

# **Macromolecular Crystallography & Structural Genomics – Recent Trends**

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Structural Genomics aims in identifying as many new folds as possible. This eventually requires faster ways of determining the three dimensional structures as there are many sequences before us for which structural information is not yet available. Although Molecular Replacement technique is still used in Crystallography for solving homologous structures, this method fails if there is not sufficient percentage of homology. The Multiwavelength Anomalous Diffraction (MAD) techniques have taken over the conventional Multiple Isomorphous Replacement (MIR) technique. With the advent of high energy synchrotron sources and powerful detectors for the diffracted intensities, developments in methodologies of macromolecular structure determination, there is a steep increase in the number of macromolecular structures determined and on an average eight new structures are deposited in the PDB every day and the total entries in the PDB is now around 29,000. Instead of using the three wavelength strategies in MAD experiments, the use of single wavelength anomalous diffraction using Sulphur anomalous scattering is recently proposed. This will reduce the data collection time to  $1/3^{\text{rd}}$ . Also, the judicious use of the radiation damage during redundant data measurements in second generation synchrotron source and also during regular data collection in the third generation synchrotron source has been pointed out recently (RIP & RIPAS).

The talk will cover these recent developments which are very useful in the area of structural genomics.