Structural Studies on Sulfurtransferase/Phosphatase Enzymes

Domenico Bordo[a], Andrea Spallarossa[a,b], Silvia Pagani[c], Timoty Larson, [d] Martino Bolognesi[b], [a]*National Cancer Research Insitute, Genova.* [b]*University of Genova.* [c]*University of Milano.* [d]*Virginia University*. E-mail: bordo@fisica.unige.it

Sulfurtransferases are widespread enzymes that *in vitro* catalyse the transfer of a sulfur atom from a donor molecule to cyanide [1]. In order to elucidate the molecular basis of sulfur transfer reaction and identify the structural determinants for enzyme selectivity, crystallographic analyses were carried out on three different sulfurtransferases: *Azotobacter vinelandii* rhodanese (RhdA) and *Escherichia coli* GlpE and *Escherichia coli* SseA, a MST enzyme.

The crystal structure of the RhdA has been determined with the method of Multiple Isomorphous Replacement and refined at 1.8 Å resolution in the sulfur-free and persulfide-containing forms [2]. GlpE crystal structure has been determined at 1.06 Å and displays a three-dimensional fold similar to that of either RhdA domains [3]. Notably, GlpE is also structurally similar to the catalytic domain of the human cell cycle-control Cdc25 phosphatase. The distinct substrate specificity, sulphur for rhodanese enzymes and phosphate for Cdc25 phosphatases, appears to be primarily consequence of the different active site loop length in the two enzymes. These structural findings provide guidelines for the identification of the as yet unknown biological role of this protein. Also the crystal structure of SseA, solved at 2.8 Å resolution by molecular replacement method [4].

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