

Grant Number: DE-FG03-03ER63517

Conference Title: Proteomics: Technologies and Applications

Dates of meeting: March 25-30, 2003

Conference Organizer/ P.I.: Ruedi Aebersold

Organization conducting the conference: Keystone Symposia

#### Meeting Summary:

The meeting took place at the Keystone, Colorado resort from March 25-30, 2003. It was attended by 206 participants, of which 35 were students; 39% of attendees submitted abstracts. The meeting had 30% returning attendees and 70% new attendees. The group of speakers was composed of internationally recruited junior and senior experts in their respective fields. The group included representatives from academia and the private sector, highlighting the convergence of proteomics efforts in the two sectors.

The completion of the genome sequences of a large number of prokaryotic and eukaryotic species has catalyzed new research approaches to study the structure, function and control of biological processes. They are characterized by the systematic and in many cases quantitative analysis of all the molecules of a particular type expressed by a cell or tissue. The systematic analysis of proteins has been termed "proteomics".

In an initial phase, most of the proteomics efforts were focused on large-scale protein identification. More recently, the objectives and technologies of proteomics have been diversified and expanded. Current proteomics research attempts to systematically and, where applicable, quantitatively determine the many properties of proteins and their biological function, including: protein abundance, state of modification, specific activity, interaction with other biomolecules, half-life, subcellular location, structure and more. Significant current challenges include the development of suitable technologies to determine these properties on a proteome-wide scale, the interpretation of the large amounts of data obtained, and the integration of different types of data into a coherent model describing a biological process.

The scientific program of the meeting intended to provide an up-to-date overview of the breadth of proteomics research and of emerging and mature technologies. Special emphasis was placed on discussing how proteomics technologies intersect with biological and clinical research. This was accomplished by bringing together leading experts from the different areas of proteomics research with biologists applying these technologies. Additionally, several talks featured comparisons of work in model systems and in mammalian cells, and others discussed computational approaches to mine large datasets of proteomic results in order to obtain biological insights into various processes.

The keynote lecture delivered by Dr. Tony Pawson, a leading researcher in signal transduction, described the dynamics and complexity of cell signaling systems and provided an excellent introduction to the technical challenges facing the proteomics field. The lecture highlighted the need to analyze proteins systematically and quantitatively, to determine the state of modification of the signaling proteins, to identify their interacting partners and subcellular location and to analyze and integrate the large amounts of diverse data. Each of these themes was expanded upon and further developed in subsequent sessions.

In this meeting, the attendees obtained a broad and expert overview of the current status of proteomics technologies and approaches and were presented with previews of emerging directions to be realized in the next few years. Biologists and clinicians intending to apply proteomics strategies in their research were presented with examples of prototypical studies that highlighted the present, considerable power of proteomics as well as the challenges that remain.