Organization and Function in the Cell Nucleus; Contents; Preface; List of Contributors; 1: Deciphering DNA Sequence Information; 1.1: Introduction; 1.2: Genes and Transcribed Regions; 1.2.1: Open Reading Frames; 1.2.2: Mapping Transcriptional Start Sites; 1.2.3: Mapping Untranslated Regions on mRNA; 1.3: Non-Coding Genomic Elements; 1.3.1: Pseudogenes; 1.3.2: Repeats; 1.3.3: Structural Variants; 1.3.4: Methods for SV Detection; 1.3.5: Transposons and Retrotransposons; 1.4: Regulatory Information; 1.4.1: Classes of Regulatory Elements; 1.4.2: Transcription Factor Binding Motifs

1.4.3: Allele-Specific Expression1.5: Individual Genetic Polymorphisms and Their Effect on Gene Expression; 1.6: Conclusion; 2: DNA Methylation; 2.1: Introduction; 2.1.1: Discovery of 5-Methylcytosine in DNA; 2.1.2: Epigenetic Control of Gene Expression; 2.2: Eukaryotic DNA Methyltransferases; 2.2.1: Dnmt1; 2.2.2: The Dnmt3 Family; 2.2.3: Cooperative Function of Dnmts; 2.3: Distribution of 5-Methylcytosine in the Mammalian Genome; 2.3.1: Spatial Distribution of 5-Methylcytosine; 2.3.2: CpG Islands and Promoter Regulation; 2.3.3: Repetitive DNA Sequences
2.3.4: Temporal Distribution of 5-Methylcytosine2.4: Control of Gene Expression by DNA Methylation; 2.4.1: Loss of Transcription Factor Binding; 2.4.2: Methyl-CpG Binding Proteins; 2.4.3: Interconnection of DNA Methylation with Other Epigenetic Pathways; 2.4.4: DNA Methylation, Higher Order Chromatin Structure, and Nuclear Architecture; 2.5: DNA Demethylation; 3: Nucleosomes as Control Elements for Accessing the Genome; 3.1: Introduction and Basic Terminology; 3.2: Nucleosomes are the Building Blocks of Chromatin; 3.2.1: Histones; 3.2.2: Protein DNA Interactions in the Nucleosome
3.2.3: The Structure of Nucleosomal DNA3.3: Nucleosomes Are Dynamic Macromolecular Assemblies; 3.3.1: Mechanisms to Promote Histone Exchange In Vivo; 3.3.2: In Vitro Determination of Nucleosome Stability; 3.4: Histone Variants and Their Effect on Nucleosome Structure and Dynamics; 3.4.1: Variant Nucleosome Structures; 3.5: Histone Modifications in Nucleosome and Chromatin Structure; 3.6: DNA Sequence and Nucleosome Positioning; 3.6.1: Mechanisms for Nucleosome Exclusion; 3.6.2: Features that Promote Nucleosome Formation; 3.7: Histone Chaperones and Chromatin Dynamics; 3.7.1: Transcription
3.7.2: DNA Replication3.7.3: DNA Repair; 3.7.4: Mechanism of Chaperone-Mediated Nucleosome Assembly and Disassembly; 3.8: Outlook and Concluding Remarks; 4: Histone Modifications and Their Role as Epigenetic Marks; 4.1: The Complexity of Histone Modifications; 4.2: Regulating Histone Modifications in Chromatin; 4.3: The ""Histone Code"" Hypothesis; 4.3.1: Defining Histone ""Marks."" Why Is Histone Modification so Complex?; 4.3.2: Recognizing Histone Modifications: ""Reader"" Domains; 4.4: Exploiting the Complexity of the Histone Code: ""Crosstalk"" Between Different Modifications
4.4.1: Histone ""Crosstalk"": Increased Code Complexity and Signal Integration

Sommario/riassunto

By way of its clear and logical structure, as well as abundant highresolution illustrations, this is a systematic survey of the players and pathways that control genome function in the mammalian cell nucleus. As such, this handbook and reference ties together recently gainedknowledge from a variety of scientific disciplines and approaches, dissecting all major genomic events: transcription, replication, repair,recombination and chromosome segregation. A special emphasis is put on transcriptional control, including genome-wide interactions andnon-coding RNAs, chromatin structure, ep

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Sommario/riassunto	This proceedings volume gathers the outcomes of the International Conference on Engineering Research and Applications (ICERA 2019), which was held at Thai Nguyen University of Technology, Vietnam, on December 1–2, 2019 and provided an international forum for disseminating the latest theories and practices in engineering research and applications. The conference focused on original research work in a broad range of areas, including Mechanical Engineering, Materials and Mechanics of Materials, Mechatronics and Micromechatronics, Automotive Engineering, Electrical and Electronics Engineering, and Information and Communication Technology. By sharing the latest advances in these fields, the book will help academics and professionals alike to revisit their thinking on sustainable development.