

1. Record Nr.	UNIORUON00153472
Autore	TENZIN Gyatso, Dalai lama
Titolo	Kalachakra Tantra. Rite of initiation : For the Stage of Generation. A commentary on the text of Kay-drup-ge-lek-sang-bo by Tenzin Gyatso the fourteenth Dalai Lama and the text itself / edited, translated and introduced by Jeffrey Hopkins
Pubbl/distr/stampa	Boston, : Wisdom Publications, 1989
Titolo uniforme	Kay-drup-ge-lek-bel-sang-bo / Tenzin Gyatso
ISBN	08-617-1028-2
Edizione	[Reprint 1991]
Descrizione fisica	511 p. ; 20 cm
Classificazione	TIB VII
Soggetti	BUDDHISMO - TIBET - TANTRA RITI DI INIZIAZIONE
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

2. Record Nr.	UNINA9910953706603321
Titolo	Bioinformatics : high performance parallel computer architectures / / edited by Bertil Schmidt
Pubbl/distr/stampa	Boca Raton, FL, : CRC Press, 2010
ISBN	0-429-13222-0 1-4398-1489-9
Edizione	[1st ed.]
Descrizione fisica	1 online resource (372 p.)
Collana	Embedded multi-core systems
Altri autori (Persone)	SchmidtBertil
Disciplina	572.80285
Soggetti	Bioinformatics - Data processing Parallel processing (Electronic computers)
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	Front cover; Contents; Editor; Contributors; Chapter 1: Algorithms for Bioinformatics; Chapter 2: Introduction to GPGPUs andMassively Threaded Programming; Chapter 3: FPGA: Architecture and Programming; Chapter 4: Parallel Algorithms forAlignments on the Cell BE; Chapter 5: Orchestrating the PhylogeneticLikelihood Function on EmergingParallel Architectures; Chapter 6: Parallel Bioinformatics Algorithmsfor CUDA-Enabled GPUs; Chapter 7: CUDA Error Correction Method forHigh-Throughput Short-Read Sequencing Data; Chapter 8: FPGA Acceleration of SeededSimilarity Searching Chapter 9: Seed-Based Parallel Protein SequenceComparison Combining Multithreading,GPU, and FPGA TechnologiesChapter 10: Database Searching with Profi le-HiddenMarkov Models on Reconfi gurableand Many-Core Architectures; Chapter 11: COPACOBANA: A Massively ParallelFPGA-Based Computer Architecture; Chapter 12: Accelerating String Set Matching forBioinformatics Using FPGA Hardware; Chapter 13: Reconfi gurable Neural System and ItsApplication to Dimeric ProteinBinding Site Identification; Chapter 14: Parallel FPGA Search Enginefor Protein Identification; Index; Back cover
Sommario/riassunto	New sequencing technologies have broken many experimental barriers to genome scale sequencing, leading to the extraction of huge quantities of sequence data. This expansion of biological databases

established the need for new ways to harness and apply the astounding amount of available genomic information and convert it into substantive biological understanding. A compilation of recent approaches from prominent researchers, *Bioinformatics: High Performance Parallel Computer Architectures* discusses how to take advantage of bioinformatics applications and algorithms o
