Molecular Analysis of Cancer
64. Dendritic Cell Protocols, edited by Stephen P. Robinson and Andrew J. Stagg, 2001
50. Colorectal Cancer: Methods and Protocols, edited by Steven M. Powell, 2001
40. Diagnostic and Therapeutic Antibodies, edited by Andrew J. T. George and Catherine E. Urch, 2000
Molecular Analysis of Cancer

Edited by

Jacqueline Boultwood

and

Carrie Fidler

Leukaemia Research Fund Molecular Haematology Unit,
University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK
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.

*Jackie Boultwood  
Carrie Fidler*
Contributors

BINAIFER R. BALSARA • Human Genetics Program, Division of Population Sciences, Fox Chase Cancer Center, Philadelphia, PA

MICHAEL L. BITTNER • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

JACQUELINE BOULTWOOD • Leukaemia Research Fund Molecular Haematology Unit, University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK

DAVID BOWTELL • Research Division, Peter MacCallum Cancer Institute, Melbourne, Australia

DOMINIQUE BROCCOLI • Medical Sciences Division, Department of Medical Oncology, Fox Chase Cancer Center, Philadelphia, PA

MARTIN M. CORCORAN • Molecular Biology Laboratory, Royal Bournemouth Hospital, Bournemouth, UK

CARRIE FIDLER • Leukaemia Research Fund Molecular Haematology Unit at the University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK

YINENG FU • Department of Pathology, Beth Israel-Deaconess Medical Center and Harvard Medical School, Boston; and Department of Pathology, Ardais Corporation, Lexington, MA

ARTHUR A. GLATFELTER • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

ANDREW K. GODWIN • Medical Sciences Division, Department of Medical Oncology, Fox Chase Cancer Center, Philadelphia, PA

MARIANNA GOLDRICK • Ambion RNA Diagnostics, Austin, TX

GERALD C. GOODEN • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

KERSTEN GRØNBEK • Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, Denmark

PER GULDBERG • Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, Denmark

KERSTIN HESELMEYER-HADDAD • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD

EVA HILGENFELD • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD
Contributors

ANDREAS HOCHHAUS • III. Medizinische Universitätsklinik, Klinikum Mannheim der Universität Heidelberg, Mannheim, Germany
RACHEL E. IBBOTSON • Molecular Biology Laboratory, Royal Bournemouth Hospital, Bournemouth, UK
RINA J. JAJU • Leukaemia Research Fund Molecular Haematology Unit, University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK
YUAN JIANG • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD
YUNFANG JIANG • Laboratory of Lymphoma Biology, Department of Lymphoma and Myeloma, University of Texas MD Anderson Cancer Center, Houston, TX
LYNDAL KEARNEY • MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, Oxford, UK
JAVED KHAN • Oncogenomics Section, Pediatric Oncology Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD
CHUANG FONG KONG • Research Division, Peter MacCallum Cancer Institute, Melbourne, Australia
NICHOLAS R. LEMoine • Imperial Cancer Research Fund Oncology Unit, Imperial College School of Medicine, Hammersmith Hospital, London, UK
ARTHUR B. MCKIE • Imperial Cancer Research Fund Oncology Unit, Imperial College School of Medicine, Hammersmith Hospital, London, UK
L. JEFFREY MEDEIROS • Department of Hematopathology, University of Texas MD Anderson Cancer Center, Houston, TX
PAUL S. MELTZER • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD
KEN MILLS • Department of Haematology, University of Wales College of Medicine, Heath Park, Cardiff, Wales, UK
CRISTINA MONTAGNA • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD
KAZUMA OHYASHIKI • First Department of Internal Medicine, Tokyo Medical University, Tokyo, Japan
JUNKO H. OHYASHIKI • First Department of Internal Medicine, Tokyo Medical University, Tokyo, Japan and the Division of Virology, Medical Research Institute, Tokyo Medical and Dental University, Tokyo, Japan
HESED PADILLA-NASH • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD
JIANGMING PEI • Human Genetics Program, Division of Population Sciences, Fox Chase Cancer Center, Philadelphia, PA
JOHN T. PHELAN II • Rochester General Hospital, Rochester, NY
Contributors

JOSEF T. PRCHAL • Department of Medicine Hematology and Oncology, Baylor College of Medicine, Houston, TX

JAMES PRESCOTT • UroCor, Inc., Oklahoma City, OK

THOMAS RIED • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD

LAO H. SAAL • Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

ANDREAS H. SARRIS • Laboratory of Lymphoma Biology, Department of Lymphoma and Myeloma, University of Texas MD Anderson Cancer Center, Houston, TX

LUCY SIDE • Leukaemia Research Fund Molecular Haematology Unit at the University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK

VORAPAN SIRIVATANAUKSORN • Imperial Cancer Research Fund Oncology Unit, Imperial College School of Medicine, Hammersmith Hospital, London, UK

YONGYUT SIRIVATANAUKSORN • Department of Surgery, Anaesthetics and Intensive Care, Imperial College School of Medicine, Hammersmith Hospital, London, UK

LINDA STAPLETON • Genetics Department, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD

AMANDA STRICKSON • Leukaemia Research Fund Molecular Haematology Unit at the University of Oxford, NDCLS, John Radcliffe Hospital, Oxford, UK

PER THOR STRATEN • Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, Denmark

HARUO SUGIYAMA • Department of Clinical Laboratory Science, Osaka University Medical School, Yamada-Oka, Suita City

JOSEPH R. TESTA • Human Genetics Program, Division of Population Sciences, Fox Chase Cancer Center, Philadelphia, PA

SABRINA TOSI • MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, Oxford, UK

TOSHIKI UCHIDA • First Department of Internal Medicine, Nagoya University School of Medicine, Showa-ku, Nagoya, Japan

IGOR VORECHOVSKY • Department of Biosciences at NOVUM, Karolinska Institute, Huddinge, Sweden

JESPER WORM • Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, Denmark

JESPER ZEUTHEN • Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, Denmark