Producing Diffraction Quality Powders from Soluble Lysozyme and Thaumatin

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The pioneer effort on insulin and lysozyme has revealed the possibility of acquiring powder diffraction profile from proteins. These powder profiles were shown to be of sufficient quality to extract structural information. These results imply the idea of using protein powder diffraction for the identification of ligand complexes.

Our effort is to develop a general method to obtain polycrystalline powder from protein in solution. Our approach takes advantage of the crystallization conditions known to produce single crystal. Lysozyme and thaumatin were used as test case in this study. The crystallizaton conditions explored for lysozyme were from NaCl in Acetate buffer pH 4.5 and the Na/K tartrate in MES buffer pH 6.5 for thaumatin.

In order to generate protein powder, we increased the number of nucleation sites by increasing the concentration of protein and/or precipitant. In both cases, the proteins were first dissolved in the appropriate buffer and then the precipitant was added. Powder diffraction profiles were collected on the high-resolution powder beam line X3B1 at the National Synchrotron Light Source and could be interpreted from the known single crystal lattice. Our results suggest that polycrystalline powder can be produce from soluble lysozyme and thaumatin and further analysis is in progress to apply this approach to other proteins.

Keywords: protein crystallography, powder diffraction, protein crystallization