

Dynamic Nuclear Polarization for Neutron Macromolecular Crystallography

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Neutron Macromolecular Crystallography is a powerful technique for the determination of the structure of proteins. The sensitivity of the neutron scattering cross section to the presence of hydrogen gives this technique a unique advantage compared to the more widely used X-ray crystallography. The problem with neutron crystallography is the low flux of even the most advanced neutron sources requires experimenters to use crystal samples orders of magnitude larger than those used at modern X-ray facilities. The requirement for large crystals greatly limits the proteins whose structures can be determined. Dynamic Nuclear Polarization (DNP) of the crystals allows provides a means to overcome the limitations imposed by low neutron flux by taking advantage of the strong spin dependence of the neutron-hydrogen scattering cross section to increase the coherent scattering from hydrogen by a factor of as much as twenty. As prototype test system has been built to measure neutron diffraction from DNP polarized protein crystals. The system has been successfully tested at the High Flux Isotope Reactor at Oak Ridge National Laboratory. Results of these measurements will be presented, as will plans for improvements to the system and potential applications of DNP to other neutron scattering techniques.

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