

Editorial

There are occasionally times when I feel that the field of proteomics is a mixed blessing. The promise of the field is clear and the technologies for measuring, quantifying and characterizing proteins from living systems are evolving rapidly and leading to new biological paradigms. On the other hand, there are many examples of research efforts that swim in a 'sea of data' that demand a substantial effort to mine and interpret the data, often without achieving the expected benefits. These challenges are not unique to proteomics as the DNA microarray community faces similar challenges. However, the proteomics community has an additional burden which is that the methods for acquiring the data are still evolving rapidly and the instrumentation used is reasonably diverse. One example of the excitement and challenge of new methods is the paradigm of shotgun proteomics—the analysis of complex mixtures of proteins that begins with a proteome-wide proteolytic digestion followed by separations and then mass spectrometry. These methods have received significant attention of late because of their ability to study and quantify a large number of proteins in a single experiment. What is not obvious to many investigators are the challenges and difficulties of performing such experiments. In this issue, we bring together a number of articles from laboratories that have recorded experience in shotgun proteomics with the goal of building an issue that will serve as a useful reference for those interested in shotgun proteomics. Because the field is at a nascent stage, and to help share with readers some of the benefits and challenges, I have asked the authors to include new data and findings in their contributions. Although this is a departure from what some readers of *Briefings in Functional Genomics and Proteomics* will be used to, I believe that it will be

particularly useful to readers interested in considering various issues and methods. I welcome any comments or feedback on this point.

The issue begins with an overview of the application of mass spectrometry to the analysis of complex protein mixtures from Oak Ridge National Laboratory. It provides a detailed overview of many of the techniques and technologies that have become essential to the proteomics community. The remaining articles describe the application of shotgun proteomics methods in a variety of contexts. The article from Cornell University describes issues related to the quantitation of *Escherichia coli* proteins using an isobaric tagging strategy. The articles from the University of Sheffield and Berkeley describe the application of this same quantitation method to measure changes in protein expression in a cyanobacterium and in a sulfate-reducing bacterium, respectively. The contribution from the Huntington Medical Research Institutes and ThermoElectron describes the benefits of using multiple proteases in studying cerebrospinal fluid. Finally, colleagues from the University of Washington share important insights comparing the use of high-end instrumentation versus lower-end instrumentation.

As a final thought, note that this issue is being published by Oxford Journals, a division of Oxford University Press. It is an exciting time for the journal and the change in publisher offers a unique opportunity to build on the previous foundation and successes as well as to consider new directions. The staff from Oxford Journals executed a seamless transition for this issue and I would like to congratulate them.

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