Preface

About three years ago, I received an e-mail from Mr. Stanford Chong, director and publisher at Pan Stanford Publishing, just after returning from BIT Life Sciences' Second Symposium on Enzymes and Biocatalysis (2011). He proposed that I write a book on enzymes. After several e-mail exchanges, we agreed to publish this book.

The prominent nature of enzymes is to enhance the rate of reaction, and most enzymes are composed of proteins. Therefore, the first half of the book describes the kinetic aspects of enzymes following a discussion on the general properties of enzymes in Chapter 1. Moreover, in Chapter 1, readers will learn how interesting enzymes are. This part describes the overall reaction kinetics by introducing historical works. The methods to analyze the effect of various factors on the enzyme activity and the practical way to determine the rate constants of the enzymatic reactions are also presented. The second half of the book describes the structural aspect of enzymes. Chapters 6 and 7 describe the general properties of proteins and the method to determine the overall and the active site structures of proteins. Chapter 8 describes the control of enzyme activity. It also discusses enzyme regulation by non-covalent interaction and by covalent modification. Protein kinase A is discussed in the section on regulation by the side chain phosphorylation, though the enzyme itself is activated with cAMP. Chapter 9 describes the standard methods of enzyme preparation. The functional and structural aspects of a phenylalanine oxidase (deaminating and decarboxylating) are discussed as a case study in Chapter 10.

A molecular simulation method that combines the quantum mechanics (QM) and molecular mechanics (MM) approaches is commonly used in chemical and biological systems. Chapter 4 shows that enzymatic reactions can be monitored experimentally at a time scale of milliseconds. A QM/MM approach simulates the reaction pathway in an enzymatic reaction under the nanosecond

to picosecond level. In Chapter 8, I make a brief mention of the QM/MM approach. Now, this method is becoming an important tool in enzymology. The 2013 Nobel Prize in Chemistry was given to three doctors, Martin Karplus, Michael Levitt, and Arieh Warshel, for their pioneering works "for the development of multiscale models for complex chemical systems."

As much as possible, I have selected original papers as reference. When it was difficult to get access to old works, I followed review papers and books. Most of the 3D structures of proteins are drawn from pdb files by PyMOL software. Some of the figures are shown by stereo view; therefore, a 3D viewer may be helpful.

For a better understanding of the text, especially the derivation of equations, a few problems are presented at the end of Chapters 2 to 10. The problems are meant to be solved independently. To aid the readers in solving the problems, solutions to difficult problems have been provided at the end of the book.

I thank the following for their comments and advice: Dr. H. Nakamoto, Saitama University (Chapters 1 to 10), Dr. K. Abe, Nagoya University (Section 1.2.2 and Box 1.1), Dr. Y. Nishina, Kumamoto University (Section 4.5.1), Dr. K. Tamura, Kitasato University (Sections 1.2.3, 6.3.2, and 7.3.2), and Dr. S. Yoneda, Kitasato University (problem 1 and its solution in Chapter 6 and Section 8.2.2.4).

Although I have carefully prepared the manuscript, the possibility of errors cannot be ruled out. Therefore, the readers are welcome to let me know if they find any error.

I would also like to express my sincere thanks to Mr. Chong for his kind advice and help, and Mr. Arvind Kanswal, senior editor, and his editorial team for their patience and kindness during the publication process.

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