



The Thursday Thing

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**The integration of theoretical aspects of protein folding
with empirical methods for protein structure prediction**

Now that the sequence of the human genome has been determined, the challenge for many molecular and structural biologists is to characterize how genome encoded proteins perform their biological function. Such an understanding requires knowledge of the three dimensional structure of these proteins. In the past 10 years, efforts geared towards protein structure prediction have progressed on two distinct fronts. The first, which has been carried out predominantly by structural and evolutionary biologists, has made use of ever growing sequence and structural databases for the prediction of structures based on sequence homology. The second, which has become the domain of physical chemists and polymer physicists, has combined experimental data and theoretical calculations for structure prediction based on first principles. My talk will focus on why there is a need to cohesively integrate aspects from both fronts in order to maximize the potential of protein prediction algorithms.

Date: Thursday, July 5, 2001
Place: MacNaughton 222
Time: 12:30 p.m.