

Report on the 2013 Biophysical Reviews Issue: Biophysics of Protein Ligand Interactions in Dilute and Crowded Media: A Special Issue in Honor of Allen Minton's 70th Birthday.

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Biophysical Reviews (BR) Issue

Format: As the official IUPAB topical review journal, *BR* publishes high quality review articles deemed to be of particular interest to members of the global biophysics community. Printed quarterly, the contents of each regular issue cover a non-themed array of topics with perspectives spanning the experimental to theoretical range.

In addition to regular issues, the Chief Editor, Jean Garnier, the *BR* editorial board and the Springer journal support staff have committed the journal to undertake the publication of a single high profile special issue each year on a topic aligned with the broadly stated IUPAB mission of promotion, development, education, recognition and sponsorship of biophysics, and biophysicists, at the international level.

Special Issue 2012: The first such special issue, published in 2012, dealt with the subject of computational methods in biophysics. That edition, edited by Haruki Nakamura and Cris dos Remedios, became the most downloaded issue in the journal's

history. The IUPAB goal of education and promotion of biophysics in that issue was met by placing the scientific emphasis on the diverse range of approaches (and problems) that could be tackled using computational methodology.

In terms of cost and manpower, computational biophysics is a relatively accessible area of science. As such, a strong motivating force behind the selection of that thematic topic was the belief that placing it in the spotlight could broadly assist with IUPAB goals in the areas of promotion, education and development of biophysics across the globe.

This goal was further enhanced by having the majority of authors in that special edition deliver a workshop style talk during the IUPAB Beijing Congress and pair with audience members at the conclusion of the question and answer session.

Special Issue 2013: The special issue theme for 2013, 'Biophysics of Protein Ligand Interactions in Dilute and Crowded Media: A

Special Issue in Honor of Allen Minton's 70th Birthday' has emerged from the twin IUPAB aims of providing recognition for a suitably deserving biophysicist, and informing the reader about recent developments in an area to which they have made significant contributions. In this instance *BR* has used the occasion of his 70th birthday to both recognize the scientific efforts of Allen Minton and to place a spotlight on the field of quantitative characterization of protein ligand interactions in dilute and crowded media that he has done so much to help develop.

In this newsletter piece I will first describe the scope of the special issue to help place its general importance in perspective. I will then provide a few words about Allen Minton's life and career achievements. Finally I will conclude with a short list of the different particular contributions from the various authors involved.

Protein Ligand Interactions in Dilute and Crowded Conditions:

Although much can be inferred about an organism by analyzing the information held in the repository of its genome it is the physical and chemical interactions between the encoded gene products that dictate the moment-to-moment interactions at the subcellular level. Indeed it would not be too dramatic to say that the goal of achieving a true molecular understanding of life processes is synonymous with the goal of

achieving a complete description of the temporal, spatial and chemical dependencies of all possible interactions in the organism.

By interaction we are referring to both chemical and physical interactions (the former defined by the breakage and/or formation of covalent chemical bonds, the latter by their absence). Such physicochemical interactions are characterized by the nature of the components involved, the reaction pathway/mechanism followed, and a quantitative index of how tightly and how quickly their reactants and products come together and depart from each other.

Recognition of the importance of the interaction in context requires a rich understanding of the underlying biological, physiological and medical aspects of the system. Defining these physicochemical interactions, the nuts and bolts of life's machinery, requires a scientist with knowledge of biology, chemistry, physics and mathematics – in short, exactly the type of problem biophysicists are uniquely trained for.

Historically two different scientific approaches have been applied towards achieving these aims. Reductionist, or bottom up strategies, have aimed to synthesize, express or purify individual components and then study their behavior in well-defined in vitro systems. Holistic, or top down approaches, have tried to

study the behavior of the individual components by monitoring their fate in the relatively undefined environment of the cultured cell, laboratory animal or human patient.

The reductionist approach has yielded definite information but with large gaps in our knowledge concerning how the interaction occurring in dilute buffer may be affected by the plethora of other components likely to be found proximal to its chemical environment within the cell or organism.

The holistic approach has yielded biologically relevant information about the particular conditions studied but with large doubts over the transferability of the information to other systems due to the lack of knowledge of the actual differences between systems as a result of the many other happenings occurring in unseen parallel of the pathway of direct observation. More recently, systems biology techniques involving large-scale spatial and temporal screening of nucleic acid, lipid, carbohydrate and protein components have sought to bridge the gap between the reductionist and holistic approaches with varying degrees of success.

However, despite these advances there is currently no predictive transferable physical theory for quantitatively estimating the range and extent of physicochemical interactions in a biological system.

Typically today's predictive models are still based on interpolative analysis of hardly won experimental evidence.

Allen Minton's Life and Contribution to Biophysics of Protein Ligand Interactions:

Towards the development of a predictive theory of physico-chemical

interactions in complex chemical environments, a number of researchers in the post-World War II period led by the



likes of Fumio Oosawa, Alexander Ogston and Torvard Laurent, adapted earlier quantitative formalisms for describing macromolecular properties (including their interactions) to include allowance for 'non-ideal' factors.

However these efforts were largely restricted to slightly non-ideal conditions not too different from dilute buffer. Beginning with his early studies of hemoglobin behavior over the 0 – 400 mg/ml range, Allen Minton helped to significantly advance and mature this field by adapting equation of state (EOS) methodology from non-ideal gas and polymer theory to examine a range of problems in

the field of biochemistry. These problems included, but were not limited to, bio-molecular structure, enzyme kinetics, surface adsorption, macromolecular diffusion, biological self-assembly and protein ligand interactions.

Working at the interface of experiment and theory Allen's research efforts have been influential across a number of fields spanning polymer physics to cell biology. He has developed and patented a range of novel experimental methods as well as contributing to the development of theory for a range of more traditional biophysical methods such as analytical ultracentrifugation, light scattering, optical biosensor technology and chromatography.

Considering his status as one of America's very highly cited chemists, the extraordinary originality of his scientific publications and his recognized seminal contributions to the development of the field of 'macromolecular crowding' he is a very appropriate first choice of scientist for *BR* to recognize via a dedication in our special issue for 2013 – the year of his 70th birthday.

Contributions from the Authors Involved in this Special Issue:

The special issue contains a wide range of experimental and theoretical articles reviewing various aspects of the topic. We thank the authors for their efforts

and briefly list their contributions below. Further information can be gained from the journal issue website

<http://link.springer.com/journal/12551/5/2/page/1>

Foreword to the biophysics of protein-protein and protein-ligand interactions in dilute and crowded media—a special issue in honor of Allen Minton's 70th birthday. D. Hall · C.G. dos Remedios

A brief look back at 45 years of research in physical biochemistry. A.P. Minton

Macromolecular interactions of the bacterial division FtsZ protein: from quantitative biochemistry and crowding to reconstructing minimal divisomes in the test tube. G. Rivas · C. Alfonso · M. Jiménez · B. Monterroso · S. Zorrilla

Protein interactions in the assembly of the tail of bacteriophage T4. F. Arisaka · S. Kanamaru

The loop hypothesis: contribution of early formed specific non-local interactions to the determination of protein folding pathways. T. Orevi · G. Rahamim · G. Hazan · D. Amir · E. Haas

Protein-protein interactions in a crowded environment. A. Bhattacharya · Y.C. Kim · J. Mittal

Computer simulations of the bacterial cytoplasm. T. Frembgen-Kesner · A.H. Elcock

Assessment and significance of protein-protein interactions during development of protein biopharmaceuticals. S. Yadav · J. Liu · T.M. Scherer · Y. Gokarn · B. Demeule · S. Kanai · J.D. Andya · S.J. Shire

Effects of macromolecular crowding agents on protein folding in vitro and in silico. A. Christiansen · Q. Wang · M.S. Cheung · P. Wittung-Stafshede

Light-scattering-based analysis of biomolecular interactions. D. Some

Analytical ultracentrifugation as a tool for studying protein interactions. P. Schuck

A historical perspective of the biophysics of the thrombin-heparin system: an example of nonspecific binding and the consequent parking problem in action. D.J. Winzor

Soft interactions and crowding. M. Sarkar · C. Li · G.J. Pielak

Hydrodynamic modeling of protein conformation in solution ELLIPS and HYDRO. J. Garcia de la Torre S.E. Harding

Simulation and modeling of crowding effects on the thermodynamic and kinetic properties of proteins with atomic details. H.-X. Zhou · S. Qin

Ratchets, red cells, and metastability. F.A. Ferrone · A. Aprelev

Entropic stabilization of the folded states of RNA due to macromolecular crowding. N.A. Denesyuk · D. Thirumalai

Modeling the structure of IgG3 wild type (WT) and mutant (M15) antibodies. General multi-subunit model for IgG antibodies employed in the HYDROSUB calculations. (Taken from the contribution by Stephen Harding and José García de la Torre, 'Hydrodynamic modeling of protein conformation in solution: ELLIPS and HYDRO' Biophys. Rev. (2013) 5:195–206)

