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## Recent Work

### Title

Redox Proteomics In Desulfovibrio vulgaris Hildenborough: Search For Proteins That Mediate Stress Response via Post-Translational Modification of the Cys Residues

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**Redox Proteomics In *Desulfovibrio vulgaris* Hildenborough: Search For Proteins That Mediate Stress Response via Post-Translational Modification of the Cys Residues.**

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*Desulfovibrio vulgaris* Hildenborough (DvH) is a sulfate reducing bacterium that grows in the absence of oxygen. From a physiological as well as ecological perspective, anaerobic bacteria have to overcome oxygen stress, the presence of which leads to the formation of reactive oxygen species (ROS). Anaerobic bacteria have evolved different mechanisms to overcome the stress induced by the presence of ROS. These include strategies to remove the ROS using post translational modification of the proteins, specifically the modifications of Cys residues in proteins, and to repair the damage in the cell to minimize the deleterious effects of the ROS associated stress. We are investigating the mechanisms by which DvH counters stress induced by oxygen as well as other redox stressors using a combination of 2D-DIGE and Isotope Coded Affinity Tag (ICAT) proteomics. All free Cys residues are blocked using N-ethylmaleimide to reduce the complexity of the sample and to specifically target the modified Cys residues. Using this approach we have identified proteins and mapped the redox active Cys residues that have function associated with redox stress in *Desulfovibrio vulgaris* Hildenborough.