

How Pre-Crystallization Analysis Can Save Your Project

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X-ray crystallography is the principal method of determination of bio-molecular structure with protein crystallization being a bottleneck in the process of structure determination. Protein crystallization is influenced by numerous factors. From these factors, protein sample properties are the most important variable. Pre-crystallization analysis of protein sample by the combination of biochemical and biophysical methods such as size-exclusion chromatography, dynamic light scattering, and thermofluor assay [1] can thus be used for the optimization of protein crystallizability. This approach is demonstrated on the crystallization of deoxyribonucleoside regulator protein (DeoR) from *Bacillus subtilis* [2]. DeoR negatively regulates the expression of enzymes required for deoxyribonucleosides and deoxyribose utilization [3], deoxyribose-5-phosphate is the preferred ligand of DeoR and induces expression of the catabolic enzymes [4].

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