1.	Record Nr.	UNINA9910629284303321
	Titolo	Nuclear, Chromosomal, and Genomic Architecture in Biology and Medicine / / edited by Malgorzata Kloc, Jacek Z. Kubiak
	Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2022
	ISBN	3-031-06573-5
	Edizione	[1st ed. 2022.]
	Descrizione fisica	1 online resource (657 pages)
	Collana	Results and Problems in Cell Differentiation, , 1861-0412 ; ; 70
	Disciplina	571.835 611.0181
	Soggetti	Cell nuclei Chromosomes Biology - Technique Genomics Biomaterials Nucleic acids Gene expression Nuclear Organization Genomic Analysis Nucleic Acid Gene Expression Analysis
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references.
	Nota di contenuto	Part I. Genome Architecture, Evolution, and Cell Fate -- Chapter 1. Networks and Islands of Genome Nano-Architecture and their Potential Relevance for Radiation Biology (A Hypothesis and Experimental Verification Hints) -- Chapter 2. A Unified Genomic Mechanism of Cell-Fate Change -- Chapter 3. Alterations to Genome Organisation in Stem Cells, Their Differentiation and Associated Diseases -- Chapter 4. How Genomes Emerge, Function, and Evolve: Living Systems Emergence - Genotype-Phenotype-Multilism - Genome/Systems Ecology -- Chapter 5. Integrating Multimorbidity into a Whole-Body Understanding of Disease Using Spatial Genomics -- Part II. Chromosomes and

Chromatin Architecture and Dynamics -- Chapter 6. Mitotic Antipairing of Homologous Chromosomes -- Chapter 7. CENP-A, a Histone H3 Variant with Key Roles in Centromere Architecture in Healthy and Diseased States -- Chapter 8. Scaling Relationship in Chromatin as a Polymer -- Chapter 9. Chromatin Dynamics during Entry toQuiescence and Compromised Functionality in Cancer Cells -- Chapter 10. Functional Aspects of Sperm Chromatin Organization -- Part III. Mechanosensitive and Epigenetic Regulators of Gene Expression and Chromatin Organization -- Chapter 11. The LINC Complex Assists the Nuclear Import of Mechanosensitive Transcriptional Regulators -- Chapter 12. Epigenetic-Mediated Regulation of Gene Expression for Biological Control and Cancer: Cell and Tissue Structure, Function, and Phenotype -- Chapter 13. Epigenetic-Mediated Regulation of Gene Expression for Biological Control and Cancer: Fidelity of Mechanisms Governing the Cell Cycle -- Chapter 14. Histone Modifications in Mouse Pronuclei and Consequences for Embryo Development -- Part IV. Nucleus, Nucleolus, and Nucleolar Organizer Architecture -- Chapter 15. Nuclear Architecture in the Nervous System -- Chapter 16. Nuclear Morphological Abnormalities in Cancer: A Search for Unifying Mechanisms -- Chapter 17. Nuclear Organization in Response to Stress: A Special Focus on Nucleoli -- Chapter 18. Simulation of Different Three-Dimensional Models of Whole Interphase Nuclei Compared to Experiment – A Consistent Scale-Bridging Simulation Framework for Genome Organization -- Chapter 19. Nucleolar Organizer Regions as Transcription-Based Scaffolds of Nucleolar Structure and Function -- Chapter 20. A Transient Mystery: Nucleolar Channel Systems -- Part V. Nuclear Actin Role in Polarization, Genome Organization, and Gene Expression -- Chapter 21. Cellular Polarity Transmission to the Nucleus -- Chapter 22. The Role of Nuclear Actin in Genome Organization and Gene Expression Regulation During Differentiation -- Chapter 23. Nuclear Actin Dynamics in Gene Expression, DNA Repair, and Cancer.

Sommario/riassunto

This volume reviews the latest research on the functional implications of nuclear, chromosomal and genomic organization and architecture on cell and organismal biology, and development and progression of diseases. The architecture of the cell nucleus and non-random arrangement of chromosomes, genes, and the non-membranous nuclear bodies in the three-dimensional (3D) space alters in response to the environmental, mechanical, chemical, and temporal cues. The changes in the nuclear, chromosomal, or genomic compaction and configuration modify the gene expression program and induce or inhibit epigenetic modifications. The intrinsically programmed rearrangements of the nuclear architecture are necessary for cell differentiation, the establishment of cell fate during development and maturation of tissues and organs including the immune, muscle, and nervous systems. The non-programmed changes in the nuclear architecture can lead to fragmentation of the nucleus and instability ofthe genome and thus cause cancer. Microbial and viral infections can lead to a clustering of centromeres, telomeres and ribosomal DNA and alter the properties of the nuclear membrane, allowing large immobile macromolecules to enter the nucleus. Recent advances in next-generation sequencing technologies combined with nucleus/chromosome conformation capture, super-resolution imaging, chromosomal contact maps methods, integrative modeling, and genetic approaches, are uncovering novel features and importance of nuclear, chromosomal and genomic architecture. This book is an interesting read for cell biologists, researchers studying the structure and function of chromosomes, and anyone else who wants to get an overview of the

field of nuclear, chromosomal and genomic architecture.

2.	Record Nr.	UNINA9910502640303321
	Titolo	Bioinformatics in Rice Research : Theories and Techniques / / edited by Manoj Kumar Gupta, Lambodar Behera
	Pubbl/distr/stampa	Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2021
	ISBN	981-16-3993-0
	Edizione	[1st ed. 2021.]
	Descrizione fisica	1 online resource (609 pages)
	Collana	Biomedical and Life Sciences Series
	Disciplina	633.18
	Soggetti	Bioinformatics Biology - Technique Genomics Gene expression Agriculture Computational and Systems Biology Genomic Analysis Gene Expression Analysis
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di contenuto	Chapter 1_Introduction to Bioinformatics -- Chapter 2_Statistics for bioinformatics -- Chapter 3_ Introduction of the databases of rice -- Chapter 4_Brief insight into the evolutionary history and domestication of wild rice relatives -- Chapter 5_3000 Genome project- A brief insight -- Chapter 6_ Databases and bioinformatics tools for data mining -- Chapter 7_Sequence Alignment -- Chapter 8_Gene identification and structure Annotation -- Chapter 9_Phylogenetic Analysis -- Chapter 10_RNA Structure Prediction. -Chapter 11_Structural Proteomics -- Chapter 12_Gene ontology and pathway enrichment analysis -- Chapter 13_High throughput sequencing technologies -- Chapter 14_Mapping algorithms in high-throughput sequencing -- Chapter 15_DNA–Protein Interaction Analysis (ChIP-Seq) -- Chapter 16_RNA–Protein Interaction Analysis -- Chapter 17_SNP

	Identification and Discovery -- Chapter 18_Microsatellite Markers from whole genome and Transcriptomic Sequences. - Chapter 19_Genome-wide association study -- Chapter 20_Expression Profiling and Discovery of microRNA -- Chapter 21_Computational approaches in identifying long non-coding RNA -- Chapter 22_circRNA in rice -- Chapter 23_ Metagenomics -- Chapter 24_RNA-Induced Gene Silencing -- Chapter 25_Single-cell RNA sequencing technologies -- Chapter 26_Recent Advancement in NGS Technologies.
Sommario/riassunto	This book provides an up-to-date review of classic and advanced bioinformatics approaches and their utility in rice research. It summarizes databases and tools for analyzing DNA, proteins and gene expression profiles, mapping genetic variations, annotation of protein and RNA molecules, phylogenetic analysis, and pathway enrichment. In addition, it presents high-throughput technologies that are widely used to provide deep insights into the genetic architecture of important traits in the rice genome. The book subsequently discusses techniques for identifying RNA-protein, DNA-protein interactions, and molecular markers, including SNP and microsatellites, in the contexts of rice breeding and genetics. Lastly, it explores various tools that are used to identify and characterize non-coding RNA in rice and their potential role in rice research.