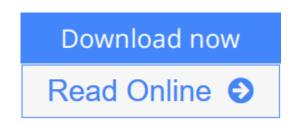


Epigenetics in Cancer (Life Science Research Fundamentals)

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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.

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