Combined X-ray approach for studying metalloproteins function/misfunction : A powerful approach to Metallogenomics

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ABSTRACT The explosion of genome sequences have posed serious challenges to the structural biology community worldwide. Despite major high throughput structural biology initiatives, particularly in Japan, USA and Europe, the structure/function paradigm on 'genome wide basis' has not even begun. The situation is even more acute in the case of metalloproteins, which quite often are not amenable to high throughput expression approaches for a variety of reasons including the fact that many of them require a specific 'metal chaperone' which lower organisms may lack. Metalloproteins are expected to make up at least a third of the genome and worldwide effort is beginning to take shape for what has recently been referred to as 'Metallogenomics'.

A variety of X-ray techniques[1] (Protein Crystallography, Solution X-ray Scattering and X-ray Absorption Fine Structure (XAFS)) have proved very powerful in studying not only structure/function relationships in metalloproteins but are proving unique in understanding misfunction of these proteins which quite often results in debilitating disease. A couple of recent examples would be highlighted[2]. In this context, the new NWSGC's beamline at the SRS, would be described. This has recently come on-line and is capable of high throughput MAD protein crystallography and single crystal XAFS as well as on-line screening of metals and their redox state.

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