

Myths and realities about the influence of electric and magnetic fields on protein crystallization and protein crystal growth

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Single crystal X-ray crystallography is a powerful technique for determining the 3D structure of biological macromolecules at very high resolution, when optimal crystals are obtained by classic or advanced methods of protein crystal growth. Although, this is not the only way to obtain the three dimensional structure of many biological macromolecules existing in living organisms. There are four additional ways to achieve this purpose: 1) Powder X-ray diffraction, 2) NMR techniques (experiments done in solution), 3) Modeling by means of using the PDB, and 4) combined methods of reconstruction by Cryo-SEM and SAXS. This contribution will show different strategies and methodologies by means of using temperature-control and high-pressure for protein crystallization that might help to increase the success rate of obtaining protein crystals, different polymorphs as well as to get high quality single crystals for crystallographic research. This paper will also present new approaches, where sophisticated methods are used not only to grow protein crystals, but also to control the size and the orientation by applying electromagnetic fields of different intensities. Finally, some case studies from the author's lab will show the advantages and disadvantages of using these non-conventional approaches for high resolution X-ray crystallography.