



# Epigenetic Regulation and Epigenomics



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# Epigenetic Regulation and Epigenomics

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## **Cover**

Simplified model of the interplay between histone modifications and small RNAs in the maintenance of pericentric heterochromatin in fission yeast (for more information see Chapter 19 "Histone Modifications", Figure 8)". Designed and drawn by Andrew Bannister and Blerta Xhemalce, The Gurdon Institute, University of Cambridge, CB2 1QN, UK.

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## Preface and Commentary

*Epigenetics* is the term given to heritable traits that occur over rounds of cell division and sometimes transgenerationally, in which the mechanisms are reversible, but do not involve changes to the underlying DNA sequence. This involves regulatory systems such as DNA methylation, histone modification, nucleosome location, and noncoding RNA. The *epigenome*, meanwhile, is a parallel to the word genome, refers to the overall epigenetic state of a cell and can be considered essentially a network of chemical switches within our cells.

Our compendium is written for university undergraduates, graduate students, faculty and investigators at research institutes. There are 33 articles with a combined length of over 1100 pages and as such is the largest in depth, up to date treatment of epigenetics presently available.

*Epigenetics Regulation and Epigenomics* differs in content and quality from all others available in five ways 1) the overall coverage was approved by our Board, which includes 11 Nobel Prize winners; 2) the selection of each article and author was validated by several reviewers from major university research centers; 3) each article was then reviewed by peers from other universities; 4) a glossary of terms with definitions is provided at the beginning of each article and 5) the articles average 35 print pages – which provides several times the depth of other such compendia.

The content is divided into five sections of articles covering key epigenetics areas. These sections are *Analytical Methods*, *Basic Molecular Mechanisms*, *The Epigenome*, *Medical Applications* and *Model Organisms*.

*Analytical Methods* articles range from chromatin immunoprecipitation (ChIP), to tag sequencing (impacting epigenomics), DNA methylation analysis, high throughput epigenotyping by mass spectrometry and includes RNA methodologies which provide an understanding of aspects of gene regulation. The *Basic Mechanisms* section covers the cell nucleus and chromatin organization and dynamics; epigenetics of stem cells; imprinting and histone modifications and methylation; as well as epigenetic aspects of prions, twins, cloning and RNA interference and all types of regulation of gene expression. The *Epigenome* coverage includes computational epigenetics and the human epigenome. *Medical Applications* include a comprehensive article on epigenetic medicine and additional detail in several articles on the of epigenetics of cancer, the immune system and aging as well as pharmaco-epigenomics to improve cancer therapies. In fact, drugs that inhibit the DNA methyltransferases, which place methyl groups on the

DNA, are now approved for clinical use in the United States for the treatment of certain cancers. This may be the beginning of a new era of cancer treatment involving epigenetic therapy. Pharmacology and emerging clinical application of RNA is also presented in this section. *Model Organisms* range from bacteria to protozoans as well as fungi and plants.

Our team of authors and peer reviewers are located at top rated epigenetics departments at institutions including the University of Cambridge, the University of Southern California, the University of California at Los Angeles, Washington University, St. Louis, and the National Institutes of Health. The team is truly global with authors or coauthors from the U.S., Sweden, Belgium, Germany, France, the UK, Austria, Spain, Hungary, Japan, India, China, Singapore, Canada and Israel.

Our team hopes that you, the reader, will benefit from our hard work – finding the content useful in your research as well as educational. We wish to thank our Managing Editor, Sarah Mellor, as well as our Executive Editor, Gregor Cicchetti for both their advice and hard work in the course of this project.

Larkspur, California, March 2012

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