# Bacterial Cell Envelope and Extracellular Sulfhydryl Binding Sites: Their Roles in Metal Binding and Bioavailability

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Although carboxyl and phosphoryl sites within the bacterial cell envelope and on extracellular polymeric substance (EPS) molecules are the most abundant metal binding sites, recent studies suggest that sulfhydryl sites control the binding of chalcophile elements under environmentally-relevant metal loading conditions. This talk will summarize our understanding of the concentration and reactivity of these important binding sites, their distribution between the cell envelope and EPS, and their role controlling bacterial bioavailability of some elements. The talk will summarize the relatively few studies that have focussed on bacterial sulfhydryl sites, and will identify areas in which future research may be most productive.

Sulfhydryl sites comprise only 5-10% of the total binding sites of bacterial cell envelopes, but exhibit such a high affinity for some metals that under low metal loading conditions, sulfhydryl binding is responsible for nearly all of the adsorbed metal budget. The concentration and distribution of sulfhydryl sites between the cell envelope and cell-produced EPS are dependent on the species, growth phase, and growth conditions. For example, the cell envelope sulfhydryl site concentrations of *Bacillus subtilis* increase with increasing glucose concentration in the growth medium. *Shewanella oneidensis* cells contain high concentrations of sulfhydryl sites within their cell envelopes with much lower concentrations present on within its EPS, while *Pseudomonas putida* cells exhibit the opposite. We apply a proteomics approach to explain the observed differences in sulfhydryl distributions. The proteomics analysis indicates that the outer membrane proteins of *S. oneidensis* contains a high concentration of cysteine residues, while the cell surface proteins of *P. putida* are relatively cysteine-poor, with cysteine-rich proteins of *P. putida* associated with the EPS. This proteomics analysis demonstrates the potential to identify the range of possible protein hosts for metal binding sulfhydryl sites, and the approach represents a means for predicting the concentration and distribution of sulfhydryl binding sites on bacterial cells and EPS molecules.