
Preface

Lymphomas are lymphoid malignancies derived from B or T lymphocytes. Although they are only listed around position 10–12 among the most frequent cancers in the Western world, their study has been and still is paradigmatic for many aspects of cancer research. The aim of this book is to present and discuss key methods that are used in lymphoma research. These methods are partly specific for lymphoma research, but many can be adopted to the study of other cancers. Several chapters describe assays based on the usage of the highly diverse B cell and T cell receptor gene rearrangements in B and T cell lymphomas, respectively. These somatic gene rearrangements are ideal clonal markers to study minimal residual disease and intraclonal tumor diversification. Moreover, chromosomal translocations involving the immunoglobulin or T cell receptor gene loci are frequent oncogenic events in many lymphomas, and the cloning of translocation breakpoint regions has led to the identification of numerous novel oncogenes. The study of deregulated mRNA and miRNA expression has revealed many novel insights into lymphoma pathogenesis and has led to the identification of disease subsets. Further topics include the analysis of epigenetic alterations, the search for viruses in lymphoma cells, the role of the B cell receptor in driving B cell lymphoma proliferation, and the usage of cell lines and mouse models in lymphoma research. By covering this broad variety of molecular studies of lymphomas, this book should be of interest not only for hematologists, hematopathologists, and immunologists but also for scientists interested in other fields of cancer research as well as human genetics.

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