

Structural Dynamics of the C-Terminal Region in Human Glutathione Transferase A1-1: A Crystallographic and Calorimetric Study

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The first protein crystal structure determined in Africa is that of the I219A mutant of human glutathione transferase A1-1 (hGST A1-1). This protein plays an important role in molecular toxicology in that, as a Phase two enzyme, it catalyses the conjugation of harmful compounds to the thiol of glutathione. In addition, hGST A1-1 is an important ligand-binding protein in the cytosol. Unlike other gene classes, the class Alpha GST A1-1 has a unique C-terminal region that makes a significant contribution to ligand binding and catalysis. This presentation will address the conformational dynamics of the C-terminal region and the role it plays in the binding of ligands and in catalysis. Our findings from crystallographic, calorimetric, and stability studies will be presented.