

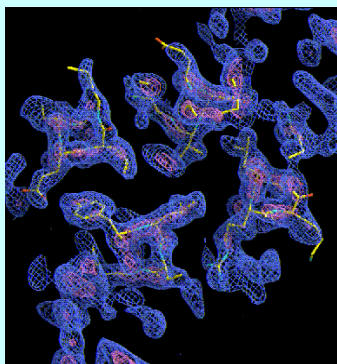


Institute For Pure and Applied Mathematics
University of California, Los Angeles presents a program in

Proteomics: Sequence, Structure, Function

March 8 - June 11, 2004

Members of the organizing committee include **Tim Chen** (Program in Molecular and Computational Biology/CS/Math, USC), **David Eisenberg** (Chem/Biochem, UCLA), **Scott Fraser** (Biological Imaging Center, Caltech), **Simon Tavaré** (Program in Molecular and Computational Biology /Math/Preventive Medicine, USC), and **David Wild** (Keck Graduate Institute)



Scientific Overview

According to one source, the term “proteome” was coined by an Australian postdoc, Marc Wilkins, about 8 years ago. Whoever coined the term, this is definitely a new field, and one which will be taking off at the time proposed for the program.

An organism’s proteome is the collection of all proteins that the organism makes. This differs from the genome in a number of ways. There are pre-translational events (for example, alternative splicing, in which several coding regions of DNA (“exons”) are joined together, but it is known that this can be done in more than one way, and that which way the exons are spliced is one way that protein expression is regulated) and post-translational events (phosphorylation, which may sometimes determine whether a protein is active or not.) Which proteins are present and in what quantities in a given cell at a given time is highly variable, whereas the genome is static.

Proteomics of necessity involves a greater level of complexity than genomics. The human proteome -- the collection of all proteins generated by the human genome -- is estimated to contain 10 million to 20 million proteins -- about 2-3 orders of magnitude higher than the number of human genes. Proteomics is of importance to basic science, for elucidating the fundamental mechanisms of biology. It is also of great interest to the biotech industry, since proteins whose function and active regions are known provide potential targets for drugs. The following workshops are scheduled during the program.

- **Tutorials: March 9-12, 2004**
- **Workshop 1: High Throughput Technologies and Methods of Analysis, March 22-26, 2004**
Organizing Committee: Tim Ting Chen (Chair), Vineet Bafna, Joseph Loo, Pavel Pevzner
- **Workshop 2: Medical Applications and Protein Networks, April 19-23, 2004**
Organizing Committee: Austin Yang (Chair), David Eisenberg, Lisa Ellerby, Bradford Gibson, Katheryn Resing
- **Workshop 3: Structural Proteomics, May 10-14, 2004**
Organizing Committee: David Wild (Chair), Tom Blundell, Steven Brenner, Adam Godzik
- **Workshop 4: Molecular Machines, May 24-28, 2004**
Organizing Committee: Robijn Bruinsma (Chair), Carlo Montemagno, Jacques Prost, Hong Qian, Shimon Weiss
- **Culminating Conference at UCLA Lake Arrowhead Conference Center, June 6-11, 2004**

Participation

The long-term program will involve a community of researchers. The intent is for long-term participants to have an opportunity to learn about proteomics from the perspectives of many different fields --mathematics, statistics, biology and medicine--and to meet a diverse group of people and have an opportunity to form new collaborations. Core participants will participate in the above events and in addition there will be lectures, seminars and mini-workshops throughout the program. Financial support at all academic levels is available. Please go to our website for more information. We are especially interested in applicants who are interested in becoming core participants and participating in the entire program (March 8-June 11, 2004), but give due consideration to applications for shorter periods. Encouraging the careers of women and minority mathematicians and scientists is an important component of IPAM's mission and we welcome their applications.

Please visit our website at <http://www.ipam.ucla.edu/programs/prot2004>
or email questions to prot2004@ipam.ucla.edu

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