of class I WSCP to visible light [1]. WSCP from *Chenopodium album* (*C. album* WSCP), belonging to class I WSCP, was extracted from leaves.The crystals were obtained using a reservoir solution containing 3.0 M KSCN and 26% PEG monomethyl ether 2,000. All of the experiments were performed in a dark room to avoid the photoconversion. X-ray data were collected at beamline BL-6A of the Photon factory (Tsukuba, Japan). The structure was determined at 2.0 Å by the MAD method with a reconstituted *C. album* WSCP with Chl containing Zn instead of Mg. *C. album* WSCP is a homotetramer assembled with crystallographic 222 symmetry. Each subunit consists of 147 residues and contains one Chl molecule. The Chl binding mode of classes I and II WSCP are completely different from eath other. As for class II WSCP, four Chl molecules reside at the subunits' interface and at the center of a tetramer, therefore the four Chl molecules interact intimately, whereas each Chl molecule of *C. album* WSCP is accommodated in the subunit, and isolated from each other.

[1] Horigome, D., Satoh, H., Itoh, N., Mitsunaga, K., Oonishi, I., Nakagawa, A., and Uchida, A. (2007) *J. Biol. Chem.* **282**, 6525-6531

Keywords: water-soluble chlorophyll protein, photoconvertibility, pigment protein

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Multiple coordination and quaternary states of fish hemoglobin re-open the root effect question

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The Root effect is a widespread property in fish hemoglobins (Hbs) that produces a drastic reduction of cooperativity and oxygen-binding ability at acidic pH. Up to now, the structural explanation of the Root effect has been based on the two-state model, and is related to an over-stabilization of the T quaternary structure. Here, we report the crystal structure of the deoxy and carbomonoxy form of the non-Root effect major component Hb isolated from the Antarctic fish Trematomus newnesi (Hb1Tn). In the deoxy state, the inter-aspartic hydrogen bond at the $\alpha 1\beta 2$ interface between Asp95α and Asp101 β is observed. In the carbomonoxy Hb1Tn crystals, both a T-like state and a R/T intermediate quaternary structure are observed. In these crystals, three of four independent CO coordination states are not assisted by the hydrogen bond with the distal histidine, that goes out of the heme pocket. This un-assisted CO coordination states are associated with unusually small thermal fluctuations which characterise both α and β CD corners. The accessibility of ligated states within three different quaternary structure (T, R and R/T intermediate) suggests a novel structural explanation of protein allostery based on a three state Edelstein's model. Grant Sponsor: PNRA.

Keywords: allostery, hemoglobins, Raman scattering

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Crystal structure of human cystathionine gamma lyase: A key enzyme in hydrogen sulfide production

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Impairment of the formation or action of hydrogen sulfide (H_2S), an endogenous gasotransmitter, is associated with various diseases such as hypertension, diabetes mellitus, septic and haemorrhagic shock and pancreatitis. Cystathionine-beta-synthase (CBS) and cystathionine-gamma-lyase (CSE) are two pyridoxal-5-phosphate (PLP)-dependent enzymes largely responsible for the production of H_2S in mammals. CBS is expressed predominantly in the central nervous system and the regulation of CBS has been well studied whereas CSE is mainly responsible for the production of H_2S outside of the nervous system and its regulatory mechanisms are less well understood. Here we report the crystal structure of human CSE at 2.4 A resolution. Structural characterization, combined with literature provides new insights into the CSE-mediated production of H_2S. Structure of the different forms of CSE reveal an open form, a hitherto not reported for any PLP dependent enzymes, and closed conformation of human CSE. Our results will be a starting point to facilitate structure-based design of novel inhibitors to aid in the development of therapies for diseases involving derangement of sulfur metabolism.

Keywords: hydrogen sulfide, cystathionine gamma lyase, crystal structure

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Structural characterization of the bacterial glutaminyl cyclase from *Zymomonas mobilis.*

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N-terminal pyroglutamate (pE) formation is an event catalyzed in biological systems by glutaminyl cyclases QC, (EC 2.3.2.5), which can be classified into two families, the plant and the mammalian family of QCs. Strong evidence exists for a direct participation of human QC in the onset and progression of Alzheimer's disease by generation of pE modified amyloid peptides. The plant enzymes, which show no sequence homology to the mammalian enzymes, have been implicated in defense mechanisms. Analysis of microbial genomes reveals a series of genes with peptide sequences homologous to plant QC enzymes. Here we show that these bacterial sequences indeed code for glutaminyl cyclases. The putative