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2.4: 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 DNA
3.3: 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 Replication
3.7.3: 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 and non-coding RNAs, chromatin structure, ep
