

The McGill-Montreal Chapter

Sigma Xi :: The Scientific Research Society ::



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## PUBLIC LECTURE

## When:

Monday

March 22, 2010

6:00 P.M.

Where:

McGill University Otto Maass Chemistry Building Room 10



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Talk will be preceded by a members-only reception at 5:30 PM in the Ruttan Room (3<sup>rd</sup> floor)

## Sigma Xi

Presents

## Observing Biological Dynamics with Atomic Resolution Using NMR and Calorimetry

Proteins are central players in an enormous variety of cellular processes, thus understanding how they function is critical to understanding the molecular basis of life. Proteins are highly flexible molecules, and there is growing evidence that their internal dynamics play an essential, but still poorly understood, role in their biological activities. Protein motions are difficult to characterize because they can involve weak interactions with energies not much greater than  $k_BT$ , transient structures with lifetimes on the order of milliseconds or microseconds, and subtle changes in structure on the scale of angstroms.

Recent advances in Nuclear Magnetic Resonance (NMR), isothermal titration calorimetry (ITC) and differential scanning calorimetry (DSC) are providing fresh insight into the fundamental behavior of biological molecules. NMR simultaneously detects the signals arising from hundreds of individual atoms within proteins, yielding exquisitely detailed structural and dynamic information. ITC measures the heat absorbed or released when proteins interact with other molecules. DSC detects the heat absorbed or released by changes in protein structure.

Information from these three techniques can be combined to produce models of biological processes that explain WHAT happens, in terms of atomic-resolution structure and dynamics, and also WHY it happens, in terms of the laws of thermodynamics. Several recent examples from our own work will be discussed, including the characterization of millisecond-timescale molecular recognition, elucidation of a microsecond-timescale protein folding mechanism, and identification of a novel mode of cooperative communication between protein binding sites.