

1. Record Nr.	UNINA9910298296503321
Titolo	Histone Recognition / / edited by Ming-Ming Zhou
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015
ISBN	3-319-18102-5
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (284 p.)
Disciplina	572.6 610 611.01816
Soggetti	Gene expression Post-translational modification Proteins Medical genetics Gene Expression Posttranslational Modification Protein-Ligand Interactions Gene Function
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
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.
