



Informatics In Proteomics

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The handling and analysis of data generated by proteomics investigations represent a challenge for computer scientists, biostatisticians, and biologists to develop tools for storing, retrieving, visualizing, and analyzing genomic data. Informatics in Proteomics examines the ongoing advances in the application of bioinformatics to proteomics research and analysis.

Through computer simulations, scientists can determine more about how diseases affect cells, predict how various drug interventions would work, and ultimately use proteins as therapeutic targets. This book first addresses the infrastructure needed for public protein databases. It discusses information management systems and user interfaces for storage, retrieval, and visualization of the data as well as issues surrounding data standardization and integration of protein sequences recorded in the last two decades. The authors subsequently examine the application of statistical and bioinformatic tools to data analysis, data presentation, and data mining. They discuss the implementation of algorithms, statistical methods, and computer applications that facilitate pattern recognition and biomarker discovery by integrating data from multiple sources.

This book offers a well-rounded resource of informatic approaches to data storage, retrieval, and protein analysis as well as application-specific bioinformatic tools that can be used in disease detection, diagnosis, and treatment. Informatics in Proteomics captures the current state-of-the-art and provides a valuable foundation for future directions.



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