

1. Record Nr.	UNINA9910823125703321
Titolo	Protein families : relating protein sequence, structure, and function // edited by Christine A. Orengo, Alex Bateman
Pubbl/distr/stampa	Hoboken, New Jersey : , : Wiley, , [2014] ©2014
ISBN	1-118-74281-8 1-118-74308-3 1-118-74285-0
Descrizione fisica	1 online resource (567 p.)
Collana	Wiley series in protein and peptide science ; ; 10
Classificazione	COM082000
Altri autori (Persone)	OrengoChristine A. <1955-> BatemanAlex <1972->
Disciplina	572/.6
Soggetti	Proteins Proteomics Molecular biology - Data processing Bioinformatics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes index.
Nota di contenuto	Cover; Title Page; Contents; Introduction; Contributors; Part I Concepts Underlying Protein Family Classification; Chapter 1 Automated Sequence-Based Approaches for Identifying Domain Families; 1.1 Introduction; 1.2 Motivation Behind Automated Classification; 1.3 Clustering the Sequence Space Graph; 1.4 Historical Overview of Sequence Clustering Algorithms; 1.5 Related Methods; 1.6 Quality Assessment; 1.7 ADDA-The Automatic Domain Delineation Algorithm; 1.8 Results; 1.9 Conclusions; References; Chapter 2 Sequence Classification of Protein Families: Pfam and other Resources; 2.1 Introduction 2.2 Pfam2.3 Smart, Prosite Profiles, CDD and Tigrfams; 2.4 Philosophy of Pfam; 2.5 HMMER3 and Jackhmmer; 2.6 Sources of New Families; 2.7 Annotation of Families; 2.8 The InterPro Collection; 2.9 The Future of Sequence Classification; References; Chapter 3 Classifying Proteins into Domain Structure Families; 3.1 Introduction; 3.2 The Classification Hierarchies Adopted by Scop and Cath; 3.3 Challenges in Identifying

Domains in Proteins; 3.4 Structure-Based Approaches for Identifying Related Folds and Homologs; 3.5 Approaches to Structure Comparison; 3.6 The DALI Algorithm
3.7 The SSAP Algorithm Used for Fold Recognition in CATH3.8 Fast Approximate Methods Used to Recognize Folds in CATH; 3.9 Measuring Structural Similarity; 3.10 Multiple Structure Alignment; 3.11 Classification Protocols; 3.12 Population of the Hierarchy; 3.13 Comparisons Between Scop and CATH; 3.14 Hierarchical Classifications Versus Structural Continuum; 3.15 Websites; References; Chapter 4 Structural Annotations of Genomes with Superfamily and Gene3D; 4.1 Introduction; 4.2 The Importance of Being High Throughput; 4.3 The Use of Structural Information; 4.4 Applications; 4.5 History
4.6 Technology4.7 Hidden Markov Models; 4.8 Building Models; 4.9 Domain Annotations; 4.10 High Throughput Computation; 4.11 Development of New Bioinformatics Algorithms; 4.12 Genomes; 4.13 e-Value Scores; 4.14 Other Sequence Sets; 4.15 Data Access; 4.16 Analysis Tools; 4.17 Conclusion; References; Chapter 5 Phylogenomic Databases and Orthology Prediction; 5.1 The Evolution of Novel Functions and Structures in Gene Families; 5.2 Homologs, Orthologs, Paralogs, and Other Evolutionary Terms; 5.3 The Standard Functional Annotation Protocol; 5.4 Orthology Identification Methods and Databases
5.5 Challenges in Phylogenetic Methods of Ortholog Identification5.6 Evaluating Ortholog Identification Methods; 5.7 Orthology Databases; 5.8 Phylogenomic Databases; 5.9 PhyloFacts; 5.10 Subfamily Classification in Phylofacts; 5.11 PhyloFacts 3.0; 5.12 PhylomeDB; 5.13 Panther; 5.14 Structural Phylogenomics: Improved Functional Annotation Through Integration of Information from Structure and Evolution; 5.15 Specific Issues in Phylogenomic Pipelines; 5.16 Improving Functional Inference using Information from Protein Structure; 5.17 Example Case Studies; 5.18 Review of Key Points; References
Part II In-Depth Reviews of Protein Families

Sommario/riassunto

"This book describes approaches for recognizing and classifying proteins into families of evolutionary related proteins. Reviewing all the major resources for classifying protein families, the book combines descriptions of general philosophies of protein family classification systems with detailed descriptions and examples of selected families found in different biological systems. Scientists in diverse areas of biology and protein science will learn how to use the various resources and databases and gain valuable insight into how proteins evolve and how new functional repertoires emerge"--
