PREFACE

The field of Biomolecular Modelling has evolved dramatically over the past 10 years. The 2013 Nobel Prize in Chemistry was awarded to pioneers in the field M. Karplus, M. Levitt, and A. Warshel, recognizing the impact of the computational and molecular modeling methods in molecular and life sciences (http://www.nobelprize.org/nobel_prizes/chemistry/) (Estrada-Tejedor, Ros-Blanco, & Teixido Closa, 2014). The enormous growth in the computer power, construction of massive parallel supercomputers, and development of novel computational methods made possible successful simulation of increasingly large biomolecular systems. Currently, it is a routine to model reaction mechanisms of solvated enzyme–substrate complexes, the dynamic behavior of proteins, nucleic acids and their complexes in nanosecond and microsecond timescale, the insertion of membrane proteins into lipid bilayer, and the docking of ligands and inhibitors to their targets. The development of the biomolecular modeling unleashed new opportunities for combined, integrated, and synergistic studies with experimental methods. For example, the QM/MM modeling of enzyme reaction mechanism can be integrated with crystallographic, mutagenesis, and kinetic studies (Christov et al., 2013; Senn & Thiel, 2009; van der Kamp & Mulholland, 2013). The atomistic molecular dynamics simulations of fast protein motions can be complemented with NMR and circular dichroism studies of larger conformational changes (Karabencheva-Christova, Carlsson, Balali-Mood, Black, & Christov, 2013; Karplus & Kuriyan, 2005; Ortega, Pons, & Millet, 2013; Zandarashvili, Esadze, & Iwahara, 2013). In bioinorganic chemistry, combining QM, QM/MM, and MD methods with multiple spectroscopic studies of metal centers (UV-Vis, MCD, EPR, and XAS) provides unique and validated insight into the interaction between the metal and the protein which govern the enzyme reactivity (Neidig & Solomon, 2005). In addition, considerable progress was achieved in integrating computational methods at different levels of theory which made easer the practical implementation of the output from one modeling study as an input for another one(Sherwood, Brooks, & Sansom, 2008). The development and improvement of molecular visualizing software including computer animations made the preparation of the inputs for computational studies and the analysis of the results much more straightforward and user friendly than before. The mentioned progress made

possible broader application of biomolecular modeling methods in biotechnology and drug design.

This thematic volume of *APCSB* is focused on some of the most recent top contributions in biomolecular modeling both in application and method developments such as the interplay between molecular modeling and chemoinformatics, computational studies of DNA polymerase, dynamic modeling of molecular assembly, stability of amyloid oligomers, coarse-grained modeling of proteins, allosteric regulations in metal sensor proteins, modeling the *N*-acylethanolamine acid amidase inhibition and action, CHARMM-GUI online server for protein nonstandard residues, and high-resolution modeling of protein structures.

TATYANA KARABENCHEVA-CHRISTOVA
Department of Applied Sciences,
Northumbria University at Newcastle,
Newcastle-upon-Tyne,
United Kingdom

REFERENCES

Christov, C. Z., Lodola, A., Karabencheva-Christova, T. G., Wan, S., Coveney, P. V., & Mulholland, A. J. (2013). Conformational effects on the pro-(S) hydrogen abstraction reaction in cyclooxygenase-1: An integrated QM/MM and MD study. *Biophysical Journal, 104*, L01–L03.

Estrada-Tejedor, R., Ros-Blanco, L., & Teixido Closa, J. (2014). Multiscale modeling for complex chemical systems: Highlights about the Nobel Prize in Chemistry 2013. *Afinidad, 71*(566), 89–94.

Karabencheva-Christova, T. G., Carlsson, U., Balali-Mood, K., Black, G. W., & Christov, C. Z. (2013). Conformational effects on the circular dichroism of human carbonic anhydrase II: A multilevel computational study. *PLoS One, 8*(2), e56874.

Karplus, M., & Kuriyan, J. (2005). Molecular dynamics and protein function. *Proceedings of the National Academy of Sciences of the United States of America, 102*(19), 6679–6685.

Neidig, M. L., & Solomon, E. I. (2005). Structure-function correlations in oxygen activating non-heme iron enzymes. *Chemical Communications, 47*, 5843–5863.

Ortega, G., Pons, M., & Millet, O. (2013). Protein functional dynamics in multiple timescales as studied by NMR spectroscopy. *Advances in Protein Chemistry and Structural Biology, 92*, 219–251.

Senn, H. M., & Thiel, W. (2009). QM/MM methods for biomolecular systems. *Angewandte Chemie International Edition in English, 48*(7), 1198–1229.

Sherwood, P., Brooks, B. R., & Sansom, M. S. P. (2008). Multiscale methods for macromolecular simulations. *Current Opinion in Structural Biology, 18*(5), 630–640.

van der Kamp, M. W., & Mulholland, A. J. (2013). Combined quantum mechanics/molecular mechanics (QM/MM) methods in computational enzymology. *Biochemistry, 52*(16), 2708–2728.

Zandarashvili, L., Esadze, A., & Iwahara, J. (2013). NMR studies on the dynamics of hydrogen bonds and ion pairs involving lysine side chains of proteins. *Advances in Protein Chemistry and Structural Biology, 93*, 37–80.