## 2001 PROGRAM

8:30 a.m.	<b>Registration and Continental Breakfast</b>
	Room 137, Chemistry-Physics Building

9:00 a.m. Welcome by Dr. Boyd E. Haley, Chairperson,
Department of Chemistry, University of
Kentucky - Room 139, Chemistry-Physics
Building

9:05 a.m. Introductory Remarks - Dr. L. Edward DeMoll,
Department of Chemistry, University of
Kentucky

9:10 a.m. Dr. Kenneth A. Walsh, University of Washington School of Medicine "The Challenge of Protein Analyses in the Post-Genome Era"

With the recent availability of genomic data, an understanding of the molecular basis of cellular function depends upon unerstanding the role of the encoded proteins. Over the years, the ate of accumulation of knowledge about protein function has been ontrolled by the rate of breakthroughs in key technologies. One uch development during the last decade has been the adaptation of Mass Spectrometry to the identification and characterization of proteins. The suitability of this methodology for answering imely biomedical questions will be discussed.

0:20 a.m. Break

0:40 a.m. Dr. Thomas C. Terwilliger, Los Alamos National Laboratory
"Structural Genomics: Foundation for the

Future of Biology?"

The genome projects have opened up the prospect of a comrehensive view and understanding of life. Structural genomics an provide a foundation for this through the determination and nalysis of protein structure on a genomic scale. Participants in he Consortium for Structural Genomics have carried out a pilot tructural genomics project based on proteins from the yperthermophile Pyrobaculum aerophilum, and are beginning a arger project to determine and analyze structures of functionally mportant proteins from Mycobacterium tuberculosis. The lesons learned in this pilot project and the prospects for the field of tructural genomics will be discussed.

11:50 p.m. Buffet Lunch, Faculty Club [Please return registration card by April 13, 2001 for reservations. Cost to be paid in advance or at registration: Faculty/Guest (\$10.00); Graduate Student (\$5.00.1

2:00 p.m. Dr. George D. Rose, The Johns Hopkins
University School of Medicine
"How Shall We Unfold Thee? Let Us Count the
Ways: Enumerating Conformations in the
Unfolded State of Globular Proteins"

The Levinthal Paradox has long been a challenge for protein folders. According to this conundrum, an unfolded protein can populate an astronomical number of conceivable conformations. The length of time needed to sift through this ensemble and find the native conformation is of order days or years. Yet proteins fold reliably in milliseconds. How can they solve this search problem? Our answer to this question provides useful insight into the unfolded state of proteins [Pappu, et. al., *PNAS*, **97**, 12565-12570 (2000)].

3:10 p.m. Break

3:30 p.m. Dr. Edward M. Marcotte, University of Texas at Austin

"Bioinformatics: A Pathway to Gene Function"

The sequences of more than 80 genomes have shown us just how few genes have been studied directly. In virtually every genome, about 1/3 to 1/2 the genes are of entirely unknown function, while most of the rest of the genes have functions inferred from their similarity to the small set of experimentally characterized genes. However, the genomes themselves contain quite a lot of information about the relationships between the genes. New methods analyze the context that genes are found in, such as their patterns of inheritance, fusion, and order on the genome. Analysis of this gene context allows assignment of function to many of the uncharacterized genes (for example, assignment of preliminary function to more than half the uncharacterized genes of yeast).

4:40 p.m. Meet with Speakers, Room 137, Chemistry-Physics Building

(http://www.chem.uky.edu/seminars/naff/welcome.html)

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Twenty-Seventh Annual Symposium on

Chemistry & Molecular Biology



established in the memory of Anna S. Naff

## **Proteomics**

## **SPEAKERS**

Edward M. Marcotte George D. Rose Thomas C. Terwilliger Kenneth A. Walsh

Friday, April 20, 2001

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