

The Active Site Architecture of *Pisum sativum* β -Carbonic Anhydrase Is a Mirror Image of That of α -Carbonic Anhydrases

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Beamline(s): X8C

Introduction: β -Carbonic anhydrase (β -CA) is an enzyme that catalyzes the reversible hydration of carbon dioxide. This enzyme has been found in species from all three kingdoms of life. It has been most intensively studied in higher plants because of the critical role it plays in the physiology of photosynthesis. The primary role of this enzyme is to minimize resistance to the diffusion of CO_2 from the stomatal air spaces to the chloroplast stroma. It is a Zn-dependent enzyme and one of the most abundant proteins on Earth.

Methods and Materials: All data were collected from flash-frozen crystals. A three wavelength Zn-MAD data set was collected at beamline X8C, NSLS, a high-resolution data set to 1.93 Å was obtained at the BioCARS beamline 14C, APS. The structure was determined by MAD making use of the anomalous signal from the intrinsic Zn-ions only. Symmetry averaging and phase extension used the 8-fold NCS.

Results: The arrangement of the functional β -CA octamer in 222 atoms in the active with an rms difference of less than 0.4 Å – provided the mirror image of one sites of β - and α -CA can be superimposed of the enzymes is used. Symmetry is novel (**Figure 1**) and requires one molecular surface to mediate two distinct types of interactions, much as is observed in viral coat proteins. Although no recognizable similarities in overall fold or sequence exist between β -CA and the two other enzymes α - and γ -CA, 11 catalytically relevant

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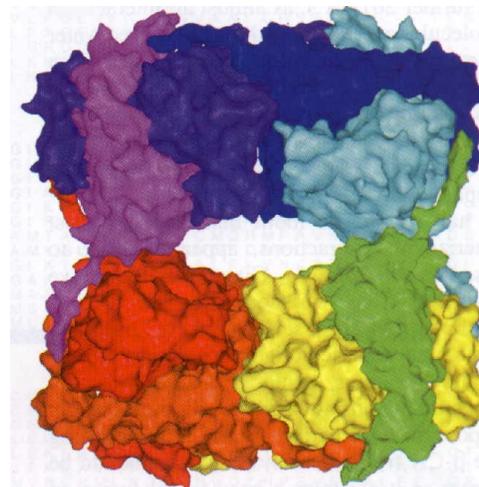


Figure 1. Molecular surface of the β -CA octamer. Each monomer is colored differently to highlight the complex interweaving of molecules, with each monomer contacting five other monomers.