Advances in our knowledge of the molecular basis of cancer are at the heart of the present revolution in clinical oncology. The identification of tumor-specific molecular alterations has led to new means of diagnosis and classification, and the characterization of critical pathways regulating tumor growth is providing the potential for less toxic, more effective targeted therapy. Nonetheless, these advances had previously occurred at an agonizingly slow pace, i.e., one gene at a time. That investigative pace has now been dramatically altered by the completion of a draft of the entire human genome and the development of miniaturized high-throughput technology for genetic analysis. These extraordinary accomplishments now permit not only the monitoring of every gene sequence in a single experiment, but also a comprehensive analysis of the complex coordinated programs and pathways that contribute to the clinical phenotype of cancers. This rapid and comprehensive approach to the investigation of tumor biology has the potential to dramatically shape the future of clinical oncology.

Expression Profiling of Human Tumors: Diagnostic and Research Applications is intended to provide an introduction and overview to comprehensive gene expression profiling of human tumors, one of the most promising new high-throughput investigative approaches in molecular biology. The intent was to provide not only a primer for the technology and analytical methods, but also an early assessment of the state-of-the-art with respect to both successes and pitfalls. These successes are significant and include methods of more precise diagnosis, and identification of prognostic markers, therapeutic targets, and gene expression patterns that predict therapeutic response. Nonetheless, there are significant challenges to further success, such as procurement and processing of appropriate samples, improvement and validation of technical approaches, and refinement of analytical methods for the resulting complex datasets. We have attempted to provide a balance between the basic science aspects of this work and its application to the clinical setting, but we have focused on the analysis of human tissue samples as providing the most direct means of translating findings to clinical practice. There are many complex issues that need to be considered as this type of work goes forward, and we hope this text will serve as a starting point for future discoveries.

The emphasis here on gene expression profiling is not intended to suggest that this should be considered the ultimate view of the molecular biology of the cancer cell. On the contrary, we all look forward to the day when analysis at the protein level is as comprehensive and provides as much detail as the present attempts of global gene transcript measurements. Obviously, the closer we come to assessment of the actual function of each molecule, the more accurate our abilities to correlate those with the clinical phenotype. Proteomics holds the promise to better achieve that goal, but is still in its
infancy, with even greater hurdles to overcome than we presently face with sequence-based expression analysis. We leave that topic for future publications.

We would like to express our deep appreciation to the many authors who have provided overviews of work in their fields. These individuals have contributed their time and effort to provide highly useful information for others (sometimes while being badgered by the Editors!). We would also like to thank Ms. Fabienne Volel and Ms. Shirley Tung for excellent assistance. Finally we thank our families for their patience and support.

Expression Profiling of Human Tumors: Diagnostic and Research Applications clearly depicts the rapid advances that are occurring in clinically important areas and that will no doubt increasingly impact clinical care. We sincerely hope that our book provides information useful to all basic or clinical investigators concerned with the molecular basis of cancer and the improvement of cancer care.

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