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Soggetti	Biophysics Proteins Physics Biomathematics Biomedical engineering Biological and Medical Physics, Biophysics Protein Structure Numerical and Computational Physics, Simulation Mathematical and Computational Biology Biomedical Engineering and Bioengineering
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Nota di contenuto	Introduction -- Physical methods for studying proteins -- Physical properties of amino acids and proteins -- Selection of a biological objects -- Mathematical simulation of complex formation of protein molecules allowing for their domain structure -- Mathematical modeling of histone dimers formation in vitro with solutions of different ionic strength in the presence of monovalent salts -- Mathematical modeling of the temperature effect on binding of monomeric proteins in aqueous solutions by example on histones H2A, H2B, H3 and H4 -- Mathematical modeling of the temperature effect on binding of different sites of protein BCL-XL in aqueous solutions -- Mathematical modeling of the phosphorylation effect on the nature formation of biological complexes P53-MDM2 and P53-P300.

Sommario/riassunto

This book is devoted to the physical and mathematical modeling of the formation of complexes of protein molecules. The models developed show remarkable sensitivity to the amino acid sequences of proteins, which facilitates experimental studies and allows one to reduce the associated costs by reducing the number of measurements required according to the developed criteria. These models make it possible to reach a conclusion about the interactions between different amino acid chains and to identify more stable sites on proteins. The models also take the phosphorylation of amino acid residues into account. At the end of the book, the authors present possible directions of application of their physical and mathematical models in clinical medicine.
