Almost three decades have elapsed since O’Farrell and Klose independently introduced high-resolution two-dimensional polyacrylamide gel electrophoresis (2D-PAGE)—often referred to as gel-based proteomics—as a core technology for analyzing the protein composition of cells, tissue, or bio fluids. Since then, many technological developments have taken place leading to improvements in the procedures for detecting, quantitating, comparing, characterizing, and storing the wealth of information generated by this method. In the early 1980s, the gel-based approach gained a new dimension with the advent of techniques to microsequence major proteins recovered from gels, and today, thanks to the development of state-of-the-art mass spectrometric techniques, it is possible to readily identify proteins that can be visualized with silver nitrate or fluorescent dyes.

The success of gel-based proteomics has relied on the fact that it provides a readily accessible, inexpensive tool for analyzing global patterns of protein expression under conditions in which all detected proteins can be studied qualitatively and quantitatively in relation to each other. There have been thousands of articles in the past 29 years documenting the usefulness of the technology and, in spite of its numerous limitations, it still plays a central role in proteomic studies, particularly in the analysis of tissue biopsy specimens.

In an effort to expedite the publication of articles that utilize gel-based proteomics, we thought it was timely to develop some guidelines as to what can be expected of such articles. First of all, it is crucial that the work in question focuses on well-defined biological questions. Second, the quality of the gel separation must be of a standard to warrant quantitative analysis of the resolved proteins, and, moreover, a significant number of samples must be analyzed to allow meaningful conclusions to be drawn, the latter being particularly important in those cases where samples from normal and pathological conditions are being compared. Significant efforts must be made to validate the results using complementary technologies such as immunofluorescence, immunohistochemistry, and antibody/protein arrays. Finally, simply presenting a list of proteins that are deregulated under a given condition without providing any new or significant biological insight will no longer be considered acceptable.

It is also becoming clear that the use of single-platform technologies may not be sufficient to deal with complex biological problems and new multiplatform integrated approaches will increasingly be required. Gel-based proteomics generates qualitative and quantitative protein behavioral data, and as such it provides a core technology to integrate information produced using various “omic” technologies. In this context, Molecular & Cellular Proteomics welcomes articles where several “omic” technologies are used to address the larger issues of systems biology. Such approaches are expected to lead to a better understanding of living cells and organisms and may shed some light as to the molecular mechanisms underlying diseases.

In the clinical area, we are steadily moving toward more precise and predictive, individualized approaches to disease treatment, which necessitates the combination of multiple parameters to subgroup patients and to derive predictions customized to the individual patient. In addition, more specific targets for therapeutic intervention will be needed, and their search will be greatly facilitated by using knowledge-based approaches. The identification and elucidation of signaling cascades and networks that are involved in the pathogenesis of diseases is a high-priority area where gel-based proteomics may play a very important role in the future. In addition, bioinformatic tools that facilitate the integration of large “omic” datasets are badly needed to make full use of the data.

Progress is achieved when a new technology is developed or when old technologies are improved. For this reason we also welcome technical notes that address any of the shortcomings of gel-based proteomics, such as articles dealing with improved detection, imaging, or quantitation. In selected cases, it may be desirable to publish large datasets recorded using gel-based proteomics, and in these cases we will consider publishing comprehensive databases that will be of interest and value to the scientific community at large.

We look forward to receiving your contribution!