

Institute for Pure and Applied Mathematics  
University of California, Los Angeles presents

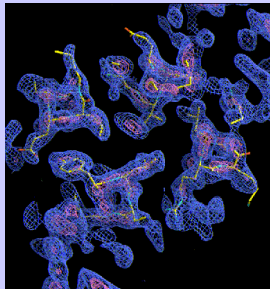
## Proteomics: Sequence, Structure, Function

### Workshop III: Structural Proteomics

May 10 - 14, 2004

Members of the organizing committee include **David Wild**, Chair (Keck Graduate Institute), **Tom Blundell** (University of Cambridge), **Steven Brenner** (UC Berkeley) and **Adam Godzik** (Burnham Institute)

**Workshop III: Structural Proteomics** is part of an active program of research activities, seminars and workshops throughout the **March 8 – June 11, 2004** period and core participants will be in residence at IPAM continuously for these 14 weeks. The program will open with tutorials, and will be punctuated by 4 major workshops and a culminating workshop at UCLA's Lake Arrowhead Conference Center. Numerous distinguished researchers will be participating. Between the workshops there will be a program of activities involving the long-term and short-term participants, as well as visitors.



#### Scientific Overview

A major obstacle to exploiting the large volume of genomic sequence data is the functional characterization of the gene products. A large proportion of the predicted protein coding regions of organisms' genomes – typically 30-40% – code for proteins of unknown function. Annotation is normally inherited from database matches to similar sequences for which the function is known. New algorithms that make use of the information contained within alignments of multiple sequences are very effective at identifying distant sequence relationships. However, the definition of a match is parameter dependent and this procedure is open to the danger of error propagation. But even using sensitive sequence similarity detection methods, a significant proportion of gene products cannot be reliably assigned function.

Recently, large-scale protein structure determination projects have gotten underway. These initiatives are variously referred to as “structural genomics” or “structural proteomics”. One goal is to carry out a comprehensive sampling of protein sequence space and the determination of structures representative of a given sequence neighborhood. Such an approach would allow the structures of other sequences in the neighborhood to be obtained by the methods of comparative (homology) modeling. Since protein three-dimensional structure is more conserved than sequence, these initiatives also open up the possibility of biochemical or biophysical functional characterization via structure. In parallel to these experimental programs are ongoing efforts to address these questions using computational techniques. The focus of this workshop will be on these computational methods and will discuss the state of the art and current challenges in a variety of topics in the field of structural proteomics, such as protein structure prediction, inferring function from sequence and structure, challenges in comparative modeling, and protein-protein interactions

#### Confirmed Speakers:

Patsy Babbitt (UCSF)	Alexander Kister (Rutgers University)	Mansoor Saqi (Barts and The London School of Medicine and Dentistry)
Steven Brenner (UC Berkeley)	Arthur Lesk (Cambridge)	Scott Schmidler (Duke University)
Ken Dill (UCSF)	Oliver Lichtarge (Baylor College of Medicine)	Jeffrey Skolnick (Buffalo)
Jacquelyn Fetrow (Wake Forest University)	Edward Marcotte (University of Texas)	Michael Sternberg (Imperial College)
Angel Garcia (LANL)	Jose N. Onuchic (UCSD)	Sarah Teichmann (MRC Laboratory)
Nick Grishin (University of Texas Southwestern Medical Center)	George Rose (Johns Hopkins University)	James Watson (European Bioinformatics Institute)
	Rob Russell (EMBL, Heidelberg)	

#### Participation

Financial support for this workshop is available for participants at all academic levels, and recent PhD's, graduate students, and researchers in the early stages of their career are especially encouraged to apply. An online application for support is available at <http://www.ipam.ucla.edu/programs/protws3>. Encouraging the careers of women and minority mathematicians and scientists is an important component of IPAM's mission and we welcome their applications. Applicants who are interested in becoming core participants and participating in the semester program (March 8 – June 11, 2004) should apply at <http://www.ipam.ucla.edu/programs/prot2004>.

Please visit our website at

<http://www.ipam.ucla.edu/programs/protws3>

or email questions to [protws3@ipam.ucla.edu](mailto:protws3@ipam.ucla.edu)

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