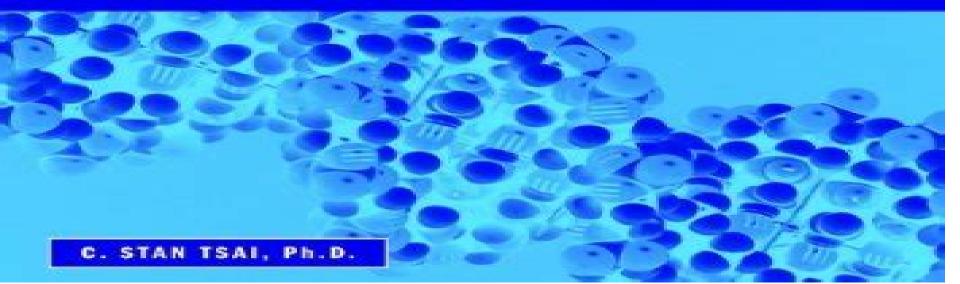


COMPUTATIONAL BIOCHEMISTRY



An Introduction To Computational Biochemistry

Raphael Guerois, Manuela López de la Paz

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textbook for undergraduates as well as postgraduates offering basic knowledge of biology Its aim is to provide state of the art information about this developing science that has the potential to replace existing biological approaches to study genes and proteins The chapters are explained in a concise yet detailed manner including ample cross references references to literature and databases tables and illustrations The book s sound approach to this intricately complex field makes it an exceptional resource for further exploration into biochemistry molecular biology genomics and drug designing fields Abundant learning features make this book the ideal teaching and learning tool KEY FEATURES Illustrations to bolster understanding of complex biochemical relations Tables for guick access to precise data Extensive end of chapter exercises and references The most basic details furnished for those who are new to biology User friendly Internet based bioinformatics tools that allow researchers to extract information from databases and analyze it Analysis of one software tool discussed in each chapter step by step from entering the input till interpretation of the results This is an in depth textbook written for the biologist who wants a thorough understanding of the popular bioinformatics programs and molecular databases currently in use It provides a broad application oriented overview of this technology Protein Design Raphael Guerois, Manuela López de la Paz,2008-02-04 Proteins have evolved through selective pressure to accomplish specific functions The functional properties of proteins depend upon their thr dimensional structures which result from particular amino acid sequences folding into tightly packed domains Thus to understand and modulate protein function rationally one definitely needs methods and algorithms to predict and decipher how amino acid sequences shape three dimensional structures Protein design aims precisely at providing the tools to achieve this goal The predictive power of rational protein design methods has dramatically increased over the past five years A broad range of studies now illustrate how the sequence of proteins and peptides can be tuned to engineer biological tools with intended properties 1 3 The extensive characterization of peptides and protein mutants has enormously benefited the understanding of protein sequence to structure relationships Synergies between computational and experimental approaches have also added momentum to the advancing limits of design methods The potential applications in fundamental biochemistry and in biotechnology justify the considerable excitement that this progress has generated within the research community The field is probably mature enough so that expert knowledge can assist researchers of diverse disciplines to rationally create or modify their favorite protein Thus the aim of Protein Design Methods and Protocols is to account for the most up to date protein design and engineering strategies so that readers can undertake their own projects with maximum confidence in a successful return The basic concepts underlying rational design of proteins are intimately related to their three dimensional structures **Globins and Other Nitric Oxide-Reactive Proteins, Part A** Robert K. Poole, 2011-09-02 The critically acclaimed laboratory standard for more than forty years Methods in Enzymology is one of the most highly respected publications in the field of biochemistry Since 1955 each volume has been eagerly awaited frequently consulted and praised by researchers and reviewers alike Now with over 400 volumes all of them

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