1. Record Nr. UNINA990006157640403321

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| Autore | Giugni, Gino <1927-2009> |
| Titolo | Diritto sindacale / di Gino Giugni ; con la collaborazione di Pietro Curzio e Mario Giovanni Garofalo |
| Pubbl/distr/stampa | Bari : Cacucci, 1993 |
| Edizione | [2. rist. della 9. ediz.] |
| Descrizione fisica | 388 p. ; 24 cm |
| Disciplina | 344.018<br>344 |
| Locazione | DDRC<br>FGBC |
| Collocazione | B-I-54/55<br>B-I-55<br>VII I 106 |
| Lingua di pubblicazione | Italiano |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |

2. Record Nr. UNICAMPANIASUN0023065

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| Autore | Grossi, Paolo <1933- > |
| Titolo | Assolutismo giuridico e diritto privato / Paolo Grossi |
| Pubbl/distr/stampa | Milano : Giuffrè, [1998] |
| ISBN | 88-14-07211-6 |
| Descrizione fisica | IX, 474 p. ; 23 cm. |
| Disciplina | 346.4009034 |
| Soggetti | Diritto civile - Europa - Storia - Sec. 19.-20 |
| Lingua di pubblicazione | Italiano |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |

3. Record Nr. UNINA9910146241703321

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| Titolo | The epigenome [[electronic resource] ] : molecular hide and seek / / edited by S. Beck and A. Olek |
| Pubbl/distr/stampa | Weinheim ; ; [Cambridge], : Wiley-VCH, c2003 |
| ISBN | 1-280-52085-X<br>9786610520855<br>3-527-60597-5<br>3-527-60151-1 |
| Descrizione fisica | 1 online resource (190 p.) |
| Altri autori (Persone) | OlekA (Alexander)<br>BeckStephan (Stephan G.) |
| Disciplina | 599.935<br>611.01816 |
| Soggetti | Human genome<br>Medical genetics<br>Nature and nurture<br>Genome, Human<br>Genomics - methods<br>Cytosine - physiology<br>Electronic books. |

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| 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 Epigenome Molecular Hide and Seek; Preface; Contents; 1 Five Not Four: History and Significance of the Fifth Base; Summary; 1.1 Historical Introduction; 1.2 Sequencing 5-methylcytosine (5-mC) Residues in Genomic DNA; The Bisulfite Method; 1.3 Gene Silencing; 1.4 Development; 1.5 Abnormal DNA Methylation in Cancer Cells; 1.6 Nuclear Transfer; 1.7 Aging; 1.8 The Future; References; 2 (Epi)genetic Signals: Towards a Human Genome Sequence of All Five Nucleotides; Summary; 2.1 A Linguistic Prologue; 2.2 Towards the Complete Sequence of the Human Genome with Five Nucleotides<br>2.3 Patterns of DNA Methylation - the Scaffold for Building a Functional Genome2.4 DNA Methylation Patterns in Segments of the Human Genome and in Viral Genomes; 2.4.1 On Viral Genomes and Foreign DNA Integrates (Table 2.1); 2.4.2 DNA Methylation Patterns in the Human Genome (Table 2.1); 2.5 Insertions of Foreign DNA into Established Mammalian Genomes; 2.6 De Novo Methylation of Integrated Foreign DNA; 2.6.1 Ad12 Genomes in Hamster Tumor Cells; 2.6.2 De Novo Methylation of Foreign DNA Integrated into the Mouse Genome by Homologous or Heterologous Recombination [23]<br>2.7 Genome-wide Perturbations in the Mammalian Genome upon Foreign DNA Insertion2.8 Outlook and Recommendations; References; 3 Epi Meets Genomics: Technologies for Finding and Reading the 5(th) Base; Summary; 3.1 The Development of 5(th)-Base Technologies; 3.1.1 Unusual DNA-cutting Enzymes; 3.1.2 A Unique Chemical Reaction that Modifies Methylated DNA; 3.1.3 The Advance of 5(th) Base Technologies in Epigenomic Research; 3.2 Restriction Landmark Genomic Scanning (RLGS): Finding the 5(th)-base Signposts in the Genomic Atlas; 3.2.1 Principle; 3.2.2 How Does RLGS Work?; 3.2.3 Applications<br>3.3 Methylation-sensitive Arbitrarily Primed (AP) PCR: Fishing for the 5 (th) Bases in Genomic Ponds3.3.1 Principle; 3.3.2 How Does MS AP-PCR Work?; 3.3.3 Applications; 3.4 Differential Methylation Hybridization (DMH): Identifying the 5(th) Bases in the Genomic Crossword Puzzle; 3.4.1 Principle; 3.4.2 How Does DMH Work?; 3.4.3 Applications; 3.5 MethyLight: Finding 5(th)-base Patterns in Genomic Shadows; 3.5.1 Principle; 3.5.2 How Does MethyLight Work?; 3.5.3 Applications; 3.6 Exploring the Epigenome; References; 4 Mammalian Epigenomics: Reprogramming the Genome for Development and Therapy Summary4.1 Introduction; 4.2 DNA Methylation; 4.3 Histone Modifications; 4.4 Imprinting; 4.5 Reprogramming and Cloning; 4.6 Epimutations and Epigenetic Inheritance; 4.7 Epigenomics: The Future; 4.7 Conclusions; References; 5 At the Controls: Genomic Imprinting and the Epigenetic Regulation of Gene Expression; Summary; 5.1 Introduction; 5.2 Genomic Imprinting; 5.2.1 The Role of DNA Methylation in Imprinted Gene Expression; 5.2.3 Organization of Imprinted Genes<br>5.2.4 The Mechanism of Imprinting at the Mouse Igf2r Imprinted Domain Requires a Cis-acting Noncoding Antisense Transcript Regulated by DNA Methylation (Fig. 5.2 a) |
| Sommario/riassunto | This is the first book that describes the role of the Epigenome (cytosine methylation) in the interplay between nature and nurture. It focuses and stimulates interest in what will be one of the most exciting areas of |

post-sequencing genome science: the relationship between genetics and the environment. Written by the most reputable authors in the field, this book is essential reading for researchers interested in the science arising from the human genome sequence and its implications on health care, industry and society.