

## **Bottlenecks and Roadblocks in High-Throughput XAS for Structural Genomics**

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High-throughput X-ray absorption spectroscopy (HT XAS) is being developed as a 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.). 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 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. HT XAS suffers compared to other genomic and proteomic technologies because of the inherent inability of XAS to analyze mixtures. It is likely that solution of this initial "separations science" problem will be the key to removing a major roadblock to the creation of this technology.