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Titolo	Protein families : relating protein sequence, structure, and function / / edited by Christine A. Orengo, Alex Bateman
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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"--

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Autore	Patel Ayyub
Titolo	Biochemical Techniques for Analyzing Protein-Lipid Interactions / / edited by Ayyub Patel
Pubbl/distr/stampa	Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2024
ISBN	9789819754373 9789819754366
Edizione	[1st ed. 2024.]
Descrizione fisica	1 online resource (183 pages)
Collana	Biomedical and Life Sciences Series
Disciplina	570.28
Soggetti	Biology - Technique Analytical biochemistry Biophysics Proteins Biological Techniques Analytical Biochemistry Biophysical Methods Protein Biochemistry
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Chapter 1. Challenges and opportunities for analyzing protein-ligand interactions -- Chapter 2. The Landscape of Lipid Protein Interaction -- Chapter 3. NMR Spectroscopy -- Chapter 4. X-ray crystallography -- Chapter 5. Lipisome microarray based assay -- Chapter 6. protein-lipid overlay assay -- Chapter 7. Quantitative Analysis of Protein-Lipid Interactions Using Tryptophan Fluorescence -- Chapter 8. Liposome Sedimentation Assay -- Chapter 9. Affinity purification lipodomics -- Chapter 10. Advanced Techniques for Analyzing The Protein-Lipid Interactions.
Sommario/riassunto	The book reviews cutting-edge advancements and their implications across various domains of molecular diagnostics. It covers foundational topics like protein-ligand interactions, lipid-protein interactions within biological membranes, and the application of NMR spectroscopy in understanding membrane structures. The book also explores advanced

techniques such as X-ray crystallography, liposome microarray assays, and protein-lipid interaction studies. By integrating experimental and computational methods, it provides a comprehensive guide to understanding the complexities of molecular diagnostics, from basic principles to innovative approaches in drug discovery and therapeutic development. Each chapter offers detailed discussions on specific topics, supported by experimental data and methodological insights, making it an invaluable resource for researchers, clinicians, and students seeking to enhance their knowledge and expertise in molecular diagnostics.