

A Novel and Easy Method for Phasing Protein Structures

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Abstract No. daut1539

Beamline(s): **X9B**

A novel method for solving protein structures has been developed at the beamline X9B. This method makes it possible to derivatize the protein crystals very quickly, which otherwise takes a long time (days to month) using classical heavy-atom derivatization techniques. In this method protein crystals are soaked in a cryo-protectant containing ~1M halide salt (eg. NaBr or KI). Soaking the protein crystals in this cryo-protectant for as short as fifteen seconds leads to incorporation of halide ions as ordered sites around the protein molecules in the crystal. The anomalous/isomorphous signal from these halide sites can be used to solve the phase problem in macromolecular crystallography. The feasibility of this method was tested on four known protein structures (Lysozyme, RNAase A, Subtilisin and Xylanase). The practical application of this method was proved by determining the structure of five unknown protein structures.