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Andrew Emili, Jack Greenblatt, Shoshana Wodak (Eds.)

Systems Analysis of Chromatin-Related Protein Complexes in Cancer

- Defining high-quality protein-protein interaction networks and the physical and functional characterization of the protein machines underlying the human chromatin interactome
- Identification of RNA molecules associated with various chromatin-modifying machines that direct or regulate the complexes to various target genes
- Exploring the biological significance of chromatin machines in cancer (and the development and differentiation of stem cells)?

Epigenetic modifications underlie all aspects of human physiology, including stem cell renewal, formation of cell types and tissues. They also underlie environmental impacts on human health, including aging and diseases like cancer. Consequently, cracking the epigenetic "code" is considered a key challenge in biomedical research. Chromatin structure and function are modified by protein complexes, causing genes to be turned "on" or "off" and controlling other aspects of DNA function. Yet while there has been explosive growth in the epigenetics field, human chromatin-modifying machines have only recently started to be characterized. To meet this challenge, our book explores complementary experimental tracks, pursued by expert international research groups, aimed at the physical and functional characterization of the diverse repertoire of chromatin protein machines - namely, the "readers, writers and erasers" of epigenomic marks. These studies include the identification of RNA molecules and drugs that interact selectively with components of the chromatin machinery. What makes this book distinctive is its emphasis on the systematic exploration of chromatin protein complexes in the context of human development and disease networks.

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