

1.	Record Nr.	UNISA990000447140203316
	Autore	GALBIATI, Enrico
	Titolo	La fede nei personaggi della Bibbia / Enrico Galbiati
	Pubbl/distr/stampa	Milano : Jaca Book, copyr. 2000
	ISBN	88-16-30364-6
	Descrizione fisica	219 p. ; 23 cm
	Collana	Già e non ancora ; 264
	Disciplina	220.8
	Soggetti	Bibbia - Concetto di fede
	Collocazione	II 2 1988(XIV 1231)
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
2.	Record Nr.	UNISALENTO991002409889707536
	Titolo	L'analisi del linguaggio teologico : il nome di Dio : atti del Convegno indetto dal Centro internazionale di studi umanistici e dall'Istituto di studi filosofici, Roma 5-11 gennaio 1969 / a cura di Enrico Castelli
	Pubbl/distr/stampa	Roma : Istituto di studi filosofici, 1969
	Descrizione fisica	550 p. ; 25 cm
	Altri autori (Persone)	Castelli, Enrico
	Disciplina	291
	Soggetti	Teologia - Linguaggio - Congressi
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	In testa al front.: Centro internazionale di studi umanistici, Roma

3.	Record Nr.	UNIORUON00103594
	Titolo	Stories from China's past : Han dynasty pictorial tomb reliefs and archaeological objects from Sichuan province, People's Republic of China. Exhibition organized by Lucy Lim in cooperation with the Sichuan Cultural Department People's Republic of China (Chinese Culture Center S. Francisco : April 11-May 31, 1987) / foreword by Alexander C. Soper, introduction by Richard C. Rudolph
	Pubbl/distr/stampa	S. Francisco, : The Chinese Culture Foundation of S. Francisco, 1987
	Descrizione fisica	209 p. : ill. ; 28 cm
	Classificazione	CIN IX L
	Soggetti	Arte cinese - esposizioni e mostre
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
4.	Record Nr.	UNINA9910346695903321
	Autore	Russ B Altman
	Titolo	Pacific Symposium on Biocomputing 2012 Kohala Coast, Hawaii, USA, 3-7 January 2012
	Pubbl/distr/stampa	World Scientific Publishing Co, 2011 [Place of publication not identified], : World Scientific Pub Co, 2012
	Descrizione fisica	1 online resource (442 p.) : ill. (some col.)
	Disciplina	572.8
	Soggetti	Engineering & Applied Sciences Computer Science
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	Bibliographic Level Mode of Issuance: Monograph
	Nota di bibliografia	Includes bibliographical references.
	Nota di contenuto	Identification of aberrant pathway and network activity from high-

throughput data. Session introduction / Rachel Karchin ... [et al.].

SSLPred : predicting synthetic sickness lethality / Nirmalya Bandyopadhyay, Sanjay Ranka, and Tamer Kahveci. Predicting the effects of copy-number variation in double and triple mutant combinations / Gregory W. Carter ... [et al.]. Integrative network analysis to identify aberrant pathway networks in ovarian cancer / Li Chen ... [et al.] -- Role of synthetic genetic interactions in understanding functional interactions among pathways / Shahin Mohammadi, Giorgos Kollias, and Ananth Grama -- Discovery of mutated subnetworks associated with clinical data in cancer / Fabio Vandin ... [et al.] -- Intrinsically disordered proteins : analysis, prediction, simulation, and biology. Session introduction / Jianhan Chen, Jianlin Cheng, and A. Keith Dunker. Quasi-anharmonic analysis reveals intermediate states in the nuclear co-activator receptor binding domain ensemble / Virginia M. Burger ... [et al.]. Efficient construction of disordered protein ensembles in a Bayesian framework with optimal selection of conformations / Charles K. Fisher, Orly Ullman, and Collin M. Stultz. Correlation between posttranslational modification and intrinsic disorder in protein / Jianjiong Gao and Dong Xu. Intrinsic disorder within and flanking the DNA-binding domains of human transcription factors / Xin Guo, Martha L. Bulyk, and Alexander J. Hartemink. Intrinsic protein disorder and protein-protein interactions / Wei-Lun Hsu ... [et al.]. Subclassifying disordered proteins by the CH-CDF plot method / Fei Huang ... [et al.]. Coevolved residues and the functional association for intrinsically disordered proteins / Chan-Seok Jeong and Dongsup Kim. Cryptic disorder: an order-disorder transformation regulates the function of nucleophosmin / Diana M. Mitrea and Richard W. Kriwacki. Functional annotation of intrinsically disordered domains by their amino acid content using IDD navigator / Ashwini Patil ... [et al.]. On the complementarity of the consensus-based disorder prediction / Zhenling Peng and Lukasz Kurgan. Modulating protein-DNA interactions by post-translational modifications at disordered regions / Dana Vuzman, Yonit Hoffman, and Yaakov Levy -- Microbiome studies: analytical tools and techniques. Session introduction / James A. Foster ... [et al.]. Estimating population diversity with unreliable low frequency counts / John Bunge ... [et al.]. Comparisons of distance methods for combining covariates and abundances in microbiome studies / Julia Fukuyama ... [et al.]. Proteotyping of microbial communities by optimization of tandem mass spectrometry data interpretation / Alys Hugo ... [et al.]. phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data / Paul J. McMurdie and Susan Holmes. SEPP: SATE-enabled phylogenetic placement / Siavash Mirarab, Nam Nguyen, and Tandy Warnow. Artificial functional difference between microbial communities caused by length difference of sequencing reads / Quan Zhang, Thomas G. Doak, and Yuzhen Ye. MetaDomain: a profile HMM-based protein domain classification tool for short sequences / Yuan Zhang and Yanni Sun. Modeling host-pathogen interactions: computational biology and bioinformatics for infectious disease research. Session introduction / Jason E. McDermott ... [et al.]. Structural models for host-pathogen protein-protein interactions: assessing coverage and bias / Eric A. Franzosa and Yu Xia. Identification of cell cycle-regulated, putative hyphal genes in *Candida Albicans* / Raluca Gordan, Saumyadipta Pyne, and Martha L. Bulyk. Determining confidence of predicted interactions between HIV-1 and human proteins using conformal method / Ilia Nouretdinov ... [et al.] -- Personalized medicine: from genotypes and molecular phenotypes towards computed therapy. Session introduction

/ Oliver Stegle ... [et al.]. Finding genome-transcriptome-phenome associations with structured association mapping and visualization in GenAMap / Ross E. Curtis ... [et al.]. Interpretome: a freely available, modular, and secure personal genome interpretation engine / Konrad J. Karczewski ... [et al.]. A kinase inhibition map approach for tumor sensitivity prediction and combination therapy design for targeted drugs / Ranadip Pal and Noah Berlow. Mixture model for sub-phenotyping in GWAS / David Warde-Farley ... [et al.] -- Text and knowledge mining for pharmacogenomics: genotype-phenotype-drug relationships. Session introduction / Kevin Bretonnel Cohen ... [et al.]. The extraction of pharmacogenetic and pharmacogenomic relations - A case study using PharmGKB / Ekaterina Buyko, Elena Beisswanger, and Udo Hahn. Linking PharmGKB to phenotype studies and animal models of disease for drug repurposing / Robert Hoehndorf ... [et al.]. Integrating VA's NDF-RT drug terminology with PharmGKB: preliminary results / Jyotishman Pathak ... [et al.]. Discovery and explanation of drug-drug interactions via text mining / Bethany Percha, Yael Garten, and Russ B. Altman. Ranking gene-drug relationships in biomedical literature using latent Dirichlet allocation / Yonghui Wu ... [et al.] -- Workshops. The structure and function of chromatin and chromosomes / William Stafford Noble ... [et al.]. Law, bioethics and the current status of ownership, privacy, informed consent in the genomic age / Greg Hampikian and Eric M. Meslin. Systems pharmacogenomics-bridging the gap / Marylyn Ritchie ... [et al.].

Sommario/riassunto

The Pacific Symposium on Biocomputing (PSB) 2012 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in the problems of biological significance. Presentations are rigorously peer-reviewed and are published in an archival proceedings volume. PSB 2012 will be held on January 3 - 7, 2012 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2012 will bring together top researchers from the US, the Asian Pacific nations, and countries around the world to exchange research results and address open issues in all aspects of computational biology. It is a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling, and other computational methods as applied to biological problems, with emphasis on the applications in the data-rich areas of molecular biology. The PSB has been designed to be responsive to the need for critical mass in sub-disciplines within biocomputing. For that reason, it is the only meeting whose sessions are defined dynamically each year in response to specific proposals. PSB sessions are organized by leaders of research in biocomputing's "hot topics". In this way, the meeting provides an early forum for serious examination of emerging methods and approaches in this rapidly changing field.