

## A Frozen Spin Target for Neutron Diffraction Measurements of Proteins Crystals

*Thursday 17 September 2015 09:30 (30 minutes)*

Neutron scattering off of protein crystals has been used successfully to determine protein structure. This technique achieves its best results when used with large crystal samples, or with samples that are amenable to techniques such as deuteration. In the case of small or delicate protein crystals, sample polarization has been identified as a method to greatly increase the signal to noise ratio in neutron diffraction studies of protein structure. The strong polarization dependence of the neutron scattering cross section of hydrogen would allow us to use Dynamic Nuclear Polarization to drastically reduce the time it takes to get reliable data from protein crystal diffraction, and enable measurements of protein structures that are currently impossible. We present a new frozen spin target being built at Oak Ridge to polarize single protein crystals on the IMAGINE beamline at the High Flux Isotope Reactor. This target will be optimized for very small samples, and built largely from “off-the-shelf” commercial items.

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**Session Classification:** Session 10