
Preface

Over the past 20 years, technological advances in molecular biology have proven invaluable to the understanding of the pathogenesis of human cancer. The application of molecular technology to the study of cancer has not only led to advances in tumor diagnosis, but has also provided markers for the assessment of prognosis and disease progression. The aim of *Molecular Analysis of Cancer* is to provide a comprehensive collection of the most up-to-date techniques for the detection of molecular changes in human cancer. Leading researchers in the field have contributed chapters detailing practical procedures for a wide range of state-of-the-art techniques.

Molecular Analysis of Cancer includes chapters describing techniques for the identification of chromosomal abnormalities and comprising: fluorescent *in situ* hybridization (FISH), spectral karyotyping (SKY), comparative genomic hybridization (CGH), and microsatellite analysis. FISH has a prominent role in the molecular analysis of cancer and can be used for the detection of numerical and structural chromosomal abnormalities. The recently described SKY, in which all human metaphase chromosomes are visualized in specific colors, allows for the definition of all chromosomal rearrangements and marker chromosomes in a tumor cell. Protocols for the detection of chromosomal rearrangements by PCR and RT-PCR are described, as well as the technique of DNA fingerprinting, a powerful tool for studying somatic genetic alterations in tumorigenesis. A number of approaches to identify mutations are detailed, and include SSCP, DGGE, the nonisotopic RNase cleavage assay, the protein truncation assay, and DNA sequencing. A change in DNA methylation status is commonly observed in cancer, and specific methodology for methylation analysis is also provided by this volume.

The analysis of gene expression represents a key area of research in the study of human cancer and a number of chapters in *Molecular Analysis of Cancer* address this subject. Global RNA expression analysis using microarray technology allows the identification of genes that are differentially expressed in tumor versus normal tissues. This is a powerful approach for identifying genes that are central to disease development or progression and can also identify new prognostic markers.

A reduction in telomere length, together with expression of the telomere maintenance enzyme, telomerase, has been described in a wide range of human cancers. To complete the volume, we include chapters describing the measurement of telomere length and telomerase levels, an area of extensive study in the field of cancer research.

We wish to thank the authors of the various chapters of *Molecular Analysis of Cancer* for their excellent contributions. Clearly, they share our hope that this volume will assist other researchers in the analysis and detection of genetic abnormalities occurring in human malignancy, and lead to a better understanding of the molecular pathogenesis of cancer.

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