SII-4-2

Crystal Structure of the Mitochondrial Cytochrome bc1 Complex, a Bioenergetic Membrane Protein

Hoeon Kim*[1], Di Xia[1], Chang-An Yu[2], and Johann Deisenhofer[1]
HHMI and University of Texas Southwetern Medical Center[1]
Oklahoma State University[2]

The atomic structure of the cytochrome bc1 complex from bovine mitochondria was solved by X-ray crystallography. It is a membrane protein complex that consists of 11 protein subunits and four redox centers with a molecular weight of 240,000 daltons. The crystallographic studies of the bc1 complex with various inhibitors showed that the two separate pockets in the structure of cytochrome b provide binding sites for two major types of inhibitors (Qo and Qi), and that Qo inhibitors bind to slightly different sectors in the Qo pocket, depending on their functionally characterized subtypes. Furthermore, some of Qo inhibitors could induce the global conformational change of the iron-sulfur protein (ISP). The result suggests that the mobility of the ISP is essential in electron transfer and proton pumping in the bc1 complex.

SII-4-3

Fibrinolytic protease in *Pleurotus ostreatus*

Hye-Seon Choi
Department of Microbiology, University of Ulsan

Fibrinolytic protease significantly increased during differentiation in *Pleurotus ostreatus*. The specific activities of fibrinolytic protease were 0.88 and 6.1 u/mg for mycelial culture and fruit body, respectively. The enzyme was purified from fruit body 52-fold with a 5% recovery. The enzyme cleaved not only fibrin but also Bβ and γ chain of human fibrinogen. There was no activity against the azocasein, azoalbumin and elastin substrate. The protease was specific for hydrophobic and bulky amino acids in the P'1 position. The enzyme was sensitive to metal chelating agents such as 1,10-phenanthroline and EDTA. Phenanthroline-inactivated enzyme was recovered by addition of Zn^{2+} or Co^{2+}. The presence of Zn^{2+} was detected by ICP mass spectral analysis as 0.77 mol of Zn^{2+} per mol protease. The enzyme is likely to be a Zn^{2+} metalloprotease.