Friday, June 04, 2010 at 11 a.m.

IGBMC Auditorium

Special Seminar

Mapping and Measuring Proteomes

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The human genome project has taught us that a complete map—in the case of the genome project the complete genomic sequence—along with computational tools to navigate the map—represent invaluable resources for experimental and theoretical biologists. A main consequence of such a complete map is that all the biological processes have to be explainable with the components that constitute the map. Proteomics has not reached the stage that complete maps are available but the urgent need for their generation is now widely recognized.

In this presentation we will discuss experimental and computational challenges related to the generation of complete proteomic maps using mass spectrometry, and instrumentation and methods to use the information contained in proteome maps for targeted proteomic experiments. We will also discuss recent technical advances towards complete proteome analysis and describe software tools and data resources that will transform proteomics from perpetual proteome mapping to accurate proteome measurement.