Do the Strong Magnetic Fields Modify the 3D Structure of Proteins?

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In this work we explore the feasibility of a new method to increase the crystal quality of biological macromolecules for X-ray crystallography. The method consist of growing protein crystals in capillary tubes containing a gelled protein/precipitant solution under the presence of a strong magnetic field of 10 Tesla. The strong magnetic field applied to the crystal growth cell was the conventional NMR magnet normally used in Chemistry laboratories.

From our preliminary results by solving the 3D structure of these analyzed protein crystals and controls, it was observed that crystals grown under the presence of a strong magnetic field in gel/capillary tubes improved substantially their electron density maps where electron density was not observed in all controls.

This promising methodology will help most of biocrystallographers to increase the crystal quality, a typical problem in most of the research laboratories for structural biology. Because of the existence of two different gels (double protective-chamber), this methodology seems to be also an available way to transport safely crystals to the synchrotron facilities without using the classical heavy laboratory Dewars for data collection.

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