Epigenetics is the study of changes in gene expression caused by mechanisms other than changes in the DNA sequence. Epigenetics is a rapidly advancing field with an increasing impact on biological and medical research.

The editors of this book have assembled top-quality scientists from diverse fields of epigenetics to produce a major new volume. Comprehensive and cutting-edge, the 26 chapters in this book constitute a key reference manual for everyone involved in epigenetics, DNA methylation, cancer epigenetics and related fields. Topics include: early life environment, DNA methylation and behavior, histone acetyltransferase biology, transgenerational epigenetic inheritance, mammalian X inactivation, epigenetic memory in plants, polycomb-group regulation, centromeres and telomeres, DNA sequence contribution to nucleosome distribution, macrosatellite epigenetics, histones, cell-fate specification and reprogramming, DNA methylation in cancer, variant histone H2A and cancer development, RNA modification, paramutation in plants, DNA sequence contribution to nucleosome distribution, macrosatellite epigenetics, histones, cell-fate specification and reprogramming, DNA methylation in cancer, variant histone H2A and cancer development, RNA modification, paramutation in plants, DNMT3L dependent methylation during gametogenesis, non-coding RNA, bisulphite-enabled technologies, rapid analysis of DNA methylation, microarray mapping, DNA methylation profiling, ChIP-sequencing, genome-wide DNA methylation analysis, and epigenetics in maize. In addition there are useful chapters on bioinformatics in epigenomics, online resources and tools for epigeneticists, and educational resources for epigenetics.

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