



	Experiment title: Italian BAG-1: Enzymes related to pathogenesis of diseases, viral proteins, receptors and redox processes.	Experiment number: MX-129
Beamline: ID14-4	Date of experiment: from: 27/2/2004 to: 28/2/2004	Date of report: 9/7/2004
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Report:

Introduction

Carbonic anhydrase is a zinc metalloenzyme found in almost all organisms and is one of the fastest enzymes known. The enzyme catalyzes the reversible hydration of carbon dioxide to bicarbonate: $\text{CO}_2 + \text{H}_2\text{O} \leftrightarrow \text{HCO}_3^- + \text{H}^+$. The very long and still growing interest in this enzyme goes beyond its importance for survival of the biological organism and diseases. Despite this the knowledge about the binding mode of CO_2 and HCO_3^- is until now fuzzy at best. Combining a non standard method for substrate delivery with x-ray crystallography we have obtained the structures of human carbonic anhydrase II in complex with CO_2 and in complex with HCO_3^-

Better diffracting crystals of the complexes (1A) have been recently obtained, giving the possibility to enhance the enzyme working mechanism knowledge.

Dataset collected

Enzyme – substrate Complex at high resolution.

Results achieved

The crystals presented high mosaicity and multiple lattices, resulting in low quality data.

