
Preface

The field of epigenetics has grown exponentially in the past decade, and a steady flow of exciting discoveries in this area has served to move it to the forefront of molecular biology. Although epigenetics may previously have been considered a peripheral science, recent advances have shown considerable progress in unraveling the many mysteries of nontraditional genetic processes. Given the fast pace of epigenetic discoveries and the groundbreaking nature of these developments, a thorough treatment of the methods in the area seems timely and appropriate and is the goal of *Epigenetics Protocols*.

The scope of epigenetics is vast, and an exhaustive analysis of all of the techniques employed by investigators would be unrealistic. However, this volume of *Methods in Molecular Biology*[™] covers three main areas that should be of greatest interest to epigenetics investigators: (1) techniques related to analysis of chromatin remodeling, such as histone acetylation and methylation; (2) methods in newly developed and especially promising areas of epigenetics such as telomere position effects, quantitative epigenetics, and ADP ribosylation; and (3) an updated analysis of techniques involving DNA methylation and its role in the modification, as well as the maintenance, of chromatin structure.

The protocols presented in *Epigenetics Protocols* are intended to provide investigators with a contemporary set of tools that can be applied to research in the field. These tools include recent breakthroughs in epigenetic analysis such as techniques for determining changes in native chromatin, methods of microarray analysis as applied to epigenetics, and methylation-sensitive single-strand conformation techniques. These methods, as well as many others provided in *Epigenetics Protocols*, have strong potential for further facilitating developments in this promising and rapidly developing field.

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