

## FOREWORD

Proteins are termed “molecules of life”. In the living organisms, they serve as the building material of cells and tissues, catalyze chemical reactions (enzymes), participate in signal transduction and transmission of genetic information, and are crucial in pathogen identification and immunoresponses. In a physiological conditions, these unique molecules have dynamic, yet unique three-dimensional structures which except for the so-called “plastic” or “natively-unfolded” proteins are determined solely by their amino-acid sequences. On the other hand, errors in sequence (mutations) or partial enzymatic digestion resulting in chain fragmentation often lead to malfunction resulting in cancer and formation of amyloid deposits that cause the notorious diseases commonly termed as amyloidoses. Thus, the protein structure and dynamics determine their function and biological role. Consequently, the formation and disruption of a protein three-dimensional structure (folding and unfolding) and protein dynamics have been subjected to intense research since the '70s of the 20th century and this research area is a place where experimental and theoretical biology, biophysics, chemistry, as well as physics, bioinformatics, applied mathematics, and computer science meet.

Research on the protein structure, dynamics and folding would not be possible without interdisciplinary and international collaboration. Researchers from the University of Gdansk and the Korean Institute for Advanced Study (KIAS), Republic of Korea, have been very active in the research of proteins and the two institutions have had a long-time history of collaboration in this field. This collaboration brought about the idea of organizing a series of *Korean-Polish/Polish Korean Conferences on Protein Folding: Theoretical and Experimental Approaches* held in Seoul and in Gdansk, on an alternating basis, to promote collaboration in protein research and related fields and exchange between Korean and Polish scientists, as well as scientists from other countries in Asia and Europe. The first conference of the series was held in Seoul in 2015. The *Second Polish Korean Conference on Protein Folding: Theoretical and Experimental Approaches* took place in the Leźno Palace hotel near

Gdansk from May 28 to June 1, 2016. The conference was attended by nearly 60 participants, including 20 invited speakers, mainly from Poland and the Republic of Korea but also from Japan, China, France, Germany, Spain, Sweden, and the USA. The conference covered a wide spectrum of topics regarding theoretical and experimental protein research, including protein-structure prediction, modeling protein structures and dynamics, empirical force fields, the physics of protein folding, protein free-energy landscapes, knotted proteins, experimental techniques, and the biological role of proteins.

The variety and high quality of the research presented at the conference brought about the idea to produce a special issue of *TASK Quarterly*, a journal with which the Polish organizers have a long-term relationship, to publish the conference papers. This special issue includes 3 papers from the invited speakers and 6 from other participants.

We would like to thank the institutions and companies that financed the conference or supported it in other ways: the National Science Centre of Poland (NCN), the Polish Ministry of Science and Higher Education, Hydro-Lab, Binder, Air Liquide, Shim-Pol, and Fundacja Inicjatyw Zawodowych i Społecznych “PERSPEKTYWA”, which facilitated the conference, and the Faculty of Chemistry, University of Gdansk for their help with logistics. Special thanks are expressed to the staff of “PERSPEKTYWA” as well as the graduate students and postdocs of the Molecular Modeling group of the Faculty of Chemistry at the University of Gdansk: Ms. Agnieszka Karczyńska, Ms. Agnieszka Lipska, Robert Ganzynkiewicz PhD, and Tomasz Wirecki PhD who helped to organize and run the event. Last but not least, we would also like to thank Prof. Jarosław Rybicki, the Editor-in-Chief of *TASK Quarterly*, for making this special issue available to publish the conference follow-up papers, as well as all the contributors who have decided to publish the results of their research in this special issue.

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