Thermodynamics Of Ligand Protein Interactions

Complex networks of protein-ligand interactions underpin cellular function and communication. Disease can arise from disruption of these networks through the alteration of protein-ligand interaction affinities, for example by protein mutation or ligand modification. Understanding the mechanisms and principles that define affinity is therefore critical to both understanding and engineering biomolecular interactions, e.g. optimising drug molecules to interact effectively with their biomolecular targets. Thermodynamics reveals that affinity can be expressed in terms of the Gibbs free energy change upon interaction. In turn, this is composed of enthalpic and entropic terms, which can be thought of loosely as arising from structural and dynamic factors respectively. Though enthalpic terms can be estimated to a reasonable degree using structural data, a better understanding of entropic contributions from dynamic processes is required. The mouse major urinary protein (MUP) has been successfully established as a model system to investigate the thermodynamics of protein-ligand interactions. This work uses MUP, and employs a wide range of biophysical techniques, to develop our understanding of the dynamic factors in the thermodynamics of protein-ligand interactions. Four factors are addressed. Protein solvation is addressed by investigating proposed entropic solvation of the MUP binding pocket, and the possibility of engineering a new binding profile through manipulation of sidechains and solvation in the binding pocket. Ligand conformational entropy is addressed by performing the first systematic assessment of the widely predicted, yet inconsistently observed, benefits of removing and restricting ligand bonds. The greatest entropic loss upon binding, that of ligand rotational and translational entropy, is addressed by assessing MD predictions of significant residual translation and rotational motion of IBMP bound to MUP. This is achieved by using a combination of NMR techniques. Finally, protein dynamics are addressed by undertaking a preliminary investigation of a potentially promising novel technique for probing site-specific changes in protein dynamics upon ligand binding.
This Special Issue examines state-of-the-art in-cell NMR spectroscopy as it relates to biological systems of increasing complexity. The compendia of research and recent innovations from prominent laboratories in the field of solid state and solution in-cell NMR spectroscopy, metabolomics and technology development are presented. The work establishes in-cell NMR spectroscopy as the premier method for determining the structures and interaction capabilities of biological molecules at high resolution within the delicately intricate interior of living cells, and the means of utilizing cells as living laboratories to directly assess the effects of exogenous and endogenous stimuli on cell physiology.]
This detailed book collects modern and established computer-based methods aimed at addressing the drug discovery challenge from disparate perspectives by exploiting information on ligand-protein recognition. Beginning with methods that allow for the exploration of specific areas of chemical space and the designing of virtual libraries, the volume continues with sections on methods based on docking, quantitative models, and molecular dynamics simulations, which are employed for ligand discovery or development, as well as methods exploiting an ensemble of protein structures for the identification of potential protein targets. Written for the highly successful Methods in Molecular Biology series, chapters include introductions to their respective topics, lists

of the necessary materials, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, Protein-Ligand Interactions and Drug Design provides detailed practical procedures of solid computer-aided drug design methodologies employed to rationalize and optimize protein-ligand interactions, for experienced researchers and novices alike.

This book provides a complete overview of current techniques to identify ligands, characterise their binding sites and understand binding mechanisms. Suitable for biomolecular scientists at graduate or post-doctoral level in academia and industry. Biologists and chemists will also find it a useful introduction to the techniques available.

Protein structure is integral to its function. For the past 70 years differential scanning calorimetry has been used to measure protein structural stability. More recently it has been used to study macromolecular interactions. Interactions between proteins and ligands can manifest on differential scanning calorimetry melting curves or thermograms. Utilizing differential scanning calorimetry thermograms to detect or diagnose diseases has been a major goal in disease diagnostics. However, correlating specific ligand-protein interactions, as manifested in a thermogram, with a disease-specific plasma thermogram, has proven elusive. Modified human serum albumin was utilized to develop a process to capture and retrieve ligands from plasma. This process was demonstrated for two ligands that bind human serum albumin and subsequently perturb plasma thermograms. Human serum albumin was covalently modified by attachment of biotin to lysine residues. An investigation was performed to determine if modifications of human serum albumin affected the ability of the protein to bind ligands, in order to design better capture reagents. An analytical differential scanning calorimetry method was devised for determining, quantitatively accurate, ligand binding constants to human serum albumin. To further validate our method, an additional 29 drug/ligands were examined to determine their binding constants to human serum albumin.

This book is dedicated to studying the thermodynamic bases of the structure-function relationship of proteins. It moves from the elementary principles of physical chemistry to the most current topics of biochemistry, including those that may be subject to some controversy. It considers thermodynamic properties related to the stability and function of proteins from the point of view of physics in a language that, without sacrificing conceptual rigor, is easy to read. Detailing the thermodynamics of protein-ligand interactions, protein naturation, allostery, oxidative phosphorylation and protein phosphorylation, the book will be of interest to students and teachers of chemistry, physics, biochemistry and biotechnology.

Innovative and forward-looking, this volume focuses on recent achievements in this rapidly progressing field and looks at future potential for development. The first part provides a basic understanding of the factors governing protein-ligand interactions, followed by a comparison of key experimental methods (calorimetry, surface plasmon resonance, NMR) used in generating interaction data. The second half of the book is devoted to insilico methods of modeling and predicting molecular recognition and binding, ranging from first principles-based to approximate ones. Here, as elsewhere in the book, emphasis is placed on novel approaches and recent improvements to established methods. The final part looks at unresolved challenges, and the strategies to address them. With the content relevant for all drug classes and therapeutic fields,

this is an inspiring and often-consulted guide to the complexity of protein-ligand interaction modeling and analysis for both novices and experts.

This inter-disciplinary guide to the thermodynamics of living organisms has been thoroughly revised and updated to provide a uniquely integrated overview of the subject. Retaining its highly readable style, it will serve as an introduction to the study of energy transformation in the life sciences and particularly as an accessible means for biology, biochemistry and bioengineering undergraduate students to acquaint themselves with the physical dimension of their subject. The emphasis throughout the text is on understanding basic concepts and developing problem-solving skills. The mathematical difficulty increases gradually by chapter, but no calculus is required. Topics covered include energy and its transformation, the First Law of Thermodynamics, Gibbs free energy, statistical thermodynamics, binding equilibria and reaction kinetics. Each chapter comprises numerous illustrative examples taken from different areas of biochemistry, as well as a broad range of exercises and references for further study.

Strategies to reduce medical uncertainty and build evidence have become critical to the advancement of medical knowledge and modern medical practice. As new techniques and strategies have arisen, so has the need for a current reference work. Drug Discovery and Design examines the latest research in the development of these new strategies. Some of the topics covered include angiotensin converting enzyme inhibitors, HIV protease inhibitors, PPAR agonists for diabetes, and glucan synthase antifungal agents.

This practical reference for medicinal and pharmaceutical chemists combines the theoretical background with modern methods as well as applications from recent lead finding and optimization projects. Divided into two parts on the thermodynamics and kinetics of drug-receptor interaction, the text provides the conceptual and methodological basis for characterizing binding mechanisms for drugs and other bioactive molecules. It covers all currently used methods, from experimental approaches, such as ITC or SPR, right up to the latest computational methods. Case studies of real-life lead or drug development projects are also included so readers can apply the methods learned to their own projects. Finally, the benefits of a thorough binding mode analysis for any drug development project are summarized in an outlook chapter written by the editors.

With contributions by numerous experts

This volume provides methods on microcalorimetry approaches to investigate complex biological molecular systems. Chapters guide readers through Differential Scanning Calorimetry (DSC), Isothermal Titration Calorimetry (ITC), and advanced data processing. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Microcalorimetry of Biological Molecules: Methods and Protocols aims to ensure successful results in the further study of this vital field.

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Birkbeck and University College London Malet Street London WC1E 7H United Kingdom Email: g. waksman@bbk. ac. uk and g. waksman@ucl. ac. uk Phone: (+44) (0) 207 631 6833 Fax: (+44) (0) 207 631 6833 URL: http://people. cryst. bbk. ac. uk/?ubcg54a Gabriel Waksman is Professor of Structural Molecular Biology at the Institute of Structural Molecular Biology at UCL/Birkbeck, of which he is also the director. Before joining the faculty of UCL and Birkbeck, he was the Roy and Diana Vagelos Professor of Biochemistry and Molecular Biophysics at the Washington University School of Medicine in St Louis (USA). The rapidly evolving ?eld of protein science has now come to realize the ubiquity and importance of protein–protein interactions. It had been known for some time that proteins may interact with each other to form functional complexes, but it was thought to be the property of only a handful of key proteins. However, with the advent of hi- throughput proteomics to monitor protein–protein interactions at an organism level, we can now safely state that protein–protein interactions are the norm and not the exception.

A study of the thermodynamics of protein-protein and protein-ligand interactions. The author explains the energetics of protein interactions and gives a thorough account of the complicated biophysics that occur when the effects of multiple, complex molecules are taken into account.

Anyone teaching physical biochemistry or structural biology will find this to be a concise and thorough guide for their lectures on protein-protein association. Students and researchers will appreciate the clarity of presentation of fundamental concepts, and the guided reading of informative classic papers.

Protein-protein recognition is a critical event controlling in a large number of cell processes and therefore is of interest to a large section of the biological community. The purpose of this book is to bring together important concepts and systems in a single volume.

Thermodynamics of Ligand-Protein InteractionsImplications For Molecular Design

Provides an updated view of the current challenges faced by computational tools to decipher the basis of ligand-receptor interaction and modeling of biomolecular systems and drug discovery.

Free energy constitutes the most important thermodynamic quantity to understand how chemical species recognize each other, associate or react. Examples of problems in which knowledge of the underlying free energy behaviour is required, include conformational equilibria and molecular association, partitioning between immiscible liquids, receptor-drug interaction, protein-protein and protein-DNA association, and protein stability. This volume sets out to present a coherent and comprehensive account of the concepts that underlie different approaches devised for the determination of free energies. The reader will gain the necessary insight into the theoretical and computational foundations of the subject and will be presented with relevant applications from molecular-level modelling and simulations of chemical and biological systems. Both formally accurate and approximate methods are covered using both classical and quantum mechanical descriptions. A central theme of the book is that the wide variety of free energy calculation techniques available today can be

understood as different implementations of a few basic principles. The book is aimed at a broad readership of graduate students and researchers having a background in chemistry, physics, engineering and physical biology.

Proteins are the cell's workers, their messengers and overseers. In these roles, proteins specifically bind small molecules, nucleic acid and other protein partners. Cellular systems are closely regulated and biologically significant changes in populations of particular protein complexes correspond to very small variations of their thermodynamics or kinetics of reaction. Interfering with the interactions of proteins is the dominant strategy in the development of new pharmaceuticals. Protein Ligand Interactions: Methods and Applications, Second Edition provides a complete introduction to common and emerging procedures for characterizing the interactions of individual proteins. From the initial discovery of natural substrates or potential drug leads, to the detailed quantitative understanding of the mechanism of interaction, all stages of the research process are covered with a focus on those techniques that are, or are anticipated to become, widely accessible and performable with mainstream commercial instrumentation. Written in the highly successful Methods in Molecular Biology series format, chapters contain introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and accessible, Protein Ligand Interactions: Methods and Applications, Second Edition serves as an ideal guide for researchers new to the field of biophysical characterization of protein interactions – whether they are beginning graduate students or experts in allied areas of molecular cell biology, microbiology, pharmacology, medicinal chemistry or structural biology.

The importance of CK2 in cancer and other diseases has generated a significant amount of literature on the protein, and an international community of CK2 researchers. The International Union of Biochemistry and Molecular Biology (IUMBMB) sponsors periodic international conferences on CK2, making the protein a natural topic for a Wiley-IUBMB publication. Protein Kinase CK2 will deal with structural aspects underlying the constitutive activity of CK2, its specific susceptibility to pharmacological inhibition and its extraordinary pleiotropy. In the second part the fundamental role of CK2 in a w.

Multiple Equilibria in Proteins covers the multiple interactions between small ions and molecules and a protein molecule. The book also deals with the physicochemical mechanisms of this interaction and the information about protein structure and the forces stabilizing that structure. The text discusses the mathematical description of complex formation, the thermodynamic analysis of binding data, and various theoretical models which can be used to describe the phenomena of small molecule-macromolecule interactions. The measurement of complex formation; the binding of neutral molecules; and hydrogen-ion equilibria are also considered. The book further tackles metal-ion binding; the binding of organic ions by proteins; as well as protein-protein interaction. Chemists and

biochemists will find the book useful.

The rapidly evolving field of protein science has now come to realize the ubiquity and importance of protein-protein interactions. It had been known for some time that proteins may interact with each other to form functional complexes, but it was thought to be the property of only a handful of key proteins. However, with the advent of high throughput proteomics to monitor protein-protein interactions at an organism level, we can now safely state that protein-protein interactions are the norm and not the exception. Thus, protein function must be understood in the larger context of the various binding complexes that each protein may form with interacting partners at a given time in the life cycle of a cell. Proteins are now seen as forming sophisticated interaction networks subject to remarkable regulation. The study of these interaction networks and regulatory mechanism, which I would like to term "systems proteomics," is one of the thriving fields of proteomics. The bird-eye view that systems proteomics offers should not however mask the fact that proteins are each characterized by a unique set of physical and chemical properties. In other words, no protein looks and behaves like another. This complicates enormously the design of high-throughput proteomics methods. Unlike genes, which, by and large, display similar physico-chemical behaviors and thus can be easily used in a high throughput mode, proteins are not easily amenable to the same treatment. It is thus important to remind researchers active in the proteomics field the fundamental basis of protein chemistry. This book attempts to bridge the two extreme ends of protein science: on one end, systems proteomics, which describes, at a system level, the intricate connection network that proteins form in a cell, and on the other end, protein chemistry and biophysics, which describe the molecular properties of individual proteins and the structural and thermodynamic basis of their interactions within the network. Bridging the two ends of the spectrum is bioinformatics and computational chemistry. Large data sets created by systems proteomics need to be mined for meaningful information, methods need to be designed and implemented to improve experimental designs, extract signal over noise, and reject artifacts, and predictive methods need to be worked out and put to the test. Computational chemistry faces similar challenges. The prediction of binding thermodynamics of protein-protein interaction is still in its infancy. Proteins are large objects, and simplifying assumptions and shortcuts still need to be applied to make simulations manageable, and this despite exponential progress in computer technology. Finally, the study of proteins impacts directly on human health. It is an obvious statement to say that, for decades, enzymes, receptors, and key regulator proteins have been targeted for drug discovery. However, a recent and exciting development is the exploitation of our knowledge of protein-protein interaction for the design of new pharmaceuticals. This presents particular challenges because protein-protein interfaces are generally shallow and interactions are weak. However, progress is clearly being made and the book seeks to provide examples of successes in this area.

The lock-and-key principle formulated by Emil Fischer as early as the end of the 19th century has still not lost any of its significance for the life sciences. The basic aspects of ligand-protein interaction may be summarized under the term 'molecular recognition' and concern the specificity as well as stability of ligand binding. Molecular recognition is thus a central topic in the development of active substances, since stability and specificity determine whether a substance can be used as a drug. Nowadays, computer-aided prediction and intelligent molecular design make a large contribution to the constant search for, e. g., improved enzyme inhibitors, and new concepts such as that of pharmacophores are being developed. An up-to-date presentation of an eternally young topic, this book is an indispensable information source for chemists, biochemists and pharmacologists dealing with the binding of ligands to proteins.

Today, calorimetry is considered an art (although some consider it a tool) that studies the energy changes that occur during a change of state. This allows physicochemical analysis to study in detail the thermodynamic systems and to evaluate the different variables that establish the characteristics of the system itself. This book illustrates how the reader can use this technique in a wide spectrum of applications.

In this volume, the editors have collected the knowledgeable insights of a number of leaders in this field - researchers who have achieved success in addressing the difficult problem of inhibiting protein-protein interactions. These researchers describe their unique approaches, and share experiences, results, thoughts, and opinions. The content of the articles is rich, and in terms of scope ranges from generalized approaches to specific case studies. There are various focal points, including methodologies and the molecules themselves. Ultimately, there are numerous lessons to be taken away from this collection, and the editors hope that this snapshot of the current state of the art in developing protein-protein inhibitors not only pays tribute to the past successes, but also generates excitement about the future potential of this field

Rapid developments in experimental techniques continue to push back the limits in the resolution, size, and complexity of the chemical and biological systems that can be investigated. This challenges the theoretical community to develop innovative methods for better interpreting experimental results. Normal Mode Analysis (NMA) is one such technique. Capable of providing unique insights into the structural and dynamical properties of complex systems, it is now finding a wide range of applications in chemical and biological problems. From the fundamental physical ideas to cutting-edge applications and beyond, this book presents a broad overview of normal mode analysis and its value in state-of-the-art research. The first section introduces NMA, examines NMA algorithm development at different resolutions, and explores the application of those techniques in the study of biological systems. Later chapters cover method developments based on or inspired by NMA but going beyond the harmonic approximation inherent in standard NMA techniques. Normal mode analysis complements traditional approaches with computational efficiency and applicability to large systems that are beyond the reach of older methods. This book offers a unique opportunity to learn from the experiences of an international, interdisciplinary panel of top researchers and explore the latest developments and applications of NMA to biophysical and chemical problems.

This book discusses a broad range of basic and advanced topics in the field of protein structure, function, folding, flexibility, and dynamics. Starting with a basic introduction to protein purification, estimation, storage, and its effect on the protein structure, function, and dynamics, it also discusses various experimental and computational structure determination approaches; the importance of molecular interactions and water in protein stability, folding and dynamics; kinetic and thermodynamic parameters associated with protein-ligand binding; single molecule techniques and their applications in studying protein folding and aggregation; protein quality control; the role of amino acid sequence in protein aggregation; muscarinic acetylcholine receptors, antimuscarinic drugs, and their clinical significances. Further, the book explains the current understanding on the therapeutic importance of the enzyme dopamine beta hydroxylase; structural dynamics and motions in molecular motors; role of cathepsins in controlling degradation of extracellular matrix during disease states; and the important structure-function relationship of iron-binding proteins, ferritins. Overall, the book is an important guide and a comprehensive resource for understanding protein structure, function, dynamics, and interaction.

Explores new applications emerging from our latestunderstanding of proteins in solution and at interfaces Proteins in solution and at interfaces increasingly serve as thestarting point for exciting new applications, from biomimeticmaterials to nanoparticle patterning. This book surveys the stateof the science in the field, offering investigators a currentunderstanding of the characteristics of proteins in solution and atinterfaces as well as the techniques used to study thesecharacteristics. Moreover, the authors explore many of the new andemerging applications that have resulted from the most recentstudies. Topics include protein and protein aggregate structure;computational and experimental techniques to study proteinstructure, aggregation, and adsorption; proteins in non-standardconditions; and applications in biotechnology. Proteins in Solution and at Interfaces is divided intotwo parts: Part One introduces concepts as well as theoretical andexperimental techniques that are used to study protein systems,including X-ray crystallography, nuclear magnetic resonance, smallangle scattering, and spectroscopic methods Part Two examines current and emerging applications,including nanomaterials, natural fibrous proteins, and biomolecularthermodynamics The book's twenty-three chapters have been contributed byleading experts in the field. These contributions are based on athorough review of the latest peer-reviewed findings as well as theauthors' own research experience. Chapters begin with a discussionof core concepts and then gradually build in complexity, concludingwith a forecast of future developments. Readers will not only gain a current understanding of proteinsin solution and at interfaces, but also will discover howtheoretical and technical developments in the field can betranslated into new applications in material design, geneticengineering, personalized medicine, drug delivery, biosensors, andbiotechnology.

Thermodynamics of Ligand-Protein Interactions: Implications for Molecular Design. Proteins continuously interact with each other to determine cell fate. Consequently, an examination of just when such protein-protein interactions occur and how they are controlled is essential for understanding the molecular mechanism of biological processes, elucidating the molecular basis of diseases, and identifying potential targets for therapeutic interventions. In Protein-Protein Interactions: Methods and Applications,

leading experts describe in detail their highly successful biochemical, biophysical, genetic, and computational techniques for studying these interactions. Their readily reproducible methods demonstrate how to identify protein interaction partners, qualitatively or quantitatively measure protein-protein interactions, monitor protein-protein interactions as they occur in living cells, and determine interaction interfaces. The techniques described utilize a variety of cutting-edge technologies, including surface plasmon resonance (SRP), fluorescence resonance energy transfer (FRET), fluorescence polarization (FP), isothermal titration calorimetry (ITC), circular dichroism (CD), protein fragment complementation assays (PCA), various two-hybrid systems, and proteomics- and bioinformatics-based approaches, such as the Scansite program for computational analysis. Each time-tested protocol includes a background introduction outlining the principle behind the technique, lists of equipment and reagents, and tips on troubleshooting and avoiding known pitfalls. Authoritative and highly practical, Protein-Protein Interactions: Methods and Applications offers both beginning and experienced investigators a full range of the powerful tools needed for deciphering how proteins interact to form biological networks, as well as for unraveling protein-protein interactions in disease in the search for novel therapeutic targets. Connects fundamental knowledge of multivalent interactions with current practice and state-of-the-art applications Multivalency is a widespread phenomenon, with applications spanning supramolecular chemistry, materials chemistry, pharmaceutical chemistry and biochemistry. This advanced textbook provides students and junior scientists with an excellent introduction to the fundamentals of multivalent interactions, whilst expanding the knowledge of experienced researchers in the field. Multivalency: Concepts, Research & Applications is divided into three parts. Part one provides background knowledge on various aspects of multivalency and cooperativity and presents practical methods for their study. Fundamental aspects such as thermodynamics, kinetics and the principle of effective molarity are described, and characterisation methods, experimental methodologies and data treatment methods are also discussed. Parts two and three provide an overview of current systems in which multivalency plays an important role in chemistry and biology, with a focus on the design rules, underlying chemistry and the fundamental principles of multivalency. The systems covered range from chemical/materials-based ones such as dendrimers and sensors, to biological systems including cell recognition and protein binding. Examples and case studies from biochemistry/bioorganic chemistry as well as synthetic systems feature throughout the book. Introduces students and young scientists to the field of multivalent interactions and assists experienced researchers utilising the methodologies in their work Features examples and case studies from biochemistry/bioorganic chemistry, as well as synthetic systems throughout the book Edited by leading experts in the field with contributions from established scientists Multivalency: Concepts, Research & Applications is recommended for graduate students and junior scientists in supramolecular chemistry and related fields, looking for an introduction to multivalent interactions. It is also highly useful to experienced academics and scientists in industry working on research relating to multivalent and cooperative systems in supramolecular chemistry, organic chemistry, pharmaceutical chemistry, chemical biology, biochemistry, materials science and nanotechnology.

New genomic information has revealed the crucial role that protein-protein interactions (PPIs)

play in regulating numerous cellular functions. Aberrant forms of these interactions are common in numerous diseases and thus PPIs have emerged as a vast class of critical drug targets. Despite the importance of PPIs in biology, it has been extremely challenging to convert targets into therapeutics and targeting PPIs had long been considered a very difficult task. However, over the past decade the field has advanced with increasing growth in the number of successful PPI regulators. Protein-Protein Interaction Regulators surveys the latest advances in the structural understanding of PPIs as well as recent developments in modulator discovery.
13.2.1 Protein Dynamics of SA WT and S1 Mutant DHFR in Apo and Bound States
Advanced researches as well as an integrated analysis of the science of thermodynamics are provided in this book. Thermodynamics is one of the most interesting parts of physical chemistry which has significantly contributed to modern science. Being focused on a broad spectrum of applications of thermodynamics, this book accumulates a series of contributions made by veteran scientists and researchers from across the planet. Significant topics such as atmospheric thermodynamics, thermodynamics of ligand-protein interactions, interfaces, nanoparticle formation in laser ablation and free-piston linear alternator are covered. This book will appeal to students engaged in post-graduate courses. It will also serve as a good source of reference for those researchers who are interested in thermodynamics.
Dr. Sergio Decherchi and Dr. Andrea Cavalli are co-founders of BiKi Technologies s.r.l. - a company that commercializes a Molecular Dynamics-based software suite for drug discovery. All other Topic Editors declare no competing interests with regards to the Research Topic subject.
Serum albumin is a large protein present in cow serum protein (BSA, Bovine Serum Albumin) rich in essential amino acids and compounds with disulfide bridges and thiol groups. This protein passes into breast milk from the bloodstream by diffusion, has antioxidant capacity and protects fats from oxidation. Albumin has the ability to inhibit tumor factors and bind to fat, mobilize them in the body to perform other functions such as obtaining energy or forming membranes. It is also able to block the conversion of angiotensin I into angiotensin II (vasoconstrictor) which gives it antihypertensive action. In addition, it has the ability to reduce cholesterol absorption, complex heavy metals and is an opioid agonist (acts on opioid receptors and promotes analgesia). BSA is the most studied and produced protein worldwide in the last 80 years. This protein brings large dividends to the world economy with a very prominent and favorable annual growth at a cost of 100 USD per gram. This book brings new contributions to the science and industry of this biopolymer. The audience of this book is very wide from students, teachers and researchers (doctors, pharmacists, biochemists and industrialists of this sector). Therefore, this book has a great future and many readers to whom it is addressed.
Protein-ligand and protein-protein interactions are critical to cellular function. Most cellular metabolic and signal tranduction pathways are influenced by these interactions, consequently molecular level understanding of these associations is an important area of biochemical research. We have examined the thermodynamics of several protein-protein associations and the protein-ligand interactions that mediate them. Using Fluorescence Correlation Spectroscopy, we have examined the putative interaction between pig heart malate dehydrogenase (MDH) and citrate synthase (CTS). We demonstrate a specific, low-affinity interaction between these enzymes. The association is highly polyethylene glycol (PEG)-dependent, and at high concentrations of NaCl or PEG, non-specific aggregates are formed. We demonstrate that oxaloacetate, the intermediate common to both CTS and MDH, induces the association at concentrations below the Km of CTS, suggesting that the open conformation of CTS is involved in the association. Using several biophysical techniques, we have examined the subunit associations of B. stearothermophilus phosphofructokinase (PFK). We demonstrate that the inhibitor bound conformation of the enzyme has reduced subunit

affinity. The kinetics and thermodynamics of the phosphoenolpyrvuate (PEP)-induced dissociation of PFK have been quantified. Binding substrate, fructose-6-phosphate (F6P), stabilizes the enzyme to inhibitor-induced dissociation by 132-fold. These data suggest that subunit associations may play a role in the allosteric inhibition of PFK by PEP. The thermodynamics of the protein-ligand associations and allosteric inhibition of E. coli phosphofructokinase have been examined using intrinsic fluorescence and hydrostatic pressure. Both ligand-binding affinity and PEP inhibition are diminished by pressure, whereas substrate-binding affinity for inhibitor-bound enzyme is pressure-insensitive. Larger entropic than enthalpic changes with pressure lead to the overall reduction in free energies. Using a fluorescence-based assay, we have developed a series of baroresistant buffer mixtures. By combining a buffer with acid dissociation of negative volume with a buffer of positive volume, a pressure-resistant mixture is produced. Alteration of the molar ratio of the two component buffers yields mixtures that are pressure-insensitive at pH values around neutrality.