1. Record Nr. UNINA990000492100403321

Autore	Millman, Jacob <1911-1991>
Titolo	Pulse, digital and swithching waveforms : devices and circuits for their generation and processing / Jacob Millman, herbert Taub
Pubbl/distr/stampa	New York : McGraw-Hill, c1965
Descrizione fisica	958 p. : ill. ; 24 cm
Collana	McGraw-Hill electrical and electronic engineering series
Altri autori (Persone)	Taub, Herbert
Disciplina	621.381'5 537.5
Locazione	FI1 DINEL
Collocazione	31-181 10 E I 60 10 E I 153
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

2. Record Nr. UNISALENTO991003925979707536

Autore	Capelle, Guy
Titolo	Avec plaisir / Guy Capelle, Albert Raasch
Pubbl/distr/stampa	Paris : Hachette FLE, c1987
ISBN	2010118707 (v. 2.3)
Descrizione fisica	171 p. : ill. ; 25 cm
Altri autori (Persone)	Raasch, Albertauthor
Disciplina	440.7
Soggetti	Lingua francese - Insegnamento
Lingua di pubblicazione	Francese
Formato	Materiale a stampa
Livello bibliografico	Monografia

3. Record Nr. UNINA9910739439803321

Titolo	Next generation sequencing in cancer research . Volume 1 Decoding the cancer genome / / Wei Wu, Hani Choudhry, editors
Pubbl/distr/stampa	New York, : Springer Science, 2013
ISBN	1-4614-7645-3
Edizione	[1st ed. 2013.]
Descrizione fisica	1 online resource (383 p.)
Altri autori (Persone)	WuWei ChoudhryHani
Disciplina	570285 599935 610 611.01816
Soggetti	Cancer - Genetic aspects Gene mapping
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	Introduction: next generation sequencing technology and cancer research -- The majority of total nuclear-encoded non-ribosomal RNA in a human cell is ‘dark matter’ unannotated RNA -- Total RNA-seq of breast cancer in hypoxia -- Altered antisense-to-sense transcript ratios in breast cancer -- Identification of piRNAs in Hela cells by massive parallel sequencing -- Discovery of new microRNAs by small RNAome deep sequencing in childhood acute lymphoblastic leukemia -- Whole-Exome Sequencing Identifies FAM20A Mutations as a Cause of Amelogenesis Imperfecta and Gingival Hyperplasia Syndrome -- Whole-exome sequencing in CIC and IDH1/2 contributing to human oligodendroglioma -- Genetic and structural variation in the gastric cancer kinome revealed through targeted deep sequencing -- Tumour evolution inferred by single-cell sequencing -- Characterization of the single-cell transcriptional landscape by highly multiplex RNA-seq -- Tracing the derivation of embryonic stem cells from the inner cell mass by single-cell RNASeq analysis -- Whole genome DNA methylation analysis based on high throughput sequencing technology -- Comparative methylome analysis of benign and malignant peripheral nerve sheath tumors -- High-resolution genome-wide mapping of HIF-binding sites by ChIP-seq -- MicroRNA transfection and AGO-bound CLIP-seq data sets reveal distinct determinants of miRNA action -- Genome-wide identification of polycomb-associated RNAs by RIP-seq -- Single-molecule sequencing: sequence methods to enable accurate quantisation -- Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells -- Reprogramming transcription by distinct classes of enhancers functionally defined by eRNA -- The genome information process for cancer research: the challenge and perspective -- Index.
Sommario/riassunto	Next Generation Sequencing (NGS) technology has placed important milestones in the life science and changed the direction in biomedical science inclucing cancer. Scientists around the world are attempting to find the root cause of cancer and they are looking for more direct and effective means to cure cancer. This journey to conquer cancer is more optimistic now with the unfolding of the cancer genome. This book focuses on the application of various NGS in the frontier cancer genome research. The 18 chapters in this volume have been written by scientists with many outstanding contributions in their area and the join effort has created comprehensive insightful view on (1) Overview of next generation sequencing technology in cancer genome research (2) Genome regulation and targeted sequencing in cancer (3) RNA transcriptome (coding and non-coding) in cancer genome (4)The challenges of computational biology for cancer genome study. This book is a state-of-the-art reference to all scientific researchers and onologists who are interested in the understanding of the cancer initiatome at whole genome scale and to those are keen to translate the ‘base pairs to bedside’ for better management of cancer patients in the era of personalized medicine.