

## CRYSTALLIZATION OF BSA (BOVINE SERUM ALBUMIN)

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The structural protein study supplied the base to start and understand the life in a molecular view. The main technique used to solve biological macromolecular three-dimensional structures is the X-ray diffraction crystallography (Blundell Johnson, 1976; Drenth, 1994). Some structural studies are important to understand the molecular interactions of some biological mechanisms. The main steps to resolve molecular structures by X-ray diffraction crystallography are macromolecular crystallization, X-ray diffraction data collection, data integrations and process, and analysis of the structure. The parameters that need to be controlled in an experiment of crystallization of a biological macromolecules are the purity of the biological macromolecule; solubility, supersaturation, nucleation, growth and ending of growth. The scope of this study is crystallization of the BSA molecule (bovine serum albumin). Although this protein is very used in laboratory, the bovine serum albumin has not a determined crystal structure. The study first determined the conditions of protein solubilization in a concentration of 80 mg/mL in water. The Crystal Screen (Hampton Research) was used for crystallization trials. Microcrystals were obtained in a condition containing only 30 % of PEG 1,500. The optimization of this primary condition was carried and the optimized condition was determined between PEG 1,000 and 2,000 in a concentration varying of 25 to 40 %.

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