1.	Record Nr.	UNINA9910798669403321
	Titolo	World employment social outlook 2016 : transforming jobs to end poverty / / International Labour Office
	Pubbl/distr/stampa	Geneva, [Switzerland] : , : International Labour Office, , 2016 ©2016
	ISBN	92-2-130388-8
	Descrizione fisica	1 online resource (192 p.)
	Disciplina	331.1
	Soggetti	Unemployment - 21st century Employment (Economic theory) - 21st century Labor market
	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.
	Sommario/riassunto	This report shows that decent work is vital to reducing poverty. Poverty has tended to decline in many emerging and developing countries, whereas it has tended to increase in the majority of advanced economies, including in terms of working poverty. The report examines the role that policy can play, particularly with economic policies, employment programmes, enterprise development, social protection and social dialogue. It also discusses the role of international labour standards.

2.

Record Nr.	UNINA9910958642403321
Titolo	Regulatory genomics : proceedings of the 3rd annual RECOMB workshop : National University of Singapore, Singapore 17-18 July 2006 / / editors, Leong Hon Wai, Sung Wing-Kin, Eleazar Eskin
Pubbl/distr/stampa	London, : Imperial College Press, c2008
ISBN	9781848162525 1848162529
Edizione	[1st ed.]
Descrizione fisica	1 online resource (144 p.)
Collana	Series on advances in bioinformatics and computational biology, , 1751-6404 ; ; 8
Altri autori (Persone)	EskinEleazar LeongHon Wai <1955-> SungWing-Kin
Disciplina	572.865
Soggetti	Genetic regulation Genomics
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	Foreword; RECOMB Regulatory Genomics 2006 Organization; CONTENTS; Keynote Papers; Computational Prediction of Regulatory Elements by Comparative Sequence Analysis M. Tompa; A Tale of Two Topics - Motif Significance and Sensitivity of Spaced Seeds M. Li; Computational Challenges for Top-Down Modeling and Simulation of Biological Pathways S. Miyano; An Improved Gibbs Sampling Method for Motif Discovery via Sequence Weighting T. Jiang; Discovering Motifs with Transcription Factor Domain Knowledge F. Chin; Applications of ILP in Computational Biology A . Dress On the Evolution of Transcription Regulation Networks R. Shamir Systems Pharmacology in Cancer Therapeutics: Iterative Informatics-Experimental Interface E. Liu; Computational Structural Proteomics and Inhibitor Discovery R. Abagyan; Characterization of Transcriptional Responses to Environmental Stress by Differential Location Analysis H. Tang; A Knowledge-based Hybrid Algorithm for Protein Secondary Structure Prediction W. L. Hsu; Monotony and Surprise (Conservative Approaches to Pattern Discovery) A . Apostolic0; Evolution of Bacterial Regulatory Systems M. S. Gelfand; Contributed Papers

Sommario/riassunto

Research in the field of gene regulation is evolving rapidly in the ever-changing scientific environment. Advances in microarray techniques and comparative genomics have enabled more comprehensive studies of regulatory genomics. The study of genomic binding locations of transcription factors has enabled a more comprehensive modeling of regulatory networks. In addition, complete genomic sequences and comparison of numerous related species have demonstrated the conservation of non-coding DNA sequences, which often provide evidence for cis-regulatory binding sites. Systematic methods to decipher