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Record Nr.	UNINA9910298331703321
Titolo	Systems analysis of chromatin-related protein complexes in cancer / / Andrew Emili, Jack Greenblatt, Shoshana Wodak, editors
Pubbl/distr/stampa	New York, : Springer Science, 2014
ISBN	1-4614-7931-2
Descrizione fisica	1 online resource (320 p.)
Altri autori (Persone)	EmiliAndrew GreenblattJack WodakShoshana J
Disciplina	570 572.6 599935 610
Soggetti	Chromosomal proteins Tumor proteins
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	Preface -- Systematic proteomic analysis of histone demethylating enzymes linked to cancer -- Histone methylating protein complexes in cancer -- Chromatin protein-protein interaction networks linked to cancer -- Structural genomics and drug discovery for chromatin-related protein complexes involved in histone tail recognition -- Transcription factories and global chromatin (enhancer) interactions in cancer -- Long ncRNAs associated with chromatin complexes and their role in cancer -- Familial and somatic mutations of histone modifying enzymes in cancer -- Chromatin regulators arising from RNAi screens of transformed cancer cell lines -- Chromatin complexes in cancer -- Exploring dynamics of chromatin complexes in cancer based on quantitative proteomics -- Regulatory ncRNAs and their targets -- ncRNA regulatory networks in cancer -- Decoding BAF remodelling complexes in cancer -- Mediator/cohesin complex in cancer -- miRNAs targeting chromatin-related protein complexes regulate epigenetic states in cancer -- Polycomb group protein complexes in cancer stem cells -- Genetic interactions between chromatin factors in

	cancer cell lines -- Chromatin complexes in DNA repair -- Chromatin complexes in chromosome segregation -- Evolution, co-expression and domain architecture of CM complexes linked to cancer -- Index.
Sommario/riassunto	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.