Identifying the Critical Residues of Protein Family OxyR that Cause Oxidative Stress Response in Bacteria.

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Abstract:

The OxyR protein found in many bacteria works as a redox switch and activates the oxidative stress response (Zaim, 2003). OxyR is a peroxide sensor and a transcription regulator, which can sense the presence of reactive oxygen species and induce antioxidant system to protect the bacteria from hydrogen peroxide (Chen, 2008). To identify the amino acid residues, critical for this function, a subset of 125 OxyR sequences was collected. These sequences covered the entire range of variability shown by all the known protein sequences in different species. A high quality multiple sequence alignment was performed to identify the specific biochemical and physiological role carried out by the amino acid residues responsible for the oxidative stress response. The phylogenetic tree will be constructed, using the aligned sequences, to study the adaptation in different environment. The structural analysis of conserved residues will be presented in the known three dimensional structure.

References:

Chen, H. “A novel OxyR sensor and regulator of hydrogen peroxide stress with one cysteine residue in Deinococcus radiodurans.” *PLoS ONE*. 2008; 3(2): e1602.

Zaim, J. “The structure of full-length LysR-type transcriptional regulators. Modeling of the full-length OxyR transcription factor dimer.” *Nucleic Acids Research*. 2003. 31(5): 1444–1454.