

## **High-Throughput X-ray Absorption Spectroscopy for Metalloproteomics**

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High-throughput X-ray absorption spectroscopy (HT XAS) is being developed as an adjunct structural genomics technology for investigating the "metalloproteome". This term refers to the collection of metal-site structures in all proteins of the proteome of a given organism grown under a given set of conditions (or of a given tissue in a given stage of development, etc.). Metalloproteomics will provide global information about the cellular response to environmental signals focused on the expression, loading, and assembly of metalloproteins. In creating a pipeline from genome to metalloproteome, several bottlenecks to high-throughput determination of metal-site structure must be overcome. For example, automation of arraying or sequencing small samples for XAS examination must be invented, automation of rapid data collection of multiple low-volume, low-concentration samples must be developed, automation of data reduction and analysis must be perfected. Feasibility studies to demonstrate this technology will be presented. The use of this technology to investigate metal-dependent expression and assembly of the metalloproteome under stress of toxic heavy metal exposure is planned.

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