## **Researchers Develop New Method for High-Pressure Cryocooling of Protein** Crystals

Protein crystallography is an essential technique in biomedical sciences. Use of this technique typically requires cooling crystals. A new high-pressure cryocooling method has been developed by Graduate Student, Chae Un Kim and his advisor, Sol Gruner,

Director of the Cornell High Energy Synchrotron Source. They have successfully used this technique to prepare protein crystals for x-ray diffraction analysis. Cryocooling, which is normally required to mitigate radiation damage during x-ray exposure, involves trial-anderror selection of cryoprotectant additives and invariably degrades the quality of the diffraction. The new method, freezing the crystals after raising them to 1.9 kbar, eliminates the need for cryoprotectants and results in higher quality diffraction data, thereby greatly facilitating the acquisition of protein structures. The diffraction pattern of an L-amino-acid oxidase crystal shows the result of cryocooling without cryoprotectants at normal pressures, while the diffraction pattern on the right is from a crystal prepared using the new method.



A poster on this method won the Oxford Cryosystems Poster award at the American Crystallographic Association annual 2005 meeting in Orlando, FL.

This work is notable because this new method of freezing protein crystals could vastly extend the range of protein structures that can be determined using x-ray diffraction. This method eliminates the need for sample additives (cryoprotectants), thereby allowing protein structures to be determined without complications and possible contamination.

See also:

CHESS Newsletter 2005 article here.