

Preface

One century ago, the coagulation of egg white by applying pressure of 700 MPa showed for the first time that pressure can denature a protein (P. W. Bridgman, J Biol Chem 19:511–512, 1914). A half century later, the protein denaturation phenomenon began to be understood on P – T plane as kinetic and thermodynamic processes (Suzuki, Rev Phys Chem Jpn 29:91–98, 1960; Hawley, Biochemistry 10:2436–2442, 1971), while independently the protein-folding phenomenon was established as a thermodynamic process (Anfinsen, Proc Natl Acad Sci USA 47:1309–1314, 1961, Nobel prize 1972). Since then, up to the present, stable folded structures of proteins and nucleic acids have been disclosed in mass quantities in crystal as well as in solution, with a hope to understand their function based on structures. However, it is now clear that generally the knowledge on these stable, and basically single, folded structures alone does not give direct answers to their function, but the knowledge on the multiple and dynamic reality of their structures is crucial. It is on this historical background that methods capable of disclosing the multiple-conformational and dynamic reality of bio-macromolecules, notably high-pressure NMR, X-ray crystallography/scattering, and others with pressure as least “invasive” perturbation, have been developed in recent years. These methods are rapidly disclosing knowledge on the hidden reality of proteins that is crucial to in-depth understanding not only of protein structures and function but also of most life phenomena such as motility, physiology/disease, and environmental adaptation/evolution, as well as to the strategic and efficient use of pressure in agricultural and medical applications in the years to come. In other words, pressure is no longer an “odd” and “foreign” parameter to life. Instead, it is a crucial variable parameter with which one can disclose the secret of nature in its very basic atomic design and, furthermore, a manageable external parameter with which one can select and enhance some important molecular events in nature to our practical needs. In short, we are currently facing a new era of high-pressure bioscience, where advanced knowledge on bio-macromolecular structure is to be shared by all people interested, to deepen our understanding of basic life phenomena and to expand the utility of pressure variable to a wide area of bioscience and biotechnology. It is in this timing and concept, marking the centennial anniversary of the first report on pressure

denaturation of proteins, that we plan this monograph covering from the basics to the application with pressure as the key variable.

The 33 chapters of this monograph are all original contributions by experts in the field. They are divided into nine parts, each of which consists of three to four chapters, which are arranged in an as much as unified manner to provide readers with a comprehensive view on the entire field of research from the basics (in Parts I through III) to the application (in Parts VI through VIII) and both (in Parts IV to V). This monograph is intended also to serve as a first comprehensive textbook on bio-macromolecular events under pressure and their possible roles in macroscopic life phenomena as well as in application to high-pressure biotechnology, for a wide audience including students and researchers in both basic and applied biosciences.

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