

Selective Extraction of Labelled Entities by Charge derivatization and Tandem mass spectrometry (SELECT): A novel approach for identification and quantitation of differential protein expression in proteomics

Gavin E. Reid

Joint Proteomics Laboratory. The Ludwig Institute for Cancer Research and The Walter and Eliza Hall Institute of Medical Research. Parkville, Victoria, Australia, 3050.

With completion of the first draft of the human genome sequence, the challenge now facing medical research is to understand gene function. However, the biological function of a gene cannot be determined from a simple examination of its sequence. Comprehensive analysis of the proteins expressed by the genome, therefore, promises to bridge the gap between the gene and its biological function. The term proteomics is synonymous with the high-throughput identification and characterization of all proteins secreted by a particular cell type, and quantitation of global changes in protein expression between healthy versus diseased cells (i.e., expression proteomics), and with the identification of components of functionally active protein complexes and characterization of the intricate protein-protein interactions involved in intracellular protein trafficking and signaling pathways (i.e., cell-mapping proteomics). Taken together, these approaches allow comprehensive examination, at the protein level, of the complex cellular changes that occur following transformation of cells from a normal to a diseased state.

Over the last few years, a variety of approaches for quantitative measurement of differential protein expression, exemplified by the isotope-coded affinity tag (ICAT) technique, have been demonstrated. However, there remains a need for the continued development of improved technologies in both expression and cell-mapping proteomics, particularly for the identification, characterization and quantitation of the trace-abundance proteins and the dynamics of their specific interactions involved in control of cellular function.

In this presentation, a novel strategy will be described, termed “Selective Extraction of Labelled Entities by Charge derivatization and Tandem mass spectrometry (SELECT), to provide enhanced selectivity and up to two orders of magnitude greater sensitivity over existing methods for protein identification and quantitation of differential protein expression.
