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Biomedicine : Human Genetics

Jurga, Stefan, Barciszewski, Jan (Eds.)

The DNA, RNA, and Histone Methylomes

- **Comprehensively reviews the chemical, regulatory, and physiological mechanisms of protein arginine and lysine methyltransferases**
- **Highlights clinical applications of epigenetic editing in cancer treatment and aging**
- **Highlights hot topics such as cellular plasticity, novel biomarkers and genome-wide association studies**

This book reviews the chemical, regulatory, and physiological mechanisms of protein arginine and lysine methyltransferases, as well as nucleic acid methylations and methylating enzymes. Protein and nucleic acid methylation play key and diverse roles in cellular signalling and regulating macromolecular cell functions. Protein arginine and lysine methyltransferases are the predominant enzymes that catalyse S-adenosylmethionine (SAM)-dependent methylation of protein substrates. These enzymes catalyse a nucleophilic substitution of a methyl group to an arginine or lysine side chain nitrogen (N) atom. Cells also have additional protein methyltransferases, which target other amino acids in peptidyl side chains or N-termini and C-termini, such as glutamate, glutamine, and histidine. All these protein methyltransferases use a similar mechanism. In contrast, nucleic acids (DNA and RNA) are substrates for methylating enzymes, which employ various chemical mechanisms to methylate nucleosides at nitrogen (N), oxygen (O), and carbon (C) atoms. This book illustrates how, thanks to their ability to expand their repertoire of functions to the modified substrates, protein and nucleic acid methylation processes play a key role in cells.

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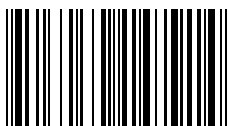
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