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Nota di contenuto	The Bromodomain as the Acetyl-Lysine Binding Domain in Gene Transcription -- PHD Fingers as Histone Readers -- Methyl-Lysine Recognition by the Royal Family Modules: Chromo, Tudor, MBT, Chromo Barrel, and PWWP Domains -- Histone Recognition by WD40 Proteins -- Methyl-Lys Recognition by Ankyrin Repeat Proteins -- Methyl-Arginine Recognition by Tudor Domains -- Histone Recognition by Tandem Modules and Modulation by Multiple PTMs -- Genome-Wide Profiling of Molecular Recognition of Histone PTMs -- BET Bromodomain Inhibition as a Therapeutic Approach in Hematological Malignancies -- Anti-Inflammatory Effects of BET Protein Inhibition Through Modulation of Gene Transcription -- Activating Latent HIV by Inhibiting Bromodomain Proteins -- Small Molecule Modulation of Methyl-Lysine Mediated Interactions.

Sommario/riassunto	This book provides a timely review of the role of histone modifications in epigenetic control of gene expression. Topics covered include: basic mechanisms of molecular recognition of histone post-translational modification (PTMs); combinatorial readout of histone PTMs by tandem epigenome reader domains; genome-wide profiling of histone PTM interactions; small molecule modulation of histone PTM interactions and their potential as a new approach to therapeutic intervention in human diseases. All chapters were written by leading scientists who made the original key discoveries of the structure and mechanism of evolutionarily conserved reader domains, which serve to direct gene transcription in chromatin through interactions with DNA-packing histones in a PTM-sensitive manner.