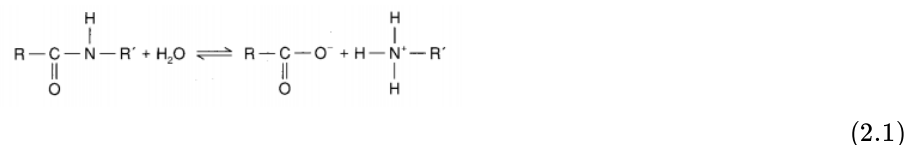


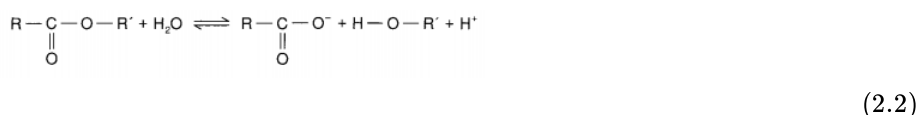
2: The Reaction Pathways of Zinc Enzymes and Related Biological Catalysts

I. Introduction

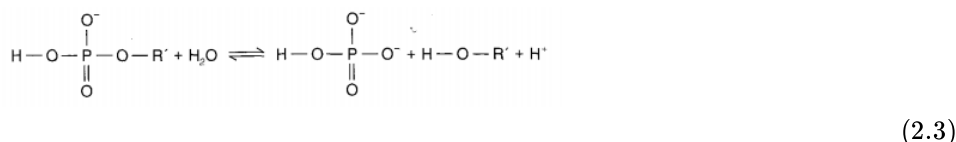
This chapter deals with metalloenzymes wherein the metal acts mainly as a Lewis acid; i.e., the metal does not change its oxidation state nor, generally, its protein ligands. Changes in the coordination sphere may occur on the side exposed to solvent. The substrate interacts with protein residues inside the active cavity and/or with the metal ion in order to be activated, so that the reaction can occur. Under these circumstances the catalyzed reactions involve, as central steps with often complex reaction pathways, the following bond-breaking and/or formation processes:



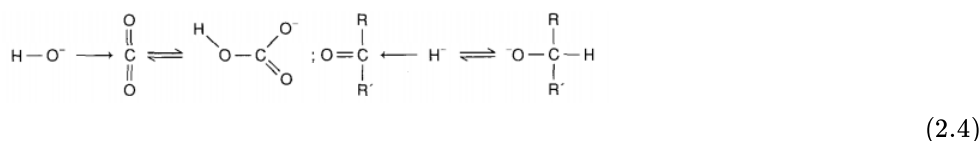
Peptide Hydrolysis



Carboxylic Ester Hydrolysis



Phosphoric Ester Hydrolysis



Nucleophilic Addition of OH⁻ and H⁺

Scheme (2.3) also pertains to the reactions which need ATP hydrolysis to promote endoenergetic reactions. We will also briefly deal with coenzyme B₁₂; this is a cobalt(III) complex that, by interacting with a number of proteins, produces an R-CH₂ radical by homolytic breaking of the Co-C bond as follows:



After an R-CH₂ radical is formed, it initiates a radical reaction. This is the only system we treat in which the oxidation state changes.

II. The Natural Catalysts

III. Strategies for the Investigation of Zinc Enzymes

A. Why Zinc?

1. The Groups to Which Zinc(II) is Bound
2. The Reactivity of Zinc(II) in Cavities
3. The Investigation of Zinc Enzymes

B.

IV. Elucidation of Structure-Function Relationships: Carbonic Anhydrase as an Example

- A. About the Enzyme
- B. Steady-State and Equilibrium Kinetics of Carbonic Anhydrase-Catalyzed $\text{CO}_2/\text{HCO}_3^-$ Interconversion
- C. What Do We Learn from Cobalt Substitution?
 - 1. Acid-base Equilibria
 - 2. Coordination Geometries
 - 3. Coordinated Water and NMR
 - 4. pH Dependence of Inhibitor Binding
- D. What Do We Learn from Copper Substitution?
- E. What Do We Learn from Manganese and Cadmium Substitution?
- F. Catalytic Mechanism
- G. Model Chemistry

V. Other Enzymatic Mechanisms and Model Chemistry

- A. Peptide Hydrolysis
- B. Ester Hydrolysis and Phosphoryl Transfer
- C. Nucleophilic Addition of OH^- and H^+
- D. Group Transfer and Vitamin B_{12}
 - 1. Group Transfer Enzymes
 - 2. The B_{12} -dependent Enzymes

VI. Perspectives

Although a great deal is known about the biophysical characteristics of the various enzyme derivatives mentioned in this chapter, we are still far from a clear understanding of their mechanisms of action, especially if we take into consideration the role of each amino-acid residue inside the active-site cavity. Although we can successfully discuss why certain metal ions are used in certain biological reactions, we still do not know why nickel(II), for example, is involved in the enzymatic hydrolysis of urea.^{199,200} If we are content with the explanations given in Sections III.A or V.D, we would need model compounds that are good catalysts and perform the job in several steps. This latter requirement would make the various models much more interesting, and would represent a new objective in the investigation of the structure-function relationship of catalytically active molecules. Indeed, the synthesis of large polypeptides may in principle provide such models. In this respect we need to know more about protein folding, for which emerging techniques like protein computer graphics and molecular dynamics are very promising.

Chemical modifications of proteins like the alkylation of carboxylate^{124,201} or histidine²⁰² residues have been performed for a long time. A newer approach toward modeling the function of a protein, and understanding the role of the active site, involves cleaving part of a naturally occurring protein through enzymatic or chemical procedures, and then replacing it with a synthetic polypeptide. The use of modern techniques of molecular genetics has allowed site-directed mutagenesis to become in principle a very powerful technique for changing a single residue in a cavity. Site-directed mutagenesis is a very popular approach, and its principal limitation with respect to the synthetic polypeptide route is that only natural amino acids can be used (aside from the technical difficulties in both approaches). Small quantities of site-directed mutants have been obtained for CPA¹²⁵⁻¹²⁷ and AP,²⁰³ whereas the expression of CA^{204,205} is now satisfactory.

Predictions of the changes in structure needed to affect the reaction pathway can nowadays be made with the aid of computers. The occurrence of the predicted change can be checked through x-ray analysis and NMR. The latter spectroscopy is today well-recognized as being able to provide structural information on small (≤ 20 kDa) proteins through 2- or 3-dimensional techniques.²⁰⁶⁻²⁰⁸ These techniques are increasingly being applied to paramagnetic metalloproteins such as many of those discussed here.^{208,209} The advantage of handling a paramagnetic metalloprotein is that we can analyze signals shifted far away from their diamagnetic

positions, which correspond to protons close to the metal ion,⁶⁹ even for larger proteins. It is possible to monitor the distances between two or more protons under various conditions, such as after the addition of inhibitors or pseudosubstrates, chemical modification, or substitution of a specific amino acid.

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210. Recently, ^{67}Zn has been used as a relaxing probe to monitor the binding of ^{13}C -enriched cyanide to zinc in carbonic anhydrase (see Section IV.C).
211. Recent work on HCA II has improved the resolution to 1.54 Å (K. Hakan *et al.*, *J. Mol. Biol.* **227** (1993), 1192). Mutants at positions 143 (R. S. Alexander, S. K. Nair, and D. W. Christianson, *Biochemistry* **30** (1991), 11064) and 200 (I. F. Krebs *et al.*, *Biochemistry* **30** (1991), 9153; Y. Xue *et al.*, *Proteins* **15** (1993), 80) also have been characterized by x-ray methods.
212. An x-ray study of the cyanate and cyanide derivatives of the native enzyme has shown that the anions sit in the cavity without binding to the metal ion (M. Lindahl, L.A. Svensson, and A. Liljas, *Proteins* **15** (1993), 177). Since NCO^- has been shown to interact with the paramagnetic cobalt(II) center, and ^{13}C -enriched cyanide has been shown to interact with ^{67}Zn -substituted CA (see Reference 67), it appears that the structures in the solid state and solution are strikingly different.
213. Recent x-ray data on the adduct of 1,2,4-triazole with HCA II confirm H-bonding with Thr-200 (S. Mangani and A. Liljas, *J. Mol. Biol.* **232** (1993), 9).
214. An HCO_3^- -complex of the His-200 mutant of HCA II has been studied by x-ray methods. The data are consistent with the coordinated oxygen being protonated and H-bonded to Thr-199 (Y. Xue *et al.*, *Proteins* **15** (1993), 80).

Contributors and Attributions

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