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Solution of Protein Crystallographic Structures by High Pressure Cryocooling and Noble Gas Phasing. Chae Un Kim, Quan Hao, Sol M. Gruner, CHESS, Cornell Univ., Ithaca, NY, USA.

Room pressure flash cryocooling of protein crystals is the standard way to reduce radiation damage during data collection. However, it is necessary to find cryoprotection conditions by trial and error, a process that can be time consuming and is not always successful. Recently a new method, high pressure cryocooling, was developed that does not require penetrative cryoprotectants and typically yields very high quality diffraction (Kim *et al.*, 2005, *Acta Cryst.* D61, 881-890). This method was successfully extended to diffraction phasing by incorporating heavy noble gas, krypton. Here, the modified high pressure cryocooling procedure is described. Porcine pancreas elastase (PPE, 240 residues, 26 kDa) prepared by the method was selected as a test case. Excellent diffraction was achieved without any penetrating cryoprotectants and a single 31 % occupied krypton (Bijvoet amplitude ratio $\langle |\Delta F| \rangle / \langle F \rangle$ of 0.53 % on PPE) was successfully used for SAD phasing at 1.3 Å resolution. The anomalous difference map showed a 100 σ peak in the krypton site and 6 additional peaks at 3.6 σ , which were assigned to naturally present sulfur atoms that had the anomalous strength of only 0.18 electrons. The modified high pressure cryocooling method has potential to greatly simplify obtaining protein structures.