CRYSTALLOGRAPHIC STRUCTURES OF OXIDIZED GLUTAREDOXIN2 (GRX2) AND GRX2-C30S COMPLEXED WITH GLUTATHIONE

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Glutaredoxins are small (9-12 kDa) heat stable proteins with at least one cysteine at their active sites that are highly conserved throughout evolution. The ubiquitous distribution of glutaredoxins is probably related to the fact that these proteins are involved in many cellular processes, including regulation of protein activity, reduction of dehydroascorbate, repair of oxidatively damaged proteins and sulphur metabolism. In the yeast *Saccharomyces cerevisiae* five glutaredoxin genes (GRX1-5) were identified: the Grx1-2 isoforms are dithiol proteins with a Cys-Pro-Tyr-Cys motif in their active site whereas Grx3-5 are monothiol proteins that contain Cys-Gly-Phe-Ser in their active site. However, the yeast Grx2 is responsible for the majority of oxidoreductase activity in the cell, suggesting that its primary function may be the detoxification of mixed disulfides that can be generated by reactive oxygen species. We elucidated the crystallographic structure of yeast Grx2 at 2.05 Å resolution in the oxidized state and the structure of yeast Grx2-C30S mutant with glutathionyl mixed disulfide at 1.91 Å resolution. We present here a comparative analysis between the structures of Grx2 from *S. cerevisiae* that allowed us to identify regions that change during the catalytical cycle and residues involved in stabilization of Grx2-glutathione complex. Furthermore, we compared Grx2 structures with glutaredoxins from other organisms and performed functional-structural relationships.