

## Preface

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The successful deciphering of the genomic sequences of both prokaryotes and eukaryotes in recent years has spurred the development of new techniques to characterize the molecular determinants of life. The completion of genomic draft sequences ahead of schedule was made possible primarily by advances in capillary array electrophoresis. Capillary electrophoresis will continue to play an important role in the post-genome era that seeks an integrated view of biology at both the molecular and structural level. While the sequencing of whole genomes represents a tremendous challenge, the proteomes are characterized by even higher structural complexity and dynamics. Moreover, combination of genomic and proteomic data will be indispensable for making progress in answering clinically and biologically relevant questions.

Analytical technologies of utmost sensitivity, specificity, speed, and sample throughput are required to be able to investigate such complex biological systems. As attested to in many of the 29 contributions to this special issue of *Journal of Chromatography B*, high-performance liquid chromatography in combination with mass spectrometry will become most likely the dominant analytical tool in elucidat-

ing molecular information. The applicability of liquid chromatography-mass spectrometry both to nucleic acid and protein analysis offers the possibility to investigate genomes and proteomes on a single instrumental platform, which should further promote the bidirectional approach to biological analysis. Intended to give perspective on the current status of genomic and proteomic technologies and their contributions to life sciences, the overall field is immense, and the contents of this volume must be combined with much other literature to give a complete picture. Nevertheless, we hope that the volume will help in shaping new ideas for future developments necessary to understand the complex networks that sustain unicellular and multicellular organisms. In this spirit, we thank all colleagues who found despite other pressing commitments the time to contribute to this issue, which reflects the commitment of the editorial board to broaden the scope of *Journal of Chromatography B* beyond classical separation techniques.

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