

## **X-Ray Structural Analysis of Carbonic Anhydrase from *Chlamydomonas reinhardtii***

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Carbonic anhydrase (CA) is a zinc-containing enzyme that catalyzes the reversible hydration of CO<sub>2</sub>. Based on the amino acid sequences, CAs are classified into three evolutionarily distinct families, designated  $\alpha$ -,  $\beta$ - and  $\gamma$ -CAs. CA from *Chlamydomonas reinhardtii* belong to the  $\alpha$  type enzyme and, homologous to CA from animal and eubacteria source. To reveal the structure, we have been engaged on X-ray study of *Chlamydomonas* CA. The enzyme was extracted from Cultured *Chlamydomonas* cells and highly purified by column chromatography [1]. The enzyme is composed of two subunits, small and large. Crystals were obtained in a solution containing ammonium sulfate. X-ray diffraction data were collected at 100K with synchrotron radiation at NW12 of PF-AR (Tsukuba). Diffraction patterns were processed with the program HKL2000. The crystal diffracted to a maximum resolution of 2.4Å. The unit-cell dimensions were  $a=b=134.6$  and  $c=120.0$ Å with a space group of  $P6_1$  or  $P6_5$ . Initial phases were derived by the molecular replacement method using the atomic coordinates of CA from *Neisseria gonorrhoeae*, which has a sequence identity of 37 % with the present CA.

[1] Yang S-Y., Tsuzuki M., Miyachi S., *Plant Cell Physiol.*,1985, **26**, 25-34.

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