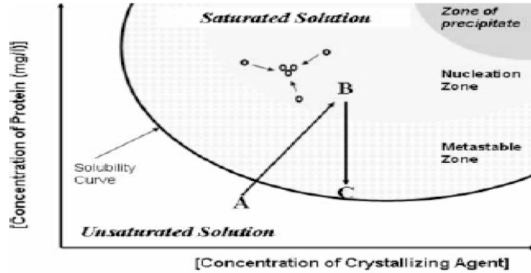


W0651

CyBi®-HTPC work station for protein crystallization. Automation of protein crystallization in sitting drop. Harris Grevelis¹, Broutin², F. Bonhoure², ¹CyBio Inc., Woburn, MA, I. Crystallography laboratory et RMN Biologiques, CNRS, Univ. of Pharmaceutical, Paris.



Recent developments in genomics and proteomics have led to an increase in the number of macromolecules requiring structural elucidation. Moreover, the increased size of complex proteins often requires the use of crystallography as a structural method. The protein structure of a gene product can then be determined by this technique, but first the crystal must be obtained. This process is inconsistent however, since it is not possible to

determine the crystallization conditions in advance using information regarding sequence and physicochemical features of a protein. Instead, the protein is tested against a matrix of varying standard conditions to determine those optimum for crystallization. The throughput and reliability of this process can be improved considerably using automation.

The behavior of a molecule dependant on variations in its environment can be described via a phase chart. The balance between the solution phase and the solid phase is called the solubility curve. Above this curve is the meta-stable zone where over saturation results in conditions that are too weak for crystal growth without any external supply of energy.

For a macromolecule to crystallize, it must go over this area without reaching the precipitation zone. The molecule will then be in an over-saturation stage which allows crystallization to commence.

Due to the numerous conditions that must be tested, it is vital to conduct all experiments with an increased focus on accuracy and reproducibility.