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Titolo	Modern genome annotation [[electronic resource]] : the BioSapiens Network / / Dmitrij Frishman, Alfonso Valencia, editors
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ISBN	1-282-50900-4 9786612509001 3-211-75123-8
Edizione	[1st ed. 2008.]
Descrizione fisica	1 online resource (506 p.)
Classificazione	BIO 110f BIO 180f
Altri autori (Persone)	FrishmanDmitrij ValenciaAlfonso
Disciplina	572.80285
Soggetti	Bioinformatics Human genome
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.
Nota di contenuto	BIOSAPIENS: A European Network of Excellence to develop genome annotation resources -- BIOSAPIENS: A European Network of Excellence to develop genome annotation resources -- Gene definition -- State of the art in eukaryotic gene prediction -- Quality control of gene predictions -- Gene regulation and expression -- Evaluating the prediction of cis-acting regulatory elements in genome sequences -- A biophysical approach to large-scale protein-DNA binding data -- From gene expression profiling to gene regulation -- Annotation and genetics -- Annotation, genetics and transcriptomics -- Functional annotation of proteins -- Resources for functional annotation -- Annotating bacterial genomes -- Data mining in genome annotation -- Modern genome annotation: the BioSapiens network -- Structure to function -- Harvesting the information from a family of proteins -- Protein structure prediction -- Structure prediction of globular proteins -- The state of the art of membrane protein structure prediction: from sequence to 3D structure -- Protein-protein complexes, pathways and networks -- Computational analysis of metabolic networks -- Protein-protein interactions: analysis and prediction -- Infrastructure for

distributed protein annotation -- Infrastructure for distributed protein annotation -- Applications -- Viral bioinformatics -- Alternative splicing in the ENCODE protein complement.

Sommario/riassunto

An accurate description of current scientific developments in the field of bioinformatics and computational implementation is presented by research of the BioSapiens Network of Excellence. Bioinformatics is essential for annotating the structure and function of genes, proteins and the analysis of complete genomes and to molecular biology and biochemistry. Included is an overview of bioinformatics, the full spectrum of genome annotation approaches including; genome analysis and gene prediction, gene regulation analysis and expression, genome variation and QTL analysis, large scale protein annotation of function and structure, annotation and prediction of protein interactions, and the organization and annotation of molecular networks and biochemical pathways. Also covered is a technical framework to organize and represent genome data using the DAS technology and work in the annotation of two large genomic sets: HIV/HCV viral genomes and splicing alternatives potentially encoded in 1% of the human genome.
